OM protein - protein search, using sw model

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          GenCore version 5.1.4_p5_4578
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Run on: March 29, 2003, 09:06:24 ; Search time 21.3633 Seconds
                                      (without alignments)
                                   2141.995 Million cell updates/sec

Title: US-09-758-173-12
Perfect score: 2549
Sequence: 1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: . 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_73:*
            1: _pir1:*
            2: _pir2:*
            3: _pir3:*
            4: _pir4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1763	69.2	330	1	GHHU	Ig gamma-1 chain C
2	1626.5	63.8	377	2	A23511	Ig gamma-3 chain C
3	1624.5	63.7	377	2	A60764	Ig gamma-3 chain C
4	1600	62.8	326	1	G2HU	Ig gamma-2 chain C
5	1586.5	62.2	327	1	G4HU	Ig gamma-4 chain C
6	1567	61.5	470	2	S22080	Ig heavy chain pre
7	1548	60.7	472	2	S31459	Ig gamma-1 chain -
8	1547	60.7	374	2	S69339	Ig heavy chain V r
9	1426.5	56.0	469	2	S37483	Ig gamma-2a chain
10	1392	54.6	446	2	S40295	Ig gamma-2a chain
11	1382.5	54.2	444	2	PC4436	monoclonal antibod
12	1369.5	53.7	475	2	S01321	Ig gamma-2b chain
13	1362	53.4	474	1	G2MS11	Ig gamma-2b chain
14	1259	49.4	328	2	I47159	Ig gamma-2a chain
15	1256	49.3	255	4	S31866	Ig gamma-1 chain C
16	1253	49.2	328	2	I47160	Ig gamma-2b chain
17	1250	49.0	234	2	PT0207	Ig gamma chain C r
18	1227	48.1	328	2	I4715B	Ig gamma 1 chain c
19	1226.5	48.1	323	1	GHRB	Ig gamma chain C r
20	1223	48.0	328	2	I47161	Ig gamma 3 chain c
21	1212.5	47.6	329	1	G2GP	Ig gamma-2 chain C
22	1157.5	45.4	308	2	C30554	Ig heavy chain C r
23	1152	45.2	289	1	G3HUWI	Ig gamma-3 heavy
24	1148	45.0	326	2	PS0017	Ig gamma-1 chain C
25	1142.5	44.8	333	2	PS0018	Ig gamma-2b chain
26	1138	44.6	324	1	G1MS	Ig gamma-1 chain C
27	1137	44.6	329	1	G3MSC	Ig gamma-3 chain C
28	1133	44.4	393	1	G1MSM	Ig gamma-1 chain C
29	1126	44.2	398	1	G3MSM	Ig gamma-3 chain C
30	1122	44.0	330	1	G2MSA	Ig gamma-2a chain
31	1119.5	43.9	335	1	G2MSAB	Ig gamma-2a chain
32	1117	43.8	399	1	G2MSAM	Ig gamma-2a chain
33	1114.5	43.7	329	2	S00847	Ig gamma-2c chain
34	1108	43.5	322	2	PS0019	Ig gamma-2a chain
35	1088.5	42.7	327	2	S06611	Ig gamma-2 chain C
36	1080	42.4	405	1	G2MSBM	Ig gamma-2b chain
37	1062	41.7	277	2	147162	Ig gamma 4 chain C
38	944	37.0	548	2	S38864	Ig epsilon chain C
39	907	35.6	220	2	A49444	Ig gamma-1 heavy c
40	827	32.4	592	2	S25705	Ig mu chain - shee
41	793.5	31.1	549	2	S04845	Ig heavy chain pre
42	757.5	29.7	572	2	B46529	Ig Y heavy chain (
43	755.5	29.6	249	2	S69340	Ig heavy chain VHI
44	727.5	28.5	241	2	S69131	Ig heavy chain (DO
45	722	28.3	627	2	S14683	Ig mu chain precur

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36867; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the Gim(17) allotypic marker, 97-Lys, and the Glm(1) marker
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the Gim(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',
A;Note: this sequence has the Gim(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni
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igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'R',98-115,'Q',117-197,'D',199-238,'E',27
A;Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOl
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the Glm(3) and Glm(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
C;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;112/Disulfide bonds: interchain (to heavy chain) (covalent) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

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Query Match       69.2%; Score 1763; DB 1; Length 330;
Best Local Similarity 99.7%; Pred. No. 3.1e-94;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 120

Qy  267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy  327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy  387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy  447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||||||||||||||||||||||||||||||
Db  301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 2

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

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Query Match       63.8%; Score 1626.5; DB 2; Length 377;
Best Local Similarity 81.7%; Pred. No. 2.4e-86;
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
         |||||||||||||:|||::|||||||||||||||||||||||||||||||||||||||||
Db    1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA----------------------- 244
         ||||||||||||||||||||||||||||||||||||||
Db   61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVELKTPLGDTHTCPRCPEPKSC 120

Qy  245 --------------------EPKSCDKTHTCPPCPAPELLGGPSVLFPPKPKDT 279
                             |||||||||||||||||||:||||||||||||
Db  121 DTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVLFPPKPKDT 180

Qy  280 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 339
         ||||||||||||||||||||:|||||||||||||||||||||:||||||||||||||||
Db  181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy  340 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399
         |||||||||||||||||||||||||||:||||||||||||:||||:|||||||||||||
Db  241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPFSREEMTKNQVSLTCLVK 300

Qy  400 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 459
         |||||||||||||:||||||| ||:::||||||||||||||||||||:::|||:||||
Db  301 GFYPSDIAVEWESSQPENNVNTTPMLDSDGSFFLYSKLTVDKSRWQQQNIFSCSVMHE 360

Qy  460 ALHNHYTQKSLSLSPGK 476
         ||||:||||||||||||
Db  361 ALHNRFTQKSLSLSPGK 377
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RESULT 3

A60764

Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

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Query Match
Best Local Similarity   63.7%;   Score 1624.5;   DB 2;   Length 377;
                        81.7%;   Pred. No. 3.2e-86;
Matches  308;   Conservative  10;   Mismatches  12;   Indels  47;   Gaps  1;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
         ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA---------------------- 244
         |||||||||||||||||||||||||||||||||||||:
Db    61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy   245 ----------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 279
                         |||||||||||||||||||||||||||||
Db   121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy   280 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 339
         ||||||||||||||||||||||| |:||||||||||||||||||||||| |||||||||
Db   181 LMISRTPEVTCVVVDVSHEDPEVQFKNYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy   340 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399
         |||||||||||||||| ||||||||||| |||||||||||||||: :||||||||||||
Db   241 QDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy   400 GFYPSDIAVEWESSNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 459
         ||||||||||||| |||||| ||||||||||||||||| |||||||||| |||||||||
Db   301 GFYPSDIAVEWESSGGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360

Qy   460 ALHNHYTQKSLSLSPGK 476
         ||||  |||||||||||
Db   361 ALHNRFTQKSLSLSPGK 377
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RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85,132-171,'ZZZ',175,'Q',177-193,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132

A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amida
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:6961124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.3-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;113-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match
Best Local Similarity   62.8%;   Score 1600;   DB 1;   Length 326;
                        90.9%;   Pred. No. 6.8e-85;
Matches  300;   Conservative  12;   Mismatches  14;   Indels  4;   Gaps  2;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
         ||||||||||||  |:|||: |||||||||||||||||||||||||||||||||||||||
Db     1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
         |||||||||||||:  |||||:|||:||||||||||:   |:---CPCPAPP-VAG 116
Db    61 GLYSLSSVVTVPSSNFGTQTYCNVDHKPSNTKVDKTVERKCCVE---CPCPAPP-VAG 116

Qy   267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
         ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||| 
Db   117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy   327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
         ||:|||||||| :|||||||||||||||| |||||||||| |||||||||||||||:||
Db   177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy   387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
          |:|||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRW 296

Qy   447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||||||||||||||||||||||||||||||
Db   297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
```

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30,81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1, 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   62.2%;   Score 1586.5; DB 1; Length 327;
Best Local Similarity 90.6%;   Pred. No. 4.1e-84;
Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

Qy 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
        |||||||||||||| :|||||||||||||||||||||||||||||||||||||||||||
Db   1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
        ||||||||||||||||||||||||||||||||||||||||| :
Db   61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117

Qy 267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
        ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db 118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy 327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
        ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||::|
Db 178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
        :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy 447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        :|||||||||||||||||||||||||||||
Db 298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327

RESULT 6
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1, 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   61.5%;   Score 1567; DB 2; Length 470;
Best Local Similarity 63.7%;   Pred. No. 8.1e-83;
Matches 305; Conservative 56; Mismatches 106; Indels 12; Gaps 8;

Qy   1 MKGHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
        |||| ||| :||||| :|||||||||||||||||||||||| :|||||||||||||||||
Db   1 MNPLWTLLFLVLSAPIGVLSQVQRESGPSLVKPSQTLSLTCTVSGFSLS-SYALTWRQA 59

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
        ||||:||| ::||: :| ||||||:|: |||||:|||||::|||:||:|:||||||| |
Db   60 PGKALEWVGGI-TSGGTTYYNPALKSRLSITKENSKQVSLSVSSVTPEDTATYYCAR-- 116

Qy 121 LFSVVGMVYNNWF-DVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
        : | || :   :||| |||||||||||||||||||||||||:|||||||||||||||
Db 117 --STYGEVGDGAIADAWGQGLLVTVSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYM 174

Qy 180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
        ||||:|||||||| |||||||||||||||||||:||||||:||| - :||:|||||||||
Db 175 PEPVTVTWNSGALKSGVHTFPAVLQSSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTK 233

Qy 240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
        ||||| || || | | |||: ||||||||||||||||||||||||||||||||| |
Db 234 VDKAVDP-TC-KPSPCDCCPPPELPGGPSVFIFPPKPKDTLTIISGTPEVTCVVVDVGHDD 291

Qy 300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
        |||||| ||||||||| :||||||||||||||||||| |||:|||||||| ||||| ||
Db 292 PEVKFSWFVDVDVEVNTATTKPREEQFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPA 351

Qy 360 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--E 417
        |||||||||||| |||||||||||: ::||||||||||||||||||||||||||||| :
Db 352 PIVRTISRTKGPAREPQVVLAPPQEELSKSTVSLLTCMVTSFYPDYIAVEWQRNGQPESE 411

Qy 418 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSLPGK 476
        |||:|||||||||| :||||||:|||||| ::||||||||||||||||||||||||| |
Db 412 DKYGTTPPQLDADSSYFLYSKLRVDRNSWQEGDTYTCVVMHEALHNHYTQKSTSKSAGK 470

RESULT 7
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

Query Match   60.7%;   Score 1548; DB 2; Length 472;

Best Local Similarity 61.9%; Pred. No. 1e-81;
Matches 297; Conservative 63; Mismatches 104; Indels 16; Gaps 6;

```
Qy    4 LWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGK 63
          ||::||||::|:||:||||||||:|||||||||:||||||||||||:|||
Db    2 LWTLLFVLSAPRGVLSQVRLQESGPGLATLLQTLSVTCTISGFSLN-NYGVDWVRQAPGK 60

Qy   64 GLEWIGSFYSSSGNTY-----YNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVR 118
          |||::  ::   : |||||||||||:||||||:|||
Db   61 ALEWLG------GSGYDEDIDYNPVLKSRLSTTKDTSKSQVSLTLSVTTEDTAVYYCAR 114

Qy  119 DRLFSSVGMYVNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 178
          ||||||||||||||||||||||||||:|||||||||||||||||||||||
Db  115 VDYDSSHAFAYAS-YDFWGPGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSY 173

Qy  179 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 238
          |||||||||||||:||||||||||||||||||||||:||||||||:|  :
Db  174 MPEPVTVTWNSGALTSGVHTFPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASST 233

Qy  239 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 298
          |||| |:| ||:: ::|  |:  ||||||||||||||||||||||||||||||:
Db  234 KVDKRVEPGCPDPCKHC-RCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQD 292

Qy  299 DPEVKFNWYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
          |||| |||| | |  |:||||||||||||||:||| :||||:|||||:||||
Db  293 DPEVQFSWFVDNVEVRTARTKPREEQYNSTFRVVSALPIQHQDWTGKEFKCKVHNEALP 352

Qy  359 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-- 416
          |||:||  |||||||||||||||||||||||||||||:||||| :||||||:||
Db  353 APIVRTISRTKGQARPQVVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPES 412

Qy  417 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db  413 EDKYGTTTSQLDADGSYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK 472
```

RESULT 8
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 60.7%; Score 1547; DB 2; Length 374;
Best Local Similarity 64.5%; Pred. No. 8.8e-82;
Matches 303; Conservative 23; Mismatches 40; Indels 104; Gaps 4;

```
Qy    8 LLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSIS-GGYGWGWIRQPPGKGLE 66
          ||||   :|||||| : :||||  :|| : :|:||  |  :|  :|:|||||||| |||
Db    8 LLLLTIPSWVLSQITLKESGPTIVKPTQTLTLTCTFSGFSLSKSGVGVGWIRQPPGQALE 67

Qy   67 WIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVG 126
          |:  :|  : |:||||:: |:|||:||||||:.  : : |||:|:|||:|:
Db   68 WLALIFWDD-DKRYSPSLRTRLTITTKDTSKNQVVLTMTNVDPADTATYYCG---YSVEG 122
```

Qy 127 MVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 186
Db 123 YGQGYRFHSWGQGTLVTVSS--- 142

Qy 187 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP 246
Db 143 --EP 144

Qy 247 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 306
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 145 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 204

Qy 307 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 205 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 264

Qy 367 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 426
          |||||||||||||||||:| :|||||||||||||||||||||||||||||||||||||||
Db 265 KAKGQPREPQVYTLPPSREEMKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 324

Qy 427 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 325 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374

RESULT 9
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 56.0%; Score 1426.5; DB 2; Length 469;
Best Local Similarity 57.2%; Pred. No. 9.3e-75;
Matches 271; Conservative 71; Mismatches 121; Indels 11; Gaps 6;

```
Qy    5 WFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKG 64
          |:|||| |  |||  ||||:|||:||||| |:.::| ||  |:|  :| |||:|:|:|:
Db    5 WIFLFLLSGTAGVHCQIQLQQSGPELVKPGASVKISCKASGYTFT-DYINWVKQKPGQG 63

Qy   65 LEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSV 124
          |:|||  :  :||||  |  |:| |:||:|:: :  |:||:|:||||||:|||:::
Db   64 LKWIGWIYPASGNTKYNENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCAR-----A 118

Qy  125 VGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 184
          :| : :||  |:|:|:|:|||||:||:|||:||||   | | ::|:||||||| :||||||
Db  119 MGAT-ATLLDYWGQGTTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVT 177

Qy  185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA 244
          ::|||| ||:||||||||||| |||||||:|||:|||:|||  :|:.| | |:|||||||
Db  178 LTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKI 236

Qy  245 EPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 302
          ||     | |||  |||||:|||||||||:||||:|||:|::| :|||||||||:::||:|
Db  237 EPRG-PTIKPCPPCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDV 295

Qy  303 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 362
          :.:|:|:|||| :| | :|:|:|||| |||||||:|:|||::|||:||||:||| ||||||
Db  296 QISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIE 355

Qy  363 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 422
          |:|| ||||||||||||||||:| ||||||||||||||||||||||||||||||||||||
Db ...
```

```
Db    356 RTISKPKGSVRAPQVVVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN 415

Qy    423 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
              :|||||||||  : :  :|||::||  |||||||  | :|||
Db    416 TEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 469


RESULT 10
S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 16-Jul-1999
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match    54.6%;   Score 1392;   DB 2;   Length 446;
Best Local Similarity   57.6%;   Pred. No. 8.4e-73;
Matches  264;   Conservative  68;   Mismatches 112;   Indels  14;   Gaps  5;

Qy    20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY 79
            ::|||| ||||:||:|||||||||||  :||||||||||||| |||:::| |:::: |
Db     1 QIQLQQSGPELVRPGASVKISCKASGYTFT-DYYIHVKQRGEGLEWIGWIYPGSGNTK 59

Qy    80 YNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWFDVWGPG 139
            |||||||||||| | ||||||||||| |||:::|||||| |: ::   :   |:|| ||
Db    60 YNEKFPKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAM-------DYWGQG 110

Qy   140 VLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 199
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111 TSVTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTF 170

Qy   200 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP-- 257
            ||||||| ||||||||||||| ||| |:|:||||||||||||||:::  ::::||: |
Db   171 PAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCK 228

Qy   258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317
            |||| ||||||||||||||||||||||  |||||||||| ||| ||:| :: |::|
Db   229 CPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQ 288

Qy   318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377
            |||||:::| ::| | |   ::: :|| |:||||::|| |:::|||  |:|||||: |||
Db   289 TQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQV 348

Qy   378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437
            | ||||||||||||||||||||||||||||||||||||:||:|||||||||||||:|||
Db   349 YVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS 408

Qy   438 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
            ||||||| ||:::   :|||  |||||  || | |||
Db   409 KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 446
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```
Db    356 RTISKPKGSVRAPQVVVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN 415


RESULT 11
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ag
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;251-320/Domain: immunoglobulin C region; immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

Query Match    54.2%;   Score 1382.5;   DB 2;   Length 444;
Best Local Similarity   56.5%;   Pred. No. 2.9e-72;
Matches  262;   Conservative  68;   Mismatches 107;   Indels  27;   Gaps  8;

Qy    20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGN-- 77
            |:|| |||||:|:|| || :|:| ::|:||||  |:|::| ||:| |||: ::||:|
Db     1 EVQXVETGGGLVRPGNSLKLSCLTSGFTFS-NYRMHWLRQPPGKRLEWIAVITVKSDNYG 59

Qy    78 TYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNW----FD 134
            |: :|::|  |||: ::   :|||  : ::::|  :  ||  :|:       :|
Db    60 AKYAESVRGRFTISRDDSKSSVYLQMNRLRBEDTATYYCCR---------TPWVYAMD 108

Qy   135 VWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 194
            |||  ||||||||||||||||||||||  |||||||||||||||||||||||| :||
Db   109 CWGQGTSVIVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSS 168

Qy   195 GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHT 254
            ||||||||| | ||||||||||| :|: |||  | ||| :  :::|:  ||:| |
Db   169 GVHTFPAVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG---- 223

Qy   255 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 312
            | |  |||| ||||||||||||||| :|:|  :  :|:||||||| |||:  :|: ||
Db   224 CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE 280

Qy   313 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 372
            | :|   | | |  ||  |:|     ::: :: :: ::| :|   |||:|| |:::| :
Db   281 VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRP 340

Qy   373 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 432
            ::  ||  ||||||||||||||||||||||||| ||||||||:||:||:||||||||||
Db   341 KAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 400

Qy   433 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            :||||||:||||| ||:::  :|||  |||||  || | |||
Db   401 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444


RESULT 12
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780, g51781; PIDN:CAA31580.1; PID:g51780, g51781
A;Note: this sequence was determined from the differentiated gene
```

C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>

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Query Match     53.7%;   Score 1369.5;   DB 2;   Length 475;
Best Local Similarity   54.5%;   Pred. No. 1.8e-71;
Matches 263;  Conservative 77;  Mismatches 128;  Indels 15;  Gaps 6;

Qy    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
          |:.||||||||| ||||:||||||||||||||||||:.|:.|:::
Db    1 MEWIWIFLLSGTAGVQSQVQLQQSGAELARPGASVKLSCKASGYTLT-SYGISWVKQR 59

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
         :|||||||| |.||.::|||||:::.||.:.|:.||.::::::|:|
Db   60 TGQGLEWIGEIYPGSGNYFNEKFKGKATLTVDKSSSTAYLHISSLTSEDSAVYFCAGPR 119

Qy  121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
         ||.|:.|:::|||||||||||||:::.|||||||||||||||
Db  120 ---QVGLLP---FGYWQOGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFP 173

Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
         |.|||.|||.||.::||||||||.||||.:.||||.|||| :|.|.:.||.|.||||.|||
Db  174 ESVTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTV 232

Qy  241 DKKAEPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 293
         |||.||.:|.||  |||||     ||||.|.||||||.|||:.||.|||||.|.||||||
Db  233 DKKLEPSGPTSTINPCPPCKECHKCCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVV 292

Qy  294 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 353
         |||.:|.:|:.|:|.|.||.::|.||..::|||:||.||||||.|.|:|||||.|.|||.:.|
Db  293 DVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVN 352

Qy  354 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 413
         ||.||||||:|||||.|| ..||||.|.|.:.||.:||||||||.|.|:.|||.||||.||
Db  353 NKDLPAPIERTISKIKGVIRAPQVYILSPPEQLSRKDVSLTCLAVGFSPEDISVEWTSN 412

Qy  414 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
         |..|.|||.|.|||||||||:|||||||..||:.:|:||||.|.|||||.:|||||||:|:|
Db  413 GHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYTLKKTISRS 472

Qy  474 PGK 476
        |||
Db  473 PGK 475
```

RESULT 13
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 01-Dec-2000
C;Accession: S25057; A02157; A02157; A26235; A26235; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: EMBL:X67210; A26235; A26233; A26233; PIDN:CAA47649.1; PIDN:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
A;Reference number: A02157; MUID:80120716; PMID:6776534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.

Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gar
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takaha
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglc
F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicced
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match     53.4%;   Score 1362;   DB 1;   Length 474;
Best Local Similarity   53.7%;   Pred. No. 4.7e-71;
Matches 260;  Conservative 75;  Mismatches 131;  Indels 18;  Gaps 5;

Qy    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
         |:.||:||:||:|||||::|||||||.|:|||.|:|:.|||.||| |:::.|:||||
Db    1 MEWSWIFLFLLSGTAGVHSEVQLQQSGPELVNPGASVKMSCKASGYTFI-TYVMHWVKQk 59

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
         ||:|||||| |.|.::|.|::|||||||.|:..||.|:.:::||:.||.|||||||||.||-
Db   60 PGQGLEWIGYINPNKDGTKFNEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARD- 118

Qy  121 LFSVVGMVYN-NWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
         :|.:.|.:::::.|||||:|:|||||||.|||:|:||||||||
Db  119 Y------YDYDWFAYWGQGTLVTVSAAKTTPPSVYPLAPGCGDTTGSSVTSGCLVKGYF 170

Qy  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
         |.|.|||:||||:||:.||.||:||||.|.:.||||.|||| :|.|.:.||.|.|||||:|
Db  171 PESVTVTWNSGSLSSSVHTLSQALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTT 230

Qy  240 VDKKAEPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 292
         |||.||.:|.||  ||||||     ||||.|.||||||.|||:.||.|||||.|.|||||
Db  231 VDKKLEPSGPISTINPCPPCKECHKCCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVV 290

Qy  293 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 352
         |||.:|.:|:.|:|.|.||.::|.||..::|||:||.||||||.|.|:|||||.|.|||
Db  293 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 352
```

```
Db  291 VDVSEDDDPVQISWFVNNVEVHATQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKV 350
        ||||.|||:.||.: .||| ||||  :|.|. :||||:||||:||||
Qy  353 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 412
Db  351 NNKDLPSPIERTISKIKGLVRAPQVYILPPAEQLSRKDVSLTCLVGFNPGDISVEWTS 410
Qy  413 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNYTQKSLSL 472
Db  411 NGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISR 470

Qy  473 SPGK 476
Db  471 SPGK 474
```

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a ...
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
F;133-202/Domain: immunoglobulin homology <IMM>

```
Query Match      49.4%;  Score 1259;  DB 2;  Length 328;
Best Local Similarity  69.3%;  Pred. No. 2.5e-65;
Matches 230;  Conservative 43;  Mismatches 53;  Indels 6;  Gaps 2;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
        |.||.||||.|||.|..|||....|||.....|||||||||.|||||.|||||||.||.|
Db    1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVLQPS 60
Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
        ||||||.:|||..|.|...||.||||...:.||||:|....|.:||:||:|.|||:.||
Db   61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116
Qy  267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
        ||||:||||||||||||||||.||||||||.|:|||:||||||||||||.||.||:||:|:
Db  117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176
Qy  327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
        |||||||||.:.|||||||||.||||.||.|||||....||||||.:|||||||||...:
Db  177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236
Qy  387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
        |::..||:||||:|||||||.||.:||:|  ||.||:||||. .||.||.|||||.||||.
Db  237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296
Qy  445 RWQQGNVFSCSVMHEALHNYTQKSLSLSPGK 476
        .|||||.|.|:|||||||||:||||:..|||
Db  297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
```

RESULT 15
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

A;Description: Screening method for protein-protein interactions of cloned gene produc

```
Query Match      49.3%;  Score 1256;  DB 4;  Length 255;
Best Local Similarity  97.1%;  Pred. No. 2.8e-65;
Matches 232;  Conservative 0;  Mismatches 7;  Indels 0;  Gaps 0;

Qy  238 TKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 297
        |.  .  |.|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76
Qy  298 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 357
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136
Qy  358 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 417
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196
Qy  418 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  197 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255
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Search completed: March 29, 2003, 09:16:21
Job time : 22.3633 secs

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                    GenCore version 5.1.4_p5_4578
            Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:      March 29, 2003, 09:06:23 ; Search time 11.3492 Seconds
                                         (without alignments)
                                         1739.566 Million cell updates/sec

Title:          US-09-758-173-12
Perfect score:  2549
Sequence:       1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:        112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_40:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1763	69.2	330	1	GC1_HUMAN	P01857 homo sapien
2	1600	62.8	326	1	GC2_HUMAN	P01859 homo sapien
3	1586.5	62.2	327	1	GC4_HUMAN	P01861 homo sapien
4	1226.5	48.1	323	1	GC_RABIT	P01870 oryctolagus
5	1212.5	47.6	329	1	GC2_CAVPO	P01862 cavia porce
6	1157	45.4	290	1	GC3_HUMAN	P01860 homo sapien
7	1148	45.0	326	1	GC1_RAT	P20759 rattus norv
8	1142.5	44.8	333	1	GCB_RAT	P20761 rattus norv
9	1138	44.6	324	1	GC1_MOUSE	P01868 mus musculu
10	1137	44.6	329	1	GC3_MOUSE	P22436 mus musculu
11	1133	44.4	393	1	GC1M_MOUSE	P01869 mus musculu
12	1126	44.2	398	1	GC3M_MOUSE	P03987 mus musculu
13	1122	44.0	330	1	GCAA_MOUSE	P01863 mus musculu
14	1119.5	43.9	335	1	GCAB_MOUSE	P01864 mus musculu
15	1117	43.8	399	1	GCAM_MOUSE	P01865 mus musculu
16	1114.5	43.7	329	1	GCC_RAT	P20762 rattus norv
17	1108	43.5	322	1	GCA_RAT	P20760 rattus norv
18	1085	42.6	336	1	GCB_MOUSE	P01866 mus musculu
19	1080	42.4	405	1	GCBM_MOUSE	P01867 mus musculu
20	489	19.2	428	1	EPC_HUMAN	P01854 homo sapien
21	483.5	19.0	429	1	EPC_RAT	P01855 rattus norv
22	465	18.2	421	1	EPC_MOUSE	P06336 mus musculu
23	458	18.0	146	1	HV2I_HUMAN	P06331 homo sapien
24	442	17.3	454	1	MUC_HUMAN	P01871 homo sapien
25	437	17.1	458	1	MUC_RABIT	P03988 oryctolagus
26	432.5	17.0	455	1	MUC_MOUSE	P01872 mus musculu
27	427	16.8	479	1	MUCM_RABIT	P04221 oryctolagus
28	425	16.7	457	1	MUC_SUNMU	P20768 suncus muri
29	422.5	16.6	476	1	MUCM_MOUSE	P01873 mus musculu
30	420	16.5	129	1	HV2F_HUMAN	P01824 homo sapien
31	420	16.5	450	1	MUC_CANFA	P01874 canis famil
32	415.5	16.3	454	1	MUC_MESAU	P06337 mesocricetu
33	403	15.8	391	1	MUCB_HUMAN	P04220 homo sapien

```
                              ALIGNMENTS
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34	396.5	15.6	137	1	HV46_MOUSE	P01822	mus musculu
35	395.5	15.5	438	1	HVC2_HETFR	P23085	heterodontu
36	394	15.5	438	1	HVCS_HETFR	P23087	heterodontu
37	385	15.1	461	1	HVCM_HETFR	P23088	heterodontu
38	384	15.1	370	1	HVC1_HETFR	P23084	heterodontu
39	383.5	15.0	353	1	ALC1_HUMAN	P01876	homo sapien
40	380.5	14.9	353	1	ALC1_GORGO	P20758	gorilla gor
41	379	14.9	340	1	ALC2_HUMAN	P01877	homo sapien
42	368	14.4	116	1	HV60_MOUSE	P18531	mus musculu
43	366.5	14.4	393	1	HVC3_HETFR	P23086	heterodontu
44	362	14.2	117	1	HV2G_HUMAN	P01825	homo sapien
45	361	14.2	116	1	HV61_MOUSE	P18532	mus musculu

```
RESULT 1
GC1_HUMAN
ID   GC1_HUMAN      STANDARD;     PRT;   330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
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RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981)
CC   -!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC       G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC       MARKER & THE G1M (NON-1) MARKERS.
CC   -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC       35,116,198,269 & 272.
CC   -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC       155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC       268-272.
CC   -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC       RESIDUES 198,267&272.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A02146; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100;
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-LINKED (GLCNAC...).
FT   MOD_RES     330    330       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (IN G1M(NON-1) MARKER).
FT                                /FTId=VAR_003888.
FT   STRAND      123    126
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FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    148
FT   STRAND      158    162
FT   TURN        163    164
FT   STRAND      165    166
FT   STRAND      175    178
FT   STRAND      183    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    206
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    240
FT   TURN        241    242
FT   STRAND      245    256
FT   STRAND      260    266
FT   TURN        267    268
FT   STRAND      269    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      306    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    324
SQ   SEQUENCE   330 AA;  36106 MW;  3770EB106C2FA33D CRC64;
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Query Match             69.2%;  Score 1763;  DB 1;  Length 330;
Best Local Similarity   99.7%;  Pred. No. 1.8e-113;
Matches   329;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy   147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS   60

Qy   207  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG  266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG  120

Qy   267  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  180

Qy   327  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE  386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE  240

Qy   387  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  300

Qy   447  QQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
          |||||||||||||||||||||||||||||||
Db   301  QQGNVFSCSVMHEALHNHYTQKSLSLSPGK  330
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RESULT 2
GC2_HUMAN
ID   GC2_HUMAN     STANDARD;      PRT;    326 AA.
AC   P01859;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-2 chain C region.
GN   IGHG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-326 FROM N.A.
RX   MEDLINE=82197621; PubMed=6804948;
RA   Ellison J.W., Hood L.E.;
RT   "Linkage and sequence homology of two human immunoglobulin gamma
RT   heavy chain constant region genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN   [2]
RP   SEQUENCE OF 88-115 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=83001943; PubMed=6811139;
RA   Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT   "Structure of human immunoglobulin gamma genes: implications for
RT   evolution of a gene family.";
RL   Cell 29:671-679(1982).
RN   [3]
RP   SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=84235992; PubMed=6329676;
RA   Krawinkel U., Rabbitts T.H.;
RT   "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT   genes.";
RL   EMBO J. 1:403-407(1982).
RN   [4]
RP   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX   MEDLINE=81007873; PubMed=6774012;
RA   Wang A.-C., Tung E., Fudenberg H.H.;
RT   "The primary structure of a human IgG2 heavy chain: genetic,
RT   evolutionary, and functional implications.";
RL   J. Immunol. 125:1048-1054(1980).
RN   [5]
RP   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX   MEDLINE=80001357; PubMed=113060;
RA   Connell G.E., Parr D.M., Hofmann T.;
RT   "The amino acid sequences of the three heavy chain constant region
RT   domains of a human IgG2 myeloma protein.";
RL   Can. J. Biochem. 57:758-767(1979).
RN   [6]
RP   SEQUENCE OF 238-275 (ZIE).
RX   MEDLINE=80114419; PubMed=118920;
RA   Hofmann T., Parr D.M.;
RT   "A note of the amino acid sequence of residues 381-391 of human
RT   immunoglobulins gamma chains.";
RL   Mol. Immunol. 16:923-925(1979).
RN   [7]
RP   REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA   Hofmann T., Parr D.M.;
RL   Submitted (MAR-1980) to the PIR data bank.
RN   [8]
RP   SEQUENCE OF 1-121 (DOT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=72033500; PubMed=4940472;
RA   Milstein C., Frangione B.;
RT   "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL   Biochem. J. 121:217-225(1971).
RN   [10]
RP   DISULFIDE BONDS.
RX   MEDLINE=69064124; PubMed=5782707;
RA   Frangione B., Milstein C., Pink J.R.L.;
RT   "Structural studies of immunoglobulin G.";
RL   Nature 221:145-148(1969).
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CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   --------------------------------------------------------------------------
DR   EMBL; J00230; AAB59393.1; -.
DR   PIR; A02148; G2HU.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5526; IGHG2.
DR   MIM; 147110; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    219       CH2.
FT   DOMAIN      220    326       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    102    102       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    103    103       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    140    200
FT   DISULFID    246    304
FT   SITE        156    156       AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT   MOD_RES     326    326       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT      60     60       S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT                                /FTId=VAR_003889.
FT   CONFLICT    109    109       C -> S (IN REF. 3).
SQ   SEQUENCE   326 AA;  35884 MW;  8310878C6878CF9C CRC64;

Query Match             62.8%;  Score 1600;  DB 1;  Length 326;
Best Local Similarity   90.9%;  Pred. No. 2.4e-102;
Matches  300;  Conservative   12;  Mismatches   14;  Indels    4;  Gaps    2;

Qy    147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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Db      1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy    207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
          ||||||||||||||  .||||||||:|||||||||||.:  || .    CPPCPAPP VAG
Db     61 GLYSLSSVVTVPSSNFGTQTYICNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy    267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
          ||||||||||||||||||||||||||||||||||||.|||||||||||||||||||||:|
Db    117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy    327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVVTLPPSRDE 386
          ||:||||||||:|||||||||||||||||.|||||||||||.|||||||||||||||| :
Db    177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVVTLPPSREE 236

Qy    387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
          :|||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db    237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy    447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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Db    297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326

RESULT 3
GC4_HUMAN
ID   GC4_HUMAN    STANDARD;    PRT;    327 AA.
AC   P01861;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
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Db  178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
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Qy  387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
        :|||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db  238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy  447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        |:|||||||||||||||||||||||||:||
Db  298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
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RESULT 4
GC_RABIT
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ID   GC_RABIT     STANDARD;      PRT;    323 AA.
AC   P01870;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma chain C region.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84030930; PubMed=6313520;
RA   Bernstein K.E., Alexander C.B., Mage R.G.;
RT   "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT   F-I haplotype.";
RL   Immunogenetics 18:387-397(1983).
RN   [2]
RP   SEQUENCE OF 1-128.
RX   MEDLINE=76135469; PubMed=1243651;
RA   Pratt D.M., Mole L.E.;
RT   "Sequence studies on the constant region of the Fd sections of rabbit
RT   immunoglobulin G of different allotype.";
RL   Biochem. J. 151:337-349(1975).
RN   [3]
RP   SEQUENCE OF 88-266 FROM N.A.
RX   MEDLINE=83299917; PubMed=6193512;
RA   Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT   "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT   heavy chain and identification of two genomic C gamma genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN   [4]
RP   SEQUENCE OF 132-161.
RX   MEDLINE=70110015; PubMed=5461106;
RA   Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT   "Sequence studies of the Fd section of the heavy chain of rabbit
RT   immunoglobulin G.";
RL   Biochem. J. 116:249-259(1970).
RN   [5]
RP   SEQUENCE OF 129-131 AND 155-322.
RA   Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL   (In) Killander J. (eds.);
RL   Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL   Stockholm (1967).
CC   -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC       104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC       MARKERS AND REF.5 THE E15 MARKER.
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DR   EMBL; M16426; AAA31289.1; -.
DR   PIR; A02161; GHRB.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR003006; Ig_MHC.
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DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-4 chain C region.
GN   IGHG4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RX   MEDLINE=83157104; PubMed=6299662;
RA   Ellison J.W., Buxbaum J.N., Hood L.E.;
RT   "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL   DNA 1:11-18 (1981).
RN   [2]
RP   SEQUENCE OF 1-30 AND 81-326.
RX   MEDLINE=70207560; PubMed=4192699;
RA   Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT   "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT   constant region of a gamma 4 chain.";
RL   Biochem. J. 117:33-47(1970).
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DR   EMBL; K01316; AAB59394.1; ALT_INIT.
DR   PIR; A02150; G4HU.
DR   HSSP; P01842; 7FAB.
DR   Genew; HGNC:5528; IGHG4.
DR   MIM; 147130; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    220       CH2.
FT   DOMAIN      221    327       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    141    201
FT   DISULFID    247    305
SQ   SEQUENCE   327 AA;   35940 MW;   3EDBD811EF208E7A CRC64;
```

```
Query Match             62.2%;  Score 1586.5;  DB 1;  Length 327;
Best Local Similarity   90.6%;  Pred. No. 2e-101;
Matches  299;  Conservative  12;  Mismatches  16;  Indels  3;  Gaps   1;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
        |||||||||||| |:|||| |||||||||||||||||||||||||||||||||||||||||
Db    1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy  207 GLYSLSSVVTVPSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTCPPCPAPELLGG 266
        |||||||||||||||||:|:|||||:|||||||||:    |  :|||| ||||:||||||
Db   61 GLYSLSSVVTVPSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117

Qy  267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
        ||||||||||||||||||||||||||||||:||||||:||||||||||||||||||||||:
Db  118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy  327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
        ||||||||||||||||||||||||||||| |::|||||||||||||||||||||||||::|
Db  178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
```

DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1
FT   VARIANT   104   104   T -> M (IN D11 MARKER).
FT   VARIANT   185   185   T -> A (IN E15 MARKER).
FT   CONFLICT   48   48   N -> E (IN REF. 2).
FT   CONFLICT   71   71   V -> VPV (IN REF. 2).
FT   CONFLICT   144   144   Q -> E (IN REF. 3 AND 4).
FT   CONFLICT   173   173   N -> D (IN REF. 5).
FT   CONFLICT   187   187   Q -> E (IN REF. 3 AND 5).
FT   CONFLICT   201   201   N -> D (IN REF. 5).
FT   CONFLICT   218   218   E -> Q (IN REF. 5).
FT   CONFLICT   233   233   N -> Q (IN REF. 5).
FT   CONFLICT   246   246   E -> G (IN REF. 5).
FT   CONFLICT   256   256   N -> D (IN REF. 5).
FT   CONFLICT   260   260   N -> D (IN REF. 5).
FT   CONFLICT   266   266   N -> W (IN REF. 5).
FT   CONFLICT   280   280   Y -> W (IN REF. 5).
FT   CONFLICT   284   284   N -> S (IN REF. 5).
SQ   SEQUENCE   323 AA;   35404 MW;   69E8AA118D579A8B CRC64;

Query Match   48.1%; Score 1226.5; DB 1; Length 323;
Best Local Similarity   69.7%; Pred. No. 7.6e-77;
Matches 228; Conservative 34; Mismatches 58; Indels 7; Gaps 2;

Qy   150 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 209
              ||||||||| ||| |:|| |||||||||||||||||||||||||||||||||:|||||
Db   4 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLY 63

Qy   210 SLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSV 269
              |||||||| :|||||||| : ||:|:||||||| :: ||||||||||||||
Db   64 SLSSVVSVTSSS--QPVTCNVAHPATNTKVDKTVAPSTCSK---PTCPPPELLGGPSV 116

Qy   270 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 329
              |||||||||||||||||||||||:| :: |||:| ::: :|:|:|:|||:||:||
Db   117 FIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWINNEQVRTARPPLREQQFNSTI 176

Qy   330 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 389
              |||:||| |||||||||||||||||||||||||||||||||||:||||| |||:|| :|
Db   177 RVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSS 236

Qy   390 NQVSLTCLVKGFYPSDIAVEWESSNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 449
              |||||||::|||||||:||||| |||:|:||||||||||||||||:::|||:|:|:|:|
Db   237 RSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRG 296

Qy   450 NVFSCSVMHEALHNHYTQKSLSLSPGK 476
              ::|||||||||||||||||::|||:|||
Db   297 DVFTCSVMHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO
ID   GC2_CAVPO   STANDARD;   PRT;   329 AA.
AC   P01862;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2 chain C region.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE OF 1-3.
RA   Trischmann T.M.;
RL   Submitted (APR-1975) to the PIR data bank.
RN   [2]
RP   SEQUENCE OF 4-68.
RX   MEDLINE=71058471; PubMed=5538606;
RA   Birshtein B.K., Hussain Q.Z., Cebra J.J.;

RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT   half-cystine joining heavy and light chains.";
RL   Biochemistry 10:18-25(1971).
RN   [3]
RP   SEQUENCE OF 69-133 AND 312-329.
RX   MEDLINE=71058486; PubMed=5538616;
RA   Turner K.J., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT   and hinge region cyanogen bromide fragments.";
RL   Biochemistry 10:9-17(1971).
RN   [4]
RP   SEQUENCE OF 134-226.
RX   MEDLINE=75036072; PubMed=4429665;
RA   Tracey D.E., Cebra J.J.;
RT   "Primary structure of the CH2 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4796-4803(1974).
RN   [5]
RP   SEQUENCE OF 227-311.
RX   MEDLINE=75036073; PubMed=4609467;
RA   Trischmann T.M., Cebra J.J.;
RT   "Primary structure of the CH3 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4804-4811(1974).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71058474; PubMed=4922544;
RA   Oliveira B., Lamm M.E.;
RT   "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL   Biochemistry 10:26-31(1971).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC   13 INBRED GUINEA PIGS.
DR   PIR; A02151; G2GP.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IGc1; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT   NON_TER   1   1
FT   DISULFID   16   16   INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID   28   79
FT   DISULFID   105   105   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   107   107   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   110   110   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   142   202
FT   CARBOHYD   178   178   N-LINKED (GLCNAC. . .).
FT   DISULFID   248   308
SQ   SEQUENCE   329 AA;   36074 MW;   5D231B7164D1FBA9 CRC64;

Query Match   47.6%; Score 1212.5; DB 1; Length 329;
Best Local Similarity   70.1%; Pred. No. 7.1e-76;
Matches 234; Conservative 28; Mismatches 63; Indels 9; Gaps 4;

Qy   146 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 205
              | ||||||||||||| ||| |:|| |||||||||||||||||||||||||||||||||
Db   1 SARTTAPSVFPLAASCVDTSGSMMLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVLQ- 59

Qy   206 SGLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKKAEPKSCDKTH--TCPPCPAPEL 263
              |||||||||||| :|||||||| : ||:|:||||||| |: |: | :|
Db   60 SGLYSLTSMVTVPSSQKAT----CNVAHPASSTKVDKTVEPIRTPZPBPCCTCPKCPPPEN 115

Qy   264 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 323
              |||||||:|||||||||||||||||||||||||:| :: |||:| ::: :|:|:|
Db   116 LGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRVE 175

Qy   324 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 383
              |:|||: : |||| |||||||||||||| |||||||||||||| :|||||||||||||

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Db  176 QYNTTFRVESVLPIQHQDWLRGKEFCKCVYNKALPAPIEKTISKTKGAPRMPDVYTLPPS 235
        |||||  :||| :|||| ::|||| :: :|| || ||||||||||||| |:   | ||||
Qy  384 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 441
        |||| :|:|| |||  |:| :  :|| ||| ||    ||| | || :| |:|||||||||
Db  236 RDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLTV 295

Qy  442 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
        |||:| ||.:.|||||||||||| ||| :|:|||
Db  296 DKSAWDQGTVTTCSVMHEALHNHVTQKAISRSPG 329
```

RESULT 6
GC3_HUMAN
```
ID   GC3_HUMAN      STANDARD;      PRT;   290 AA.
AC   P01860;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN   IGHG3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (DISEASE PROTEIN WIS).
RX   MEDLINE=81021548; PubMed=677477;
RA   Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT   "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT   gamma 3 heavy-chain disease protein Wis.";
RL   Biochemistry 19:4304-4308(1980).
RN   [2]
RP   REVISIONS TO 12-97 (PROTEIN WIS).
RX   MEDLINE=77118561; PubMed=402363;
RA   Michaelsen T.E., Frangione B., Franklin E.C.;
RT   "Primary structure of the 'hinge' region of human IgG3. Probable
RT   quadruplication of a 15-amino acid residue basic unit.";
RL   J. Biol. Chem. 252:883-889(1977).
RN   [3]
RP   REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX   MEDLINE=77021516; PubMed=823945;
RA   Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT   "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT   Structure of the Fc fragment of immunoglobulin G3.";
RL   Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN   [4]
RP   SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX   MEDLINE=82247835; PubMed=6805505;
RA   Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA   Franklin E.C., Hood L., Buxbaum J.N.;
RT   "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT   gene deletion model.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC   -!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC       INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC       NORMALLY PRESENT IN THE HINGE REGION.
CC   -!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC   -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC       REF.2.
CC   -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC       AND ALL OF THE CH1 REGION.
CC   -!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC       OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC       GAMMA-3 HEAVY CHAINS.
CC   -!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC       OR ANOTHER GAMMA CHAIN SUBCLASS.
CC   -!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC       TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC       IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC       SEGMENT (12-28).
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the 'Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00231; AAA52805.1; ALT_SEQ.
DR   PIR; A02149; G3HUWI.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5527; IGHG3.
DR   MIM; 147120;
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG like; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT   DOMAIN        12     73       HINGE.
FT   DOMAIN        74    183       CH2.
FT   DOMAIN       184    289       CH3.
FT   REPEAT        29     43
FT   REPEAT        44     58
FT   REPEAT        59     73
FT   MOD_RES        1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD       6      6       N-LINKED (GLCNAC...).
FT   DISULFID       7      7       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      24     24       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      27     27       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      33     33       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      39     39       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      42     42       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      48     48       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      54     54       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      57     57       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      63     63       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      69     69       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   DISULFID      72     72       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT   CARBOHYD     140    140       N-LINKED (GLCNAC...).
FT   MOD_RES      290    290       REMOVED POST-TRANSLATIONALLY.
FT   VARIANT      126    127       QV -> EB (IN ZUC).
FT                                 /FTId=VAR_003890.
FT   VARIANT      134    134       P -> L (IN OMM).
FT                                 /FTId=VAR_003891.
FT   VARIANT      139    139       F -> Y (IN OMM).
FT                                 /FTId=VAR_003892.
FT   VARIANT      182    182       T -> A (IN OMM).
FT                                 /FTId=VAR_003893.
FT   VARIANT      227    227       S -> N (IN OMM).
FT                                 /FTId=VAR_003894.
FT   VARIANT      227    227       MISSING (IN ZUC).
FT                                 /FTId=VAR_003895.
FT   VARIANT      279    279       F -> Y (IN OMM).
FT                                 /FTId=VAR_003896.
SQ   SEQUENCE    290 AA;  32331 MW;  E69CBC9570SB2F46 CRC64;
```

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Query Match             45.4%;  Score 1157;  DB 1;  Length 290;
Best Local Similarity   76.2%;  Pred. No. 3.7e-72;
Matches  218;  Conservative  20;  Mismatches  26;  Indels  22;  Gaps  2;

Qy  210 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV-----------------DKKAEPKSCD 250
            :|||||||||||||||||||||||||||                      ::|||||
Db    8 TVSSELKTP---LGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCD 64

Qy  251 KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 310
          |||||||||||||||||||||||||||||||||||||||||||||:|:|||
Db   65 TPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDG 124

Qy  311 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 370
          :||||||||:||||||:||:||||||||||:||||:|||||||||||||||||||||:|||
Db  125 VQVHNAKTKPRRQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTKG 184
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Qy  371  QFREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD  430
         |||||||||||:|:||||||||||||||||||||||||||||||||| ||||:||||
Db  185  QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSD  244

Qy  431  GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
         ||||||||||||:|||||||||||||||||||||||||||||||||
Db  245  GSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK  290

RESULT 7
GC1_RAT
ID  GC1_RAT           STANDARD;      PRT;    326 AA.
AC  P20759;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig gamma-1 chain C region.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89232738; PubMed=3149946;
RA  Brueggemann M.;
RT  "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL  Gene 74:473-482(1988).
DR  PIR; PS0017; PS0017.
DR  HSSP; P01842; 7FAB.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003597; Ig_c1.
DR  Pfam; PF00047; ig; 3.
DR  SMART; SM00407; IGc1; 2.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT  NON_TER        1      1
FT  DOMAIN         1     97
FT  DOMAIN        98    112       CH1.
FT  DOMAIN       113    219       HINGE.
FT  DOMAIN       220    326       CH2.
FT  DISULFID      27     82       CH3.
FT  DISULFID     102    102
FT  DISULFID     106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID     109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID     111    111       INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID     140    200
FT  DISULFID     246    304
FT  CARBOHYD     176    176       N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE     326 AA;  35946 MW;  013BAB45EF49B9DA CRC64;

Query Match             45.0%;  Score 1148;  DB 1;  Length 326;
Best Local Similarity   63.1%;  Pred. No. 1.8e-71;
Matches  210;  Conservative  52;  Mismatches  61;  Indels  10;  Gaps  4;

Qy  147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  206
         ||||||:||| :||||: ||||||||||||||||||||||||||||||||||||||||||
Db    1  AETTAPSVYPLAPGTALKSNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQ-S   59

Qy  207  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG  266
         ||||||||||||:||||||||||||||||:|||||||| :|||    :|||:| || 
Db   60  GLYTLTSSVVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCG---GDCKPC----ICTG  113

Qy  267  --PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE   323
            |:||||||||||| :|||| :||||||| :||||||||||||||||||  |  | 
Db  114  SEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEE  173

Qy  324  QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS  383
         |:||||||:||||:||||||||||||||||||||  :||||||||||||||||||||||
Db  174  QFNSTFRSVSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMSPT  233

Qy  384  RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK  443
         ::|:||||:|:|||||||||||||| :|||| |:||||||||||:::||||||::|||:
Db  234  KEEMTQNEVSITCMVKGFYPYPDDIVEWQMNGQPENYKNTPFTMDTDGSYFLYSKLNVKK  293
```

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RESULT 9
GC1_MOUSE
ID   GC1_MOUSE      STANDARD;      PRT;    324 AA.
AC   P01868;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   30-MAR-2000 (Rel. 39, Last annotation update)
DE   Ig gamma-1 chain C region.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX   MEDLINE=80202559; PubMed=6769752;
RA   Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA   Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT   "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT   cloned in a bacterial plasmid.";
RL   Gene 9:87-97(1980).
RN   [3]
RP   SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=80012837; PubMed=113776;
RA   Rogers J., Clarke P., Salser W.;
RT   "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT   heavy chain.";
RL   Nucleic Acids Res. 6:3305-3321(1979).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=78242288; PubMed=98524;
RA   Adetugbo K.;
RT   "Evolution of immunoglobulin subclasses. Primary structure of a
RT   murine myeloma gamma1 chain.";
RL   J. Biol. Chem. 253:6068-6075(1978).
RN   [5]
RP   DISULFIDE BONDS (MOPC 21).
RX   MEDLINE=73008889; PubMed=5073237;
RA   Svasti J., Milstein C.;
RT   "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL   Biochem. J. 126:837-850(1972).
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   EMBL; V00793; CAA24175.1; -.
DR   EMBL; V00795; CAA24176.1; -.
DR   PIR; A02159; G1MS.
DR   HSSP; P01842; 7FAB.
DR   GlycoSuiteDB; P01868; -.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_C1.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
```

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KW   Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC...).
FT                                /FTId=CAR_000055.
FT   DISULFID    244    302
FT   MOD_RES     324    324       REMOVED POST-TRANSLATIONALLY.
FT   CONFLICT    276    276       N -> D (IN REF. 3).
FT   CONFLICT    278    278       N -> D (IN REF. 3).
SQ   SEQUENCE   324 AA;  35704 MW;  A338812F3D1F2C93 CRC64;
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Query Match             44.6%;  Score 1138;  DB 1;  Length 324;
  Best Local Similarity   62.0%;  Pred. No. 8.5e-71;
  Matches  206;  Conservative  55;  Mismatches  61;  Indels  10;  Gaps  4;

Qy    147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
          |||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||:
Db      1 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTWNSGSLSSGVHTFPAVLQSD 60

Qy    207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 264
          |||||||||||||||||| :||||||||||||:|||||||||:||      ::||||||
Db     61 -LYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 114

Qy    265 GGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
          |||||||:||||||:||:||:|:|||||||||:|||||:||||:|:|||:|:|:|||||
Db    115 --SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 172

Qy    325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVVTLPPSR 384
          |:|||||||||||:||:|:|||:|||:||||:|||||||||||:|||:||||||||||:
Db    173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 232

Qy    385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
          ||| |:|:|:||||||||||||||| |:||||||||||||||||||||||||:|||||||
Db    233 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS 292

Qy    445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          ||| ||||:|||:|||||||||||||||||||
Db    293 NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 324
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RESULT 10
GC3_MOUSE
ID   GC3_MOUSE      STANDARD;      PRT;    329 AA.
AC   P22436;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-3 chain C region, secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR   PIR; B02156; G3MSC.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG like; 1.
DR   SMART; SM00407; IGC1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER   1   1
FT   DOMAIN   1   97   CH1.
FT   DOMAIN   98   113   HINGE.
FT   DOMAIN   114   223   CH2.
FT   DOMAIN   224   327   CH3.
SQ   SEQUENCE   329 AA; 36228 MW; F4582717418ZBAD6 CRC64;

Query Match   44.6%; Score 1137; DB 1; Length 329;
Best Local Similarity   64.0%; Pred. No. 1e-70;
Matches 212; Conservative 46; Mismatches 69; Indels   4; Gaps   3;

Qy   148 STKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 207
                 ||:||||| |||::||||| |||||||||||| ||:||||||| : :|||||| ||
Db   1 TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SG   59

Qy   208 LYSLSSVVTVPSSSLGTQYTICNVNHKPSNTKVDKKAEPKSCDKTHTCP--PCPAPELLG 265
            :|| |||||||| :| : ||| :||:|:|| |||| :: | | :||
Db   60 FYSLSSLVTVPSSTWPSQVTICNVAHPASKTELIKRIEPR-IPKPSTPPGSSCPPGNILG 118

Qy   266 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 325
            |||||:||||||| | ||| |:| ||||| | || : : | | | :|| ||| |
Db   119 GPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY 178

Qy   326 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVVTLPPSRD 385
            ||| |||| ||: | |||| ||| :||||| ||:||| : : ||||||: ||
Db   179 NSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPRE 238

Qy   386 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 445
            :||:||||||||:|||||| : |||| ||: : :|||:|||||| ||||||||||| |
Db   239 QMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDTDS 298

Qy   446 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            | || ||||||| || |||||||||| ||||
Db   299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329

RESULT 11
GC1M_MOUSE
ID   GC1M_MOUSE   STANDARD;   PRT;   393 AA.
AC   P01869;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ig gamma-1 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka Y., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]

RP   SEQUENCE OF 323-393 FROM N.A.
RX   MEDLINE=82197626; PubMed=6804950;
RA   Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT   "mRNA for surface immunoglobulin gamma chains encodes a highly
RT   conserved transmembrane sequence and a 28-residue intracellular
RT   domain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN   [3]
RP   SEQUENCE OF 323-366 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
RN   [4]
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC   SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC   GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC   BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3', END, ENCODED
CC   IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC   SEGMENT OF MU CHAINS.
CC   --
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   PIR; B02159; G1MSM.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_cl.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGC1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Transmembrane.
FT   NON_TER   1   1
FT   DOMAIN   1   97   CH1.
FT   DOMAIN   98   110   HINGE.
FT   DOMAIN   111   217   CH2.
FT   DOMAIN   218   324   CH3.
FT   DISULFID   27   82   INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID   102   102   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   104   104   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   107   107   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   109   109   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   138   198
FT   CARBOHYD   174   174   N-LINKED (GLCNAC. . .).
FT   DISULFID   244   302
FT   TRANSMEM   340   357   POTENTIAL.
FT   DOMAIN   358   393   CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match   44.4%; Score 1133; DB 1; Length 393;
Best Local Similarity   61.9%; Pred. No. 2.4e-70;
Matches 205; Conservative 55; Mismatches 61; Indels 10; Gaps   4;

Qy   147 ASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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Db      1 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 60

Qy    207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 264
          ||:|:||||   |||||  :::||||       ||||           |:|  :|||||
Db    .61 -LYTLSSSVTVPSSSRPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 114

Qy    265 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
          ||||  ||||||||||  :||:||||||||  : ||||| |:  |:|:|||| |:|||||
Db    115 --SSVFIPPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 172

Qy    325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQREPQVYTLPPSR 384
          :||||||||||:|||:||| |||||||||||  ||||||||||:|:|||||||  :|||
Db    173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 232

Qy    385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
          :::|:||||||||||||||||:|| ||:||||  |||||||||||||||||||||||||
Db    233 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVVYSKLNVQKS 292

Qy    445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
           :::|:|:||||:|||:|||||||:|||:|
Db    293 NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 323

RESULT 12
GC3M_MOUSE
ID   GC3M_MOUSE     STANDARD;      PRT;      398 AA.
AC   P03987;
DT   23-OCT-1986 (Rel. 02, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-3 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
RN   [2]
RP   SEQUENCE OF 328-398 FROM N.A.
RX   MEDLINE=84041483; PubMed=6314258;
RA   Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA   Wall R.;
RT   "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT   segment.";
RL   Nucleic Acids Res. 11:6775-6785(1983).
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; J00451; AAB59655.1; -.
DR   EMBL; V01526; CAA24767.1; ALT_SEQ.
DR   PIR; A02155; G3MSM.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER     1      1
```

```
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
FT   TRANSMEM    346    362       POTENTIAL.
FT   DOMAIN      363    398       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT    333    333       E -> G (IN REF. 2).
FT   CONFLICT    342    342       E -> Q (IN REF. 2).
FT   CONFLICT    388    388       P -> F (IN REF. 2).
SQ   SEQUENCE   398 AA;  43929 MW;  CF7F264B50A41B95 CRC64;

Query Match             44.2%;  Score 1126;  DB 1;  Length 398;
Best Local Similarity   63.8%;  Pred. No. 7.2e-70;
Matches  210;  Conservative  46;  Mismatches  69;  Indels   4;  Gaps   3;

Qy    148 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 207
          :|:|||||| |: ||||         ||||||||||| ||||  ||| |||||||||:|
Db      1 TTTAPSVYPLVPGGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SG 59

Qy    208 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTCP--PCPAPELLG 265
          ||||||||:|||||| :|||||||  || ||||||        :|:|  |:|||||:|
Db     60 FYSLSSLVTVPSSTWPSSQTVICNVAHPASKTELIKRISPR-IPKPSTPPGSSCPPGNILG 118

Qy    266 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 325
          |||||||||||||  |:|::|  || |||| |: |||:|:|::: :  || |:|||||||
Db    119 GPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY 178

Qy    326 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 385
          |:|:||||::|:||| |:|: |||||:|||||| ||||||||||||||||||||| |||
Db    179 NSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPRE 238

Qy    386 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 445
          ::|:||||:||||:|:||:||:|||  | ||  |||||||||| |:|:|:||||||:|||
Db    239 QMSKKKVSLTCLVTNFFSEAISVEWERNGELQDYKNTPPILDSDGTYFLYSKLTVDTDS 298

Qy    446 WQQGNVFSCSVMHEALHNHYTQKSLSLSP 474
          | ||:||:|||:||:|||||| :|:||:|
Db    299 WLQGEIFTCSVVHEALHNHHTQKNLSRSP 327

RESULT 13
GCAA_MOUSE
ID   GCAA_MOUSE     STANDARD;      PRT;      330 AA.
AC   P01863;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ig gamma-2A chain C region, A allele.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81076554; PubMed=677755;
RA   Sikorav J.-L., Auffray C., Rougeon F.;
RT   "The complete nucleotide sequence of mouse immunoglobin gamma 2a gene
RT   and evolution of heavy chain genes: further evidence for intervening
RT   sequence-mediated domain transfer.";
RL   Nucleic Acids Res. 9:1365-1381(1981).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81198976; PubMed=6262729;
RA   Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT   "Structure of the constant and 3' untranslated regions of the murine
RT   Balb/c gamma 2a heavy chain messenger RNA.";
RL   Nucleic Acids Res. 8:3143-3155(1980).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81223894; PubMed=6787604;
RA   Ollo R., Auffray C., Morchamps C., Rougeon F.;
RT   "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT   suggests that exons can be exchanged between genes in a multigenic
```

RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN   [4]
RP   MYELOMA PROTEIN MOPC 173.
RX   MEDLINE=74175517; PubMed=4831970;
RA   Bourgois A., Fougereau M., Rocca-Serra J.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin:amino-acid sequence of the Fc fragment.Implications
RT   for the evolution of immunoglobulin structure and function.";
RL   Eur. J. Biochem. 43:423-435(1974).
RN   [5]
RP   DISULFIDE BONDS.
RX   MEDLINE=73056887; PubMed=4565406;
RA   de Preval C., Fougereau M.;
RT   "Determination of the primary structure of a mouse gamma G2a
RT   immunoglobulin. Identification of the disulfide bridges.";
RL   Eur. J. Biochem. 30:452-462(1972).
CC   ---
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; V00798; CAA24178.1; -.
DR   PIR; A02152; G2MSA.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1   1
FT   DISULFID   15   15
FT   DISULFID   27   82
FT   DISULFID   107   107   INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID   110   110   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   112   112   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   144   204   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   250   308
FT   MOD_RES   330   330   REMOVED POST-TRANSLATIONALLY.
SQ   SEQUENCE   330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match   44.0%; Score 1122; DB 1; Length 330;
Best Local Similarity   63.6%; Pred. No. 1.1e-69;
Matches 211; Conservative   43; Mismatches   74; Indels   4; Gaps   3;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
          |||:|||| |:| |||||| | | |||||:| |:|||||:||||| |||||||||||||
Db   1 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 264
Db   61 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118

Qy   265 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
Db   119 GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED 178

Qy   325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
Db   179 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE 238

Qy   385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
Db   239 EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYMYSKLRVEKK 298

Qy   445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |:||||||| |||| ||||| :|||:|:|||
Db   299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330

RESULT 14
GCAB_MOUSE
ID   GCAB_MOUSE   STANDARD;   PRT;   335 AA.
AC   P01864;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2A chain C region, B allele.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=82037881; PubMed=6170065;
RA   Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT   "Multiple differences between the nucleic acid sequences of the
RT   IgG2aa and IgG2ab alleles of the mouse.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN   [2]
RP   SEQUENCE.
RX   MEDLINE=82037777; PubMed=6794027;
RA   Dognin M., Lauwereys M., Strosberg A.D.;
RT   "Multiple amino acid substitutions between murine gamma 2a heavy
RT   chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC   -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC   FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC   ---
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR   PIR; A02153; G2MSAB.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1   1
SQ   SEQUENCE   335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match   43.9%; Score 1119.5; DB 1; Length 335;
Best Local Similarity   61.3%; Pred. No. 1.6e-69;
Matches 206; Conservative   52; Mismatches   71; Indels   7; Gaps   2;

Qy   147 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
          |||:|||| |:| |||||| | | |||||:| |:|||||:||||: |||||||||:-|
Db   1 AKTTAPSVYPLVPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSSLSSGVHTFPALLQ-S 59

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK------SCDKTHTCPPCPA 260
Db   60 GLYTLSSSVTVSNTWPSQTITCNVAHPASSTKVDKKIEPRVPITQNPCPPHQRVPPCAA 119

Qy   261 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 320
Db   120 PDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 179

Qy   321 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380

```
Db   180  HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239
          ||||  ||||||| :  |||:||:|||:|| |||||||||||||||||||||||||||||
Qy   381  PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 440
          |:||  ||:||||:|| ||||||:||||| ||||  |:|::  |||||||:|:|:||||:
Db   240  PPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLR 299
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Qy   441  VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |:::|::|:|||||||||||||||||||: | |  |
Db   300  VQKSTWERGSLFACSVVHEVLHNHLTKTISRSLGK 335
```

```
RESULT 15
GCAM_MOUSE
ID   GCAM_MOUSE      STANDARD;       PRT;   399 AA.
AC   P01865;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2A chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC       SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC       GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC       BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC       IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC       SEGMENT OF MU CHAINS.
CC   -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC       IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC       THE A ALLELE.
CC   -------------------------------------------------------------------
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CC   -------------------------------------------------------------------
DR   EMBL; J00471; AAB59661.1; ALT_INIT.
DR   PIR; A02154; G2MSAM.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   TRANSMEM    346    363       POTENTIAL.
FT   DOMAIN      364    399       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    380    180       N-LINKED (GLCNAC...) (POTENTIAL).
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SQ   SEQUENCE   399 AA;  44020 MW;  4C3813BFAED3FF0 CRC64;

     Query Match                    43.8%;    Score 1117;  DB 1;  Length 399;
     Best Local Similarity          63.4%;    Pred. No. 3e-69;
     Matches   210;  Conservative   43;  Mismatches   74;  Indels    4;  Gaps    3;

Qy   147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
          |||:||||||||:|:|||:|||   |||||:|||| ::||:|:|||:||::|||||||||
Db     1  AKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 60

Qy   207  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 264
          |||:|| ||| |  |:|:| ||||||||::|  |:|  :|||||||||||    ||||||
Db    61  -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118

Qy   265  GGPSVFLFPPKPKDTLMISRTEPVTCVVVDVSHEDPEVKFNWYDGVEVHNAKTKPREEQ 324
          |||||:|:|||||:||:|:|||::||||||||::|:: :|||: ||||:|||  |:||:
Db   119  GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED 178

Qy   325  YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
          ||||:|||||||||||||:|||:|:|||||:||:|||||||||:|||::|||:|:||:|:
Db   179  YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVVLPPPE 238

Qy   385  DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
          :|:||||:||||||||:||||||||||||| |||||:||||||||:||||:||:||:|:
Db   239  EEMTKKQVTLTCMVTDFMPEDIVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 298

Qy   445  RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
          ||:||:|||||| ||:|||| | |  |:|:|
Db   299  NWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329
```

```
Search completed: March 29, 2003, 09:11:17
Job time : 13.3492 secs
```

```
          GenCore version 5.1.4_p5_4578
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     March 29, 2003, 09:06:23 ; Search time 43.1716 Seconds
                                        (without alignments)
                                        2271.829 Million cell updates/sec

Title:      US-09-758-173-12
Perfect score: 2549
Sequence:   1 MKHLWFFLLVAAPRWVLSQ........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
            Gapop 10.0 , Gapext 0.5

Searched:   671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:     671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  SPTREMBL_21:*
            1: sp_archea:*
            2: sp_bacteria:*
            3: sp_fungi:*
            4: sp_human:*
            5: sp_invertebrate:*
            6: sp_mammal:*
            7: sp_mhc:*
            8: sp_organelle:*
            9: sp_phage:*
           10: sp_plant:*
           11: sp_rodent:*
           12: sp_virus:*
           13: sp_vertebrate:*
           14: sp_unclassified:*
           15: sp_rvirus:*
           16: sp_bacteriap:*
           17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2102.5	82.5	471	4	Q8TC77	Q8tc77 homo sapien
2	2075	81.4	473	4	Q8TC63	Q8tc63 homo sapien
3	1473.5	57.8	463	11	Q9LC4	Q99lc4 mus musculu
4	1437.5	56.4	473	11	Q9D8L4	Q9d8l4 mus musculu
5	1434	56.3	469	11	Q8R3V9	Q8r3v9 mus musculu
6	1430.5	56.1	437	11	Q9R1A4	Q9r1a4 mus musculu
7	1416	55.6	468	11	Q99L31	Q99l31 mus musculu
8	1394.5	54.7	473	11	Q99L25	Q99l25 mus musculu
9	1367	53.6	474	11	Q8R3H6	Q8r3h6 mus musculu
10	1365.5	53.6	473	11	Q91Z05	Q91z05 mus musculu
11	1268	49.7	701	4	Q96PQ8	Q96pq8 homo sapien
12	1262.5	49.5	337	6	Q95M34	Q95m34 equus cabal
13	973	38.2	613	4	Q96EY0	Q96ey0 homo sapien
14	948.5	37.2	597	4	Q9BU10	Q9bu10 homo sapien
15	944.5	37.1	597	4	Q9BQB8	Q9bqb8 homo sapien
16	938.5	36.8	588	4	Q8WUX4	Q8wux4 homo sapien
17	938.5	36.8	618	4	Q96AA6	homo sapien
18	915	35.9	496	4	Q96KX8	homo sapien
19	770.5	30.2	597	4	Q96BB9	homo sapien
20	762	29.9	613	4	Q8WUK1	homo sapien
21	746.5	29.3	479	11	Q99M22	mus musculu
22	726	28.5	613	11	Q8VCX7	mus musculu
23	725	28.4	278	11	Q921K1	mus musculu
24	702	27.5	494	4	Q96K68	homo sapien
25	700	27.5	482	11	Q91X92	mus musculu
26	692.5	27.2	614	4	Q96GA6	homo sapien
27	667.5	26.2	497	4	Q8WY24	homo sapien
28	655.5	25.7	479	11	Q91WP5	mus musculu
29	655	25.7	488	11	Q91WR1	mus musculu
30	654.5	25.7	487	11	Q99KA4	mus musculu
31	652	25.6	486	11	Q91Z07	mus musculu
32	645	25.3	500	4	Q9BRV0	homo sapien
33	637.5	25.0	481	11	Q91WT1	mus musculu
34	636	25.0	496	4	Q96DK0	homo sapien
35	635.5	24.9	481	11	Q8VCV5	mus musculu
36	631.5	24.8	480	11	Q91XE1	mus musculu
37	626.5	24.6	489	11	Q8VCX4	mus musculu
38	623.5	24.5	484	11	Q8VEA0	mus musculu
39	614	24.1	484	11	Q99LA6	mus musculu
40	590.5	23.2	481	11	Q91WT3	mus musculu
41	583.5	22.9	150	4	Q95973	homo sapien
42	576	22.6	416	4	Q9NPP6	homo sapien
43	538	21.1	573	4	Q8WU38	homo sapien
44	503	19.7	426	11	Q9DCD9	mus musculu
45	465	18.2	384	4	Q9UP60	homo sapien

ALIGNMENTS

```
RESULT 1
Q8TC77
ID   Q8TC77        PRELIMINARY;      PRT;   471 AA.
AC   Q8TC77;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.8 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024289; AAH24289.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE  471 AA;  51791 MW;  38BF7F4CF58B660E CRC64;

Query Match           82.5%;  Score 2102.5;  DB 4;  Length 471;
Best Local Similarity 85.2%;  Pred. No. 1.1e-159;
Matches 403;  Conservative 16;  Mismatches 45;  Indels 9;  Gaps 4;

Qy     5  WFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKG  64
          |||  ||    |  | :|| |||||||||||| |:|| ||:|||  | :||||||||||
Db     7  WVF--LVAILEGVQCEVQLVESGGGLVKPGGGSLRLSCAASGFTFS-SYSMNWVRQAPGKG  63

Qy    65  LEWIGSFYSSGNTYYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSV  124
          |||:|| | :::||:| :|::|  |:|| :: |:::|::|::|||||||||| |   |
Db    64  LEWVSSMSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD-----  118

Qy   125  VGMVYNNW-FDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV  183
          :  :|:|: ||:||:|:|||||||||||||||||||||||||||||||||||||||||||
Db   119  LRQLTSYWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV  178

Qy   184  TVSWNSGALTSGVHTFPAVLQSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK  243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   179 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK 238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   417 YKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 473

Qy   244 AEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 303
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   239 VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 298

Qy   304 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 363
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   299 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 358

Qy   364 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 423
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 418

Qy   424 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   419 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
```

```
RESULT 2
Q8TC63
ID   Q8TC63          PRELIMINARY;     PRT;    473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;   51986 MW;   E29920B09BA369F5 CRC64;

Query Match             81.4%;  Score 2075;  DB 4;  Length 473;
Best Local Similarity   83.2%;  Pred. No. 1.8e-157;
Matches  397;  Conservative  29;  Mismatches  39;  Indels  12;  Gaps 5;

Qy     1 MKHLWFFLLLVAAPRWVLSQVLQESGPGLVKPSETLSLTCAVSGGSI-SGGYGWGWIRQ 59
           |: |||:|||:|||||||| ||:.: :||||:.::||||||| ::.||  :|: :|:
Db     8 MKHLWFFLLLVAAPRWVLSRIQLQESGPGLLKPSV-LSLTCTVSGDSVASSSYYWGWVRQ 67

Qy    60 PPGKGLEWIGSFYSSSGNTYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRD 119
           |||||||||||:|:|||:|:|:||| |:|||:||:::|||||||||||:||||||:||
Db    68 PPGKGLEWIGTI-NFSGNMYYSPSLRSRVTMSADMSENSFYLKLDSVTAADTAVYYCAAG 126

Qy   120 RLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
           |:    |:|| : |:|:|  |||  :| ||||||||| |||| :::|||||||||||||
Db   127 HL--VMGFGAH-----WGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF 179

Qy   180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
           |||||||||||||||||||||||||||||||||||:|||||||||:|||||||||||||
Db   180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTK 239

Qy   240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
           |:|: .|:    .||| |||  ::.||||||| |||||||||||||||||||||:|:|:|
Db   240 VDKRVESK--YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED 296

Qy   300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
           ||| ||||||||||||||||||||| ::|:|||||||||||||||||||||||||||||
Db   297 PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS 356

Qy   360 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
           |:|||||||||||||||||||||:|:||||||| ::|:|:||||||||||||||||||||
Db   357 SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 416

Qy   420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   406 NYKNTQPIMDTDGSYFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 463
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Db   417 YKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 473

RESULT 3
Q99LC4
ID   Q99LC4          PRELIMINARY;     PRT;    463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003599; Ig-4.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE   463 AA;   51007 MW;   EAA674C6BBC10783 CRC64;

Query Match             57.8%;  Score 1473.5;  DB 11;  Length 463;
Best Local Similarity   56.3%;  Pred. No. 1.9e-109;
Matches  269;  Conservative  84;  Mismatches 108;  Indels  17;  Gaps 6;

Qy     1 MKHLWFFLLLVAAPRWVLSQVLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
           |: :||||||||||||||||: ::||| :||::::|||:|||:|||||  :|: :||:
Db     1 MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFT-GYGVSWVKQR 59

Qy    61 PGKGLEWIGSFYSSSGNTYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
           .|:||||||:|:::||.| : ::||| |:|:|:::  :|:|||: :|::|||:||||||
Db    60 TGQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVVFCARSS 119

Qy   121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
           :|||   ::  : | |: |:|||| ::  | ||| |||||:|:|||||||||||||||:|
Db   120 YYSY-----DLFAYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP 173

Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
           |||||||||||:||||||||||||:|-||||||||||||||||||:|||||:|||::::|
Db   174 EPVTVTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSETVTCNVAHPASSTKV 232

Qy   241 DKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 298
           |:|:   ||:|  |||   .: : |   : :|||||||:||||:.:: || ||| : :|
Db   233 DKKIVPRDCG----CKPCICTVPEV----SSVFIFPPKPKDVLTITLFPKVTCVVVDISKD 285

Qy   299 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
           ||||::::|:|| | | :::::|:::|||||:|::|||:|: |:|||| :||||||||:|
Db   286 DPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFP 345

Qy   359 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 418
           ||:||||||:::|:|::|||| |::|:::|:::::||:||:|:||::|||:||:|:||:|
Db   346 APIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAE 405

Qy   419 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            ||:|:|:||:||| |:|||| |:||::|:||| ::::|||.||:|| |:|||| :||
Db   406 NYKNTQPIMDTDGSYFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 463
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RESULT 4
Q9D8L4
ID   Q9D8L4          PRELIMINARY;       PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810060009Rik protein.
GN   IGH-1 OR 1810060009RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE   473 AA;   51699 MW;   9DED57A514475FBB CRC64;

Query Match             56.4%;  Score 1437.5;  DB 11;  Length 473;
Best Local Similarity   55.8%;  Pred. No. 1.5e-106;
Matches  269;  Conservative  80;  Mismatches 118;  Indels  15;  Gaps  5;

Qy      1  MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60
           || ||| |||||||||||| |||||||||||||||||||| |||| || |||| :
Db      1  MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFT-DYINWVKQR  59

Qy     61  PGKGLEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYCVRDR  120
           ||||||||| || ||||| :||||| :|: |||||||||:: | ||:| |||||||
Db     60  PGQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARS- 118

Qy    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
           :||||||| ||| |||||||||||||| |||||||||||||||||||||||||||||||
Db    119  ----GYDY-DWFAYWGQGTLVTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYFP  172

Qy    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSLGTQTYICNVNHKPSNTKV  240
           |||||||||||||||||||||||||||||||||||||||||||:|||:|||||:|||||
Db    173  EPVLTWNSGSLSSGVHTFPALLQ-SGLVTLSSSSVTVTSNTWPSQTITCNVAHPASSTKV  231
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                       241  DKKAEPK------SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD  294
                            ||:|:         | |:| :|| :||||:||||||||||||||||||:|:|||||:||||
                       232  DKKIEPRVPITQNPCPLKECPCAAPDLLGGPSVFIFPPKIKDVIMISLSPMVTCVVVD  291

                       295  VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN  354
                            |||:| |||| | |||||||:|||||| :| ||||||:|||:|| |||||| | ||
                       292  VSEDDPVQISWFVNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNN  351

                       355  KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG  414
                            :||| ||||||||| :|:| |  |||:| | |::||:|:|:|||| |:|||:|||||:||
                       352  RALPSPIEKTISKPRGPVRAPQVYVLPPPAEMTKKEFSLTCMITGFLPAEIAVDWTSNG  411

                       415  QPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  474
                            :|:||||| ||||||||:| | | |||||||:|:|||||| |||| |||||:|::|| |
                       412  RTEQNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKTISRSL  471

                       475  GK  476
                            ||
                       472  GK  473
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RESULT 5
Q8R3V9
ID   Q8R3V9          PRELIMINARY;       PRT;   469 AA.
AC   Q8R3V9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024405; AAH24405.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;   51976 MW;   534793F155D05457 CRC64;

Query Match             56.3%;  Score 1434;  DB 11;  Length 469;
Best Local Similarity   57.1%;  Pred. No. 2.8e-106;
Matches  274;  Conservative  76;  Mismatches 110;  Indels  20;  Gaps  10;

Qy      4  LWF-FLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPG  62
           | | |||||||||| |||| |||||||||||||||||||:|||| ::|||||||| |||
Db      3  LMLNWIFLVTLLNGIQCEVNLVESGGGLVQPGGSLRLSCAASGFTFT-DYMSWVRQPPG  61

Qy     63  KGLEWIGSFYSSSGNTY---YNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYCVRD  119
           |||||| ||||:||| |     :||||:|:||  |:|||| :|:| :|: |  |||||::
Db     62  KALEWLG-FIRNKANGYTTEYSASVKGRFTISRDNSQSILYLQMNALRAEDSATYYCARD  120

Qy    120  RLFSVGMVYNNW-FDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  178
           | :| | | ::  |||||||||||||| |||||||||||| || :||:| |||||||||
Db    121  RRSS---YYYSGTSFAYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGY  177

Qy    179  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSLGTQTYICNVNHKPSNT  238
           ||||||||||||||||||||||||| ||| |:||||||||||||||||:|||||:||::
Db    178  FPEPVTVTWNSGSLSSGVHTFPAVLQSD-LVTLSSSVTVPSSTWPSQTVTCNVAHPASST  236

Qy    239  KVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS  296
           ||||| :|||  |||| |:   |:    || :||| ||:|| || ||||||||||||||:
Db    237  KVDKKIVPRDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTITLPKVTCVVVDIS  289

Qy    297  HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA  356
           |:| ||| ||||| ||||||||:||||||||:|:|||| :|: |:::|||||| | || |
Db    290  KDDPEVQFSWFVDDVEVHTAQFKPREEQFNSIFRSVSELPIMHQDWLNGKEFKCRVNSAA  349

Qy    357  LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP  416
           ||||||||||| |:|:| |||| |||:||||||:|:|||:|||| |:|||||||:||:||
Db    350  FPAPIEKTISKTKGRPKAPQVTIPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQP  409
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Qy   417 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                 |||||||||||||||||:||:::|||||||:|||||||:|:|||:|:||:||||
Db   410 AENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 469

RESULT 6
Q9R1A4
ID   Q9R1A4   PRELIMINARY;   PRT;   437 AA.
AC   Q9R1A4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Gamma1 heavy chain of Mab7 (Fragment).
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFv).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152372; AAD40243.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER   1   1
FT   NON_TER   437   437
SQ   SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match   56.1%; Score 1430.5; DB 11; Length 437;
Best Local Similarity   58.3%; Pred. No.4.9e-106;
Matches 267; Conservative 72; Mismatches 96; Indels 23; Gaps 7;

Qy   21 VQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYY   80
               |:||||||:|||||||::|||:|||||||||:|| :||||||||||||||:::::|
Db   1 VQLQESGGGLVKPGGSLKLSCAASGFTFS-STAMSWVRQTPEKRLEWVASF-SSGGLIYY   58

Qy   81 NPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWFDVWGPGV 140
                ::|||||||||||||:::|:|||::||||||||| :|| :||:||||||
Db   59 TDSVKGRFTIYKDKDRNILSLQMSSLRSEDTAMYYCAR----------GDYSAYWGPGT 107

Qy   141 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 200
               |||||||||||||||||||||||| :|:|||||||||||||||:|||:|||:|||||
Db   108 LVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFP 167

Qy   201 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--C 258
               |||||:|||||||||||||:::|:|||:||||||:|:||||| :||:|||||:|| |
Db   168 AVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG-----CKPCIC 222

Qy   259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
               ||:|:||||:||||||||||:|:|||||||||||||:|:|:||||:|:||||||||:|
Db   223 TVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQT 279

Qy   319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
               ||||||||||:::|| |||||||||||||||||:::|||||||||||||||:|||||||
Db   280 QPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVY 339

Qy   379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
               |:||::|:|:|||||||||||:::|||||||||:||:|::::|:|||||||||:||||:
Db   340 TIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSK 399

Qy   439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 7
Q99L31
ID   Q99L31   PRELIMINARY;   PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE 468 AA; 51661 MW; 9635232BB3332ADB CRC64;

Query Match   55.6%; Score 1416; DB 11; Length 468;
Best Local Similarity   56.7%; Pred. No. 7.7e-105;
Matches 271; Conservative 68; Mismatches 127; Indels 12; Gaps 5;

Qy   1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP   60
               |||:|||::||||::||:::|:||||||||:||:::|||||::||||::::::::::
Db   1 MKCSWVIFFLMAVVIGVNSEVQLQQGGAELVRPGASVKLSCTASGFNIKDSL-MHWVKQR   59

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
               |:|||||:||||||||||::|||:|||||::|||||:||:::|||:::|:||||||||| -
Db   60 PEQGLEWIGWIDPEDGETKYAPKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARN- 118

Qy   121 LFSVVGMVYNNWFDVWGPGVLVTVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                    :|:||||:||||||||:::|||:|||:||||:||::||||::::|||||||||
Db   119 -----LLYGGYDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFP 172

Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
               |||:|||||||||||||||||||||:|||||||||||||:::|:|||||||:|||:||
Db   173 EPVTLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVSSTWPSQSITCNVAHPASSTKV 231

Qy   241 DKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 298
               |||:||:||||||||| |:||:|:||||:||:|||||||:|:|:|:|:||||||:||
Db   232 DKKIEPRG-PTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSED 290

Qy   299 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
               |||:|:||:||||||||::|||||||:|||:|:|:||||:||||||||:||:||||||||
Db   291 DPDVQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALP 350

Qy   359 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 418
               |||||||||:|||::::|||||||:::|::||:|:|||||||:||:::||||||:||:
Db   351 APIERTISKPKGSVRAPQVYVLPPPEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTEL 410

Qy   419 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
               ||:|:|||||||||:||||||::|||||:||||:||||::::||||||:|||||:|||
Db   411 NYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTKSFSRTPGK 468

RESULT 8

Q99L25
ID   Q99L25
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE   473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match   54.7%; Score 1394.5; DB 11; Length 473;
Best Local Similarity   55.8%; Pred. No. 4.1e-103;
Matches 269; Conservative   71; Mismatches 127; Indels 15; Gaps 6;

Qy   1 MKHLWFLLLVAAPRWVLSQVLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP   60
Db   1 MEWSWVFLFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSGYTFT-DHTIHWVKQR 59

Qy   61 PGKGLEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
Db   60 PEQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRG- 118

Qy 121 LFSVVGMVNN---WFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK 176
Db 119 ----GSIYGYGLYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVK 173

Qy 177 DYFPBPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS 236
Db 174 GYFPEPVTLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSTWPSQSITCNVAHPAS 232

Qy 237 NTKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVD 294
Db 233 STKVDKKIEPRG-PTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVD 291

Qy 295 VSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 354
Db 292 VSEDDPDVQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNN 351

Qy 355 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 414
Db 352 KALPAPIERTISKPKGSVRAPQVVLPPEEMTKKQVLTCMVTDFMPEDIYVEWTNNG 411

Qy 415 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 474
Db 412 KTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVHEGLHNHHTTKSFSRTP 471

Qy 475 GK 476
Db 472 GK 473

RESULT 9
Q8R3H6
ID   Q8R3H6
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.7 kDa protein.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match   53.6%; Score 1367; DB 11; Length 474;
Best Local Similarity   54.8%; Pred. No. 6.5e-101;
Matches 261; Conservative   75; Mismatches 124; Indels 16; Gaps 5;

Qy   8 LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW 67
Db   8 LFLLSVTEGVHSQVQLLQSGPELVKPGASVKISCRASGYAFSKSW-MNWVKRRPGKGLEW 66

Qy   68 IGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGM 127
Db   67 IGRIFPGDGDTHYSGKFQGKAKLTADKSSVTAFLQLTSLTSEDSAVVFCARD------S 119

Qy 128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 187
Db 120 DYGDYFDDWGQGATVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTW 179

Qy 188 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
Db 180 NSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS 238

Qy 248 SCDKT-HTCPP------CPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
Db 239 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDP 298

Qy 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
Db 299 DVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSP 358

Qy 361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
Db 359 IERTISKIKGLVRAPQVVILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTENY 418

Qy 421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db 419 KDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474

RESULT 10
Q91Z05
ID   Q91Z05
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.9 kDa protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.

RESULT 11

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RESULT 11
Q96PQ8
ID   Q96PQ8      PRELIMINARY;    PRT;   701 AA.
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21477448; PubMed=11593034;
RA   Hu Z., Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR   EMBL; AF272774; AAK58686.1; -.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   MGD; MGI:2144967; AU044919.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein_
SQ   SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;

Query Match             53.6%;  Score 1365.5;  DB 11;  Length 473;
Best Local Similarity   55.6%;  Pred. No. 8.5e-101;
Matches  265;  Conservative  70;  Mismatches 123;  Indels  19;  Gaps   6;

Qy    7 FLLLVAAPRWLSQVLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLE 66
          ||:|: :||||||    |||||||||| ||: :|:||  :||||
Db    9 FLVLII--KGVQCEVOLVESGGGGLVKPGGSRKLSCAASGFTFS-DYGMHWVRQAPEKGLE 65

Qy   67 WIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVG 126
           :|: :|| |||   :: :|:|||| | ::||  :|: :: | :|||||:| :|
Db   66 WVAYINSGSTTIYYADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARE------- 118

Qy  127 MVYNNWFDVWGPGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPEVTVS 186
             :: ||  ||:|:|:|||||| |||:||||      :|  ::||||||:||| |:||:
Db  119 -LWLRIDYWGQGTTITVSSAKTTPPSVYPLAPGCCGDTTGSSVTLGCLVKGYFPESVTVT 177

Qy  187 WNSGALTSGVHTFPAVLQSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP 246
         |||| |:| :||||| || |||:::|:|||||| | |:| : |||||   |:||||:||
Db  178 WNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEP 236

Qy  247 KSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
         |   : |:|||      |||| | ||||||:||||::||:|||| | |||||||||| :|
Db  237 SGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDD 296

Qy  300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
         | | :::|::: |||  |: :| :|||| ||||| | :|:||| :|| :|||| ||  ||
Db  297 PDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPS 356

Qy  360 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
         ||| |||| ||  | ||:|:||| : ::||| ||||||| | |  ||:|||:|||  ::|
Db  357 PIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEEN 416

Qy  420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||  ||||||||:|::|||| |: | ||:  :|||:|:||||:|:| :|:||:|:||
Db  417 YKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 473
```

RESULT 12

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RESULT 12
Q95M34
ID   Q95M34      PRELIMINARY;    PRT;   337 AA.
AC   Q95M34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Immunoglobulin gamma 1 heavy chain constant region
DE   (Fragment).
GN   IGHC1.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagner B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98383416; PubMed=9717671;
RA   Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA   Leibold W., Radbruch A.;
RT   "Organization of the equine immunoglobulin heavy chain constant region
RT   genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL   Immunobiology 199:105-119(1998).
DR   EMBL; AJ300675; CAC44624.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT   NON_TER   1    1
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   SMART; SM00181; EGF; 2.
DR   PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW   Hydrolase; Serine protease_
SQ   SEQUENCE   701 AA;  77826 MW;  94AC6CEB42CC992F CRC64;

Query Match             49.7%;  Score 1268;  DB 4;  Length 701;
Best Local Similarity   82.7%;  Pred. No. 9.1e-93;
Matches  244;  Conservative   4;  Mismatches  29;  Indels  18;  Gaps   3;

Qy  185 VSWNSGALTSGVHTFPAVLQSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS--NTKVD 241
         ||| |||  |||     ||:  | |      |:  :| ::|:|::  ::
Db  422 VSWGQGCATVG-------HFGVY-----TRVSQYIEWLQKLMRSEPRPGVLLRAPFP 466

Qy  242 KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 301
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  467 GSAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 526

Qy  302 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 361
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  527 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 586

Qy  362 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 421
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  587 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 646

Qy  422 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  647 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 701
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SQ   SEQUENCE   337 AA; 37438 MW; A6DBF2B01DEFD1F6 CRC64;

Query Match   49.5%; Score 1262.5; DB 6; Length 337;
Best Local Similarity   69.2%; Pred. No. 9e-93;
Matches 234; Conservative   42; Mismatches   53; Indels   9; Gaps   3;

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Qy  147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
              |||||:|:||||||||||||||||||||||||||||||||:||||||||||||||||||
Db    1  ASTTAPKVFALAPGCGTTSDSTVALGCLVSGYFPEPVKVSWNSGSLTSGVHTFPSVLQSS 60

Qy  207  GLYSLSSVVTVPSSSLGTGTYICNVNHKPSNTKVDKKAEP-----KSCDKTHTCPPCPA 260
              ||||:||||:||||  :|:  |||||:::|  ||||  :     ||:|||||||| ||
Db   61  GFYSLSSMTVPASTWTSETYICNVHAASNFKVDKRIEPIPDNHQKVCDMS-KCPKCPA 119

Qy  261  PELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 320
              ||||||||||||||||||||||||||||||||:|||  :||:|::|||||||||
Db  120  PELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTRP 179

Qy  321  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380
              :||||||||||:||||||||||||:|||||||||:|:|||||||||||| :||:
Db  180  KEEQFNSTYRVVSVLRIQHQDWLSGKEFCKVNNQALPQPIERTITKTKGRSQEPQVVVL 239

Qy  381  PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK 438
              ||:|||::||| |||  :||  ||:  |||||  |||||||||||||||||||||:
Db  240  APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQDSDGSYFLYSK 299

Qy  439  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
              |||||||||||||||||||||||||||||||||||||
Db  300  LSVDRNRWQQGTFTCGVMHEALHNHYTQKNVSKNPGK 337
```

RESULT 13
Q96EY0
ID   Q96EY0   PRELIMINARY;   PRT;   613 AA.
AC   Q96EY0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:20337).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-CELL;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011857; AAH11857.1; -.
DR   InterPro; IPR003598; Ig_C2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match   38.2%; Score 973; DB 4; Length 613;
Best Local Similarity   38.5%; Pred. No. 2.8e-69;
Matches 224; Conservative   75; Mismatches   163; Indels   120; Gaps   19;

```
Qy    1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYVGWIRQP 60
              |||||||||||||||||||||||||||||||||||||||||||||||:|||:||||||
Db    1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQP 59

Qy   61  PGKGLEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLSSVTAADTAVYYCVRDR 120
              |||||||||:|:|:  :::||||||||  ||:||||||||:|:||:||||||||||: :
Db   60  AGKGLEWIGRIY-TSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCASQP 118

Qy  121  L-FSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDY 178
              : :|  ||:  |:|  ||  |||||||  ::|  |||  |  |:|   |||||||||:|
Db  119  WELPTVGLFY------WGQGTLVTVSSGSASAPTLFPLVSCENSPDTSSVAVGCLAQDF 172
```

```
Qy  179  FPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL-GTQTY-ICNVNH 233
              |:|:|:|    |:|  ||||||||||||||||||||||  ||||:|   || :|||||
Db  173  LPDSITFSWKYKNNSDISSTRGFSVLR-GGKYAATSQVLLPSKDVMQGTDEHVVCKVQH 231

Qy  234  KPSN-------------TKVDKKAEPKS-----------CDKTHTCP---------- 256
              :                  ||:|  :              |||:|||
Db  232  PNGNKEKQNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGPSPRQIQVSWLREG 291

Qy  257  --------PCPAPELLGGPS------------ 268
                       |:
Db  292  KQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASS 351

Qy  269  --------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317
                        :|:|||||  :||| |||||||||||||||||||:::|:||||||||
Db  352  MCVPDQDTAIRVFAIPPS-FASIFLTKSTKLJTCLVTDLTTYD-SVTISWTRQNGEAVKTH 409

Qy  318  TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ 376
              |:||||||||||||:||||||||||||||:|||||||||||||||||||||||  |||
Db  410  TNISESHPNATFSAVGEASICEDDWNSGERFTCVTHTDLPSPLKQTISRPKGVALHRPD 469

Qy  377  VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG 431
              |:||| |:| | |||||||||||||||||||||||||||||  ||||||||||    ||
Db  470  VVLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG 529

Qy  432  SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
              : ||||||||||||||||||||||||||||||||||
Db  530  RYFAHSIITVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS 571
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RESULT 14
Q9BU10
ID   Q9BU10   PRELIMINARY;   PRT;   597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 65.3 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
HSSP; P01825; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IG; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA; 65274 MW; 2DAFA8PB7E055851 CRC64;

Query Match   37.2%; Score 948.5; DB 4; Length 597;
Best Local Similarity   37.5%; Pred. No. 2.4e-67;
Matches 219; Conservative   76; Mismatches   176; Indels   113; Gaps   17;

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Qy    1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db    1  MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFS-GYYWSWIRQP 59

Qy   61  PGKGLEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
              |||||||||:|  :: :|||||||  |||||||||||||||||:|:||:|||||||: :
Db   60  PGKGLEWIGEI-NHSGSTNYNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVI 118
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Best Local Similarity   37.5%;   Pred. No. 5.1e-67;
Matches 219;   Conservative   75;   Mismatches 177;   Indels 113;   Gaps   17;

Qy    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
          ||||||||||||||||||||||||||||    |||||||||  |||||  : ||:||||||
Db    1 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFS-GYYWSWIRQP 59

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
          ||||||||    :   . |||||||||||| ||| .||  |||:| ||:|||| ||::
Db   60 PGKGLEWIGEI-NHSGITNYNPSLKSRVTISVDTSKKQLSLSVNAADTAVYYCARVI 118

Qy  121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYF 179
          ||||||||||||||||||||||||  ||:||||  ||||:||||||| |||| |||||||
Db  119 TRASPGTDGRYGMDVWGQGTTVTVSSGSASAPTLFPLVSCENSPDTSSVAVGCLAQDFL 178

Qy  180 PEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHK 234
          |: :|||    .||  :|.  |.||  |.   ||:|::   .|.      ||| :  ||:|:||
Db  179 PDSITFSWKYKNNSDISSTRGFPSVLR-GGKYAATSQVLLPSKDVMQGTDEHVVCKVQHP 237

Qy  235 PSN--------------TKVDKKAEPKS------------CDKTHTCP----------- 256
          ||.               .|||:||| |.            ||||:||
Db  238 NGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGK 297

Qy  257 --------PCPAPELLGGPS----- 268
                  ||||||||||:
Db  298 QVGSGVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRGLTFQQNASSM 357

Qy  269 ----------VFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
                    :|||||||.|  ::|.|.||||||||  :|:|   ||.||.||  ::|:||.|
Db  358 CVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHT 415

Qy  319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV 377
          ||| :  :.|   ||.:|..  :  :|:||||   :|:|    |||:   :|::|||:  |    ..
Db  416 NISESHPNATFSAVGEASICEDDWNSGERFTCVTHTDLPSPLKQTISRPKGVALHRPDV 475

Qy  378 YTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGS 432
          |  ||| :::|   ||:|:|||::: |.|||:  ||||:..     ::|   .|.|.    |.|:
Db  476 YLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGR 535

Qy  433 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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Db  536 YFAHSILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK 579
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Search completed: March 29, 2003, 09:14:42
Job time : 45.1716 secs

Query Match   37.1%; Score 944.5; DB 4; Length 597;

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                  GenCore version 5.1.4_p5_4578
             Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:       March 29, 2003, 09:14:52 ; Search time 18.2478 Seconds
                                         (without alignments)
                                         1531.829 Million cell updates/sec

Title:        US-09-758-173-12
Perfect score: 2549
Sequence:     1 MKHLWFFLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters:        237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Database :   Published_Applications_AA:*
              1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
              2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
              3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
              4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
              5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
              6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
              7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
              8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
              9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
             10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
             11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
             12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
             13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
             14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result          %       Query Match
No.   Score   Match   Length  DB  Length  ID                       Description
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  1   2549    100.0    476    9    476    US-10-124-905-12          Sequence 12, Appl
  2   2549    100.0    476    9    476    US-09-948-429B-12         Sequence 12, Appl
  3   2309     90.6    476    9    476    US-10-124-905-4           Sequence 4, Appl
  4   2309     90.6    476    9    476    US-09-948-429B-4          Sequence 4, Appli
  5   2127     83.4    451    9    451    US-09-925-179-66          Sequence 66, Appl
  6   2126     83.3    451   10    451    US-09-920-171-18          Sequence 18, Appl
  7   2124     83.3    451    9    451    US-09-925-179-65          Sequence 65, Appl
  8   2124     83.3    451   10    451    US-09-920-171-14          Sequence 14, Appl
  9   2124     83.3    451   10    451    US-09-920-171-16          Sequence 16, Appl
 10   2122.5   83.3    450    9    450    US-09-996-288-218         Sequence 218, App
 11   2122.5   83.3    450    9    450    US-09-996-288-250         Sequence 250, App
 12   2122.5   83.3    450   10    475    US-09-796-848A-43         Sequence 43, Appl
 13   2122.5   83.3    475   10    475    US-09-740-002-25          Sequence 25, Appl
 14   2121     83.2    451    9    451    US-09-925-179-68          Sequence 68, Appl
 15   2120.5   83.2    450   10    450    US-09-996-288-216         Sequence 216, App
 16   2120.5   83.2    450    9    450    US-09-796-848A-49         Sequence 49, Appl
 17   2119.5   83.2    450    9    450    US-09-996-288-222         Sequence 222, App
 18   2119.5   83.2    450    9    450    US-09-996-288-224         Sequence 224, App
 19   2119.5   83.2    450   10    450    US-09-796-848A-39         Sequence 39, Appl
 20   2119.5   83.2    450   10    450    US-09-796-848A-41         Sequence 41, Appl
 21   2118.5   83.1    450   10    450    US-09-996-288-220         Sequence 220, App
 22   2118.5   83.1    450   10    450    US-09-796-848A-37         Sequence 37, Appl
 23   2117.5   83.1    450    9    450    US-09-996-288-226         Sequence 226, App
 24   2117.5   83.1    450    9    450    US-09-996-288-252         Sequence 252, App
 25   2117.5   83.1    450    9    450    US-09-996-288-254         Sequence 254, App
 26   2117.5   83.1    450    9    450    US-09-996-288-256         Sequence 256, App
 27   2117.5   83.1    450   10    450    US-09-796-848A-45         Sequence 45, Appl
 28   2116.5   83.0    450    9    450    US-09-996-288-232         Sequence 232, App
 29   2116.5   83.0    450    9    450    US-09-996-288-234         Sequence 234, App
 30   2116.5   83.0    450    9    450    US-09-996-288-236         Sequence 236, App
 31   2115.5   83.0    450    9    450    US-09-996-288-212         Sequence 212, App
 32   2115.5   83.0    450    9    450    US-09-996-288-214         Sequence 214, App
 33   2115.5   83.0    450   10    450    US-09-796-848A-51         Sequence 51, Appl
 34   2115.5   83.0    450   10    450    US-09-996-288-228         Sequence 228, App
 35   2114.5   83.0    450   10    450    US-09-796-848A-53         Sequence 53, Appl
 36   2114.5   83.0    450   10    450    US-09-796-848A-47         Sequence 47, Appl
 37   2112.5   82.9    450    9    450    US-09-996-288-238         Sequence 238, App
 38   2112.5   82.9    450    9    450    US-09-996-288-242         Sequence 242, App
 39   2112.5   82.9    450    9    450    US-09-996-288-244         Sequence 244, App
 40   2112.5   82.9    450    9    450    US-09-996-288-246         Sequence 246, App
 41   2106.5   82.6    450    9    450    US-09-996-288-210         Sequence 210, App
 42   2106.5   82.6    450    9    450    US-09-996-288-240         Sequence 240, App
 43   2105.5   82.6    450    9    450    US-09-996-288-208         Sequence 208, App
 44   2105.5   82.6    450    9    450    US-09-996-288-248         Sequence 248, App
 45   2095     82.2    451    9    451    US-09-996-288-230         Sequence 230, App
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ALIGNMENTS

```
RESULT 1
US-10-124-905-12

; Sequence 12, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION:  PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;  STREET:  699 Prince Street
;  CITY:  Alexandria
;  STATE:  VA
;  COUNTRY:  USA
;  ZIP:  22314
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE:  Floppy disk
;  COMPUTER:  IBM PC compatible
;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;  SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER:  US/10/124,905
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  09/383,916
;  FILING DATE:
;  APPLICATION NUMBER:  US 08/487,550
;  FILING DATE:  07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME:  Teskin, Robin L.
;  REGISTRATION NUMBER:  35,030
;  REFERENCE/DOCKET NUMBER:  012712-131
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE:  703-836-6620
;  TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  12:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH:  476 amino acids
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;     TYPE:  amino acid
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-10-124-905-12

Query Match             100.0%;     Score 2549;  DB 9;  Length 476;
Best Local Similarity   100.0%;     Pred. No. 2.6e-129;
Matches  476;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60
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Db      1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60

Qy     61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120

Qy    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
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Db    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180

Qy    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
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Db    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240

Qy    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
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Db    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300

Qy    301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
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Db    301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360

Qy    361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
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Db    361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420

Qy    421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
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Db    421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476


RESULT 2
US-09-948-429B-12
;  Sequence 12, Application US/09948429B
;  Patent No. US20020177689A1
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, Darrell R.
;     TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;     TITLE OF INVENTION:   TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;     TITLE OF INVENTION:   PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;     TITLE OF INVENTION:   IMMUNOSUPPRESANTS"
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;        STREET:  699 Prince Street
;        CITY:  Alexandria
;        STATE:  VA
;        COUNTRY:  USA
;        ZIP:  22314
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/09/948,429B
;        FILING DATE:
;        CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  09/383,916
;        FILING DATE:
;        APPLICATION NUMBER:   US 08/487,550
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;     FILING DATE:  07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;     NAME:  Teskin, Robin L.
;     REGISTRATION NUMBER:  35,030
;     REFERENCE/DOCKET NUMBER:  012712-131
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-836-6620
;     TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:   12:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  476 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;        MOLECULE TYPE:  protein
US-09-948-429B-12

Query Match             100.0%;     Score 2549;  DB 9;  Length 476;
Best Local Similarity   100.0%;     Pred. No. 2.6e-129;
Matches  476;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60
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Db      1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60

Qy     61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120

Qy    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180

Qy    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240

Qy    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300

Qy    301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360

Qy    361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420

Qy    421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476


RESULT 3
US-10-124-905-4
;  Sequence 4, Application US/10124905
;  Patent No. US20020166136A1
;  GENERAL INFORMATION:
;     APPLICANT:  Anderson, Darrell R.
;     TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;     TITLE OF INVENTION:   TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;     TITLE OF INVENTION:   PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;     TITLE OF INVENTION:   IMMUNOSUPPRESANTS"
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;        STREET:  699 Prince Street
;        CITY:  Alexandria
;        STATE:  VA
;        COUNTRY:  USA
;        ZIP:  22314
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
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;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/10/124,905
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 09/383,916
;  FILING DATE:
;  APPLICATION NUMBER: US 08/487,550
;  FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Teskin, Robin L.
;  REGISTRATION NUMBER: 35,030
;  REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 703-836-6620
;  TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 4:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 476 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-10-124-905-4

Query Match             90.6%;  Score 2309;  DB 9;  Length 476;
Best Local Similarity   91.2%;  Pred. No. 1.7e-116;
Matches  434;  Conservative    9;  Mismatches   33;  Indels    0;  Gaps    0;

Qy    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWIRQP 60
          ||||||||||||||||||| :||::|:|||    |||||| :|||||||:|||||||||:
Db    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT 60

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
          |:||||||: | |||||:||||||:|||||||||:|||||  :|||||||||||||:
Db   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120

Qy  121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

Qy  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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;  TITLE OF INVENTION: "IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;  STREET: 699 Prince Street
;  CITY: Alexandria
;  STATE: VA
;  COUNTRY: USA
;  ZIP: 22314
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/948,429B
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 09/383,916
;  FILING DATE:
;  APPLICATION NUMBER: US 08/487,550
;  FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Teskin, Robin L.
;  REGISTRATION NUMBER: 35,030
;  REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 703-836-6620
;  TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 4:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 476 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-09-948-429B-4

Query Match             90.6%;  Score 2309;  DB 9;  Length 476;
Best Local Similarity   91.2%;  Pred. No. 1.7e-116;
Matches  434;  Conservative    9;  Mismatches   33;  Indels    0;  Gaps    0;

Qy    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWIRQP 60
          ||||||||||||||||||| :||::|:|||    |||||| :|||||||:|||||||||:
Db    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT 60

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
          |:||||||: | |||||:||||||:|||||||||:|||||  :|||||||||||||:
Db   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120

Qy  121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

Qy  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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RESULT 4
US-09-948-429B-4
; Sequence 4, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

RESULT 5
US-09-925-179-66
; Sequence 66, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
;   FILE REFERENCE: P0718P2C1D1C1US
;   CURRENT APPLICATION NUMBER: US/09/925,179
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 08/466,163
;   PRIOR FILING DATE: 1995-06-06
;   PRIOR APPLICATION NUMBER: US 08/405,617
;   PRIOR FILING DATE: 1995-03-15
;   PRIOR APPLICATION NUMBER: US 08/185,899
;   PRIOR FILING DATE: 1994-01-26
;   PRIOR APPLICATION NUMBER: PCT/US92/06860
;   PRIOR FILING DATE: 1992-08-14
;   PRIOR APPLICATION NUMBER: US 07/879,495
;   PRIOR FILING DATE: 1992-05-07
;   PRIOR APPLICATION NUMBER: US 07/744,768
;   PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8a of Tabl
US-09-925-179-66

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Query Match       83.4%;  Score 2127; DB 9;  Length 451;
Best Local Similarity  87.6%;  Pred. No. 8.5e-107;
Matches  401;  Conservative  18;  Mismatches  31;  Indels  8;  Gaps  3;

Qy   20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY 79
Db    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI-TYDGSTN 59

Qy   80 YNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMYYNNW-FDVWGP 138
Db   60 YNPSLKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHY-----FGHWHFAVWGQ 113

Qy  139 GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
Db  114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173

Qy  199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
Db  174 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC 233

Qy  259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db  234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293

Qy  319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db  294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353

Qy  379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
Db  354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413

Qy  439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db  414 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 6
US-09-920-171-18 .

; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
;   APPLICANT: Lowman, Henry B.
;   APPLICANT: Presta, Leonard G.
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Lowe, John
;   TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;   FILE REFERENCE: P1123C2US
;   CURRENT APPLICATION NUMBER: US/09/920,171
;   CURRENT FILING DATE: 2001-08-01
;   PRIOR APPLICATION NUMBER: US 08/887,352
;   PRIOR FILING DATE: 1997-07-02
;   PRIOR APPLICATION NUMBER: US 09/296,005
;   PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

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Query Match       83.4%;  Score 2126; DB 10;  Length 451;
Best Local Similarity  87.6%;  Pred. No. 9.6e-107;
Matches  401;  Conservative  17;  Mismatches  32;  Indels  8;  Gaps  3;

Qy   20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY 79
Db    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI-KYSGETK 59

Qy   80 YNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMYYNNW-FDVWGP 138
Db   60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHY-----FGHWHFAVWGQ 113

Qy  139 GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
Db  114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173

Qy  199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
Db  174 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC 233

Qy  259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db  234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293

Qy  319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db  294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353

Qy  379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
Db  354 TLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413

Qy  439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db  414 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 7
US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
;   FILE REFERENCE: P0718P2C1D1C1US
;   CURRENT APPLICATION NUMBER: US/09/925,179
;   CURRENT FILING DATE: 2001-08-08
;   PRIOR APPLICATION NUMBER: US 08/466,163

; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Tabl
US-09-925-179-65

Query Match   83.3%; Score 2124; DB 9; Length 451;
Best Local Similarity   87.3%; Pred. No. 1.2e-106;
Matches 400; Conservative 19; Mismatches 31; Indels 8; Gaps 3;

Qy   20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY 79
           ||||| ||| | ||| ||::| ||||||:|:||:|||:|:||||||||| || :::|:|
Db   1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI-TYDGSTN 59

Qy   80 YNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNW-FDVWGP 138
           ||| | | | ||||:|||| ||:::|| ||||||| :: |||:|:|| ||:
Db   60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHY------FGHWHFAVWGQ 113

Qy   139 GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173

Qy   199 FPAVLQSSGLYLSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
           ||||||||||||||||||||||||||||||||||||||||||| ||:|||:||||||||
Db   174 FPAVLQSSGLYLSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC 233

Qy   259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293

Qy   319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353

Qy   379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
           ||||:|| || |||||||||||||||||||||||||||||||||||||||||||||||||
Db   354 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413

Qy   439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ||||||||||||||||||||||||||||||||||||||
Db   414 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 8
US-09-920-171-14
; Sequence 14, Application US/0920171
; Patent No. US2002005487BA1
; GENERAL INFORMATION:
;   APPLICANT: Lowman, Henry B.
;   APPLICANT: Presta, Leonard G.
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Lowe, John
;   TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;   FILE REFERENCE: P1123C2US
;   CURRENT APPLICATION NUMBER: US/09/920,171
;   CURRENT FILING DATE: 2001-08-01
;   PRIOR APPLICATION NUMBER: US 08/887,352
;   PRIOR FILING DATE: 1997-07-02
;   PRIOR APPLICATION NUMBER: US 09/296,005

; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match   83.3%; Score 2124; DB 10; Length 451;
Best Local Similarity   87.3%; Pred. No. 1.2e-106;
Matches 400; Conservative 19; Mismatches 31; Indels 8; Gaps 3;

Qy   20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY 79
           ||||| ||| | ||| ||::| ||||||:|:||:|||:|:||||||||| || :::|:|
Db   1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI-TYDGSTN 59

Qy   80 YNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNW-FDVWGP 138
           ||| | | | ||||:|||| ||:::|| ||||||| :: |||:|:|| ||:
Db   60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHY------FGHWHFAVWGQ 113

Qy   139 GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173

Qy   199 FPAVLQSSGLYLSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
           ||||||||||||||||||||||||||||||||||||||||||| ||:|||:||||||||
Db   174 FPAVLQSSGLYLSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC 233

Qy   259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293

Qy   319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353

Qy   379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
           ||||:|| || |||||||||||||||||||||||||||||||||||||||||||||||||
Db   354 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413

Qy   439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ||||||||||||||||||||||||||||||||||||||
Db   414 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US2002005487BA1
; GENERAL INFORMATION:
;   APPLICANT: Lowman, Henry B.
;   APPLICANT: Presta, Leonard G.
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Lowe, John
;   TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;   FILE REFERENCE: P1123C2US
;   CURRENT APPLICATION NUMBER: US/09/920,171
;   CURRENT FILING DATE: 2001-08-01
;   PRIOR APPLICATION NUMBER: US 08/887,352
;   PRIOR FILING DATE: 1997-07-02
;   PRIOR APPLICATION NUMBER: US 09/296,005
;   PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

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Query Match          83.3%;  Score 2124;  DB 10;  Length 451;
Best Local Similarity 87.3%;  Pred. No. 1.2e-106;
Matches 400;  Conservative 19;  Mismatches 31;  Indels 8;  Gaps 3;

Qy   20  QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY  79
         |||||||  :||:|||||||||||||||||  :|||||||||||||||||||
Db    1  EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI-TYDGSTN  59

Qy   80  YNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNW-FDVWGP  138
         |||:  :||:||   |||||:||||||  |  ||||   :  :|||
Db   60  YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHY------FGHWHFAVWGQ  113

Qy  139  GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  198
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  114  GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  173

Qy  199  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC  258
         ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db  174  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC  233

Qy  259  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  318
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  234  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  293

Qy  319  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  378
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  294  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  353

Qy  379  TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK  438
         ||||||  :||||||||||||||||||||||||||||||||||||||||||||||||
Db  354  TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK  413

Qy  439  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
         ||||||||||||||||||||||||||||||||||||||
Db  414  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  451
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RESULT 10
US-09-996-288-218
; Sequence 218, Application US/09996288
; Patent No. US2002017126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-218

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Query Match          83.3%;  Score 2122.5;  DB 9;  Length 450;
Best Local Similarity 87.3%;  Pred. No. 1.5e-106;
Matches 400;  Conservative 18;  Mismatches 31;  Indels 9;  Gaps 3;

Qy   20  QVQLQESGPGLVKPSETLSLTCAVSGGSIS-GGYGWGWIRQPPGKGLEWIGSFYSSSGNT  78
         |||||||  :||:|||||||||||||||   :||||||  |||||||||
Db    1  QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIW-WDGKK  59

Qy   79  YYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWPDVWGP  138
          :||:|||||||| |||||:|||:||||||||| |:|||
Db   60  HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD------MIFNWYFDVWGQ  112

Qy  139  GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  198
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  113  GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  172
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Qy 199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
         |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db 173 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC 232

Qy 259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 233 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 292

Qy 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 293 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 352

Qy 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
         |||||| :||||||||||||||||||||||||||||||||||||||||||||||||
Db 353 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 412

Qy 439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||||||||||||||||||||||||||||||||||||||
Db 413 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450

RESULT 11
US-09-996-288-250
; Sequence 250, Application US/09996288
; Patent No. US2002017126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophyl
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-250

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Query Match          83.3%;  Score 2122.5;  DB 9;  Length 450;
Best Local Similarity 87.3%;  Pred. No. 1.5e-106;
Matches 400;  Conservative 18;  Mismatches 31;  Indels 9;  Gaps 3;

Qy   20  QVQLQESGPGLVKPSETLSLTCAVSGGSIS-GGYGWGWIRQPPGKGLEWIGSFYSSSGNT  78
         |||||||  :||:|||||||||||||||   :||||||  |||||||||
Db    1  QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIW-WDGKK  59

Qy   79  YYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWPDVWGP  138
          :||:|||||||| |||||:|||:||||||||| |:|||
Db   60  HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD------MIFNWYFDVWGQ  112

Qy  139  GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  198
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  113  GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  172

Qy  199  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC  258
         ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db  173  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC  232

Qy  259  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  318
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  233  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  292

Qy  319  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  378
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  293  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  352

Qy  379  TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK  438
         ||||||  :||||||||||||||||||||||||||||||||||||||||||||||||
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Db  353 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 412
            |||||||||||||||||||||||||||||||||||||||||
Qy  439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            ||||||||||||||||||||||||||||||||||||||
Db  413 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450
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RESULT 12
US-09-796-848A-43
; Sequence 43, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; TITLE OF INVENTION: Producing Them
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SEQ ID NO 43
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-43

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Query Match             83.3%;   Score 2122.5;  DB 10;  Length 450;
Best Local Similarity   87.3%;   Pred. No. 1.5e-106;
Matches 400; Conservative 18; Mismatches 31; Indels 9; Gaps 3;

Qy   20 QVQLQESGPGLVKPSETLSLTCAVSGGSIS-GGYGWGWIRQPPGKGLEWIGSFYSSSGNT 78
Db    1 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIW-WDGKK 59

Qy   79 YYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWFDVWGP 138
Db   60 HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD------MIFNWYFDVWGQ 112

Qy  139 GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
Db  113 GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 172

Qy  199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
Db  173 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC 232

Qy  259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db  233 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 292

Qy  319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db  293 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 352

Qy  379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
Db  353 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 412

Qy  439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db  413 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450
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RESULT 13

US-09-740-002-25
; Sequence 25, Application US/09740002
; Patent No. US2002001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 25
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-25

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Query Match             83.3%;   Score 2122.5;  DB 10;  Length 475;
Best Local Similarity   86.4%;   Pred. No. 1.5e-106;
Matches 406; Conservative 20; Mismatches 41; Indels 3; Gaps 3;

Qy    8 LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISG-GYGWGWIRQPPGKGLE 66
Db    8 LFLVAVATRVLSQVQLQESGPVVKPTETLLTLTCTVSGFSLSNPRMGVTWIRQPPGKALE 67

Qy   67 WIGSFYSSGNTYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVG 126
Db   68 WLGNIFSSDEKS-FSPSLKSRLTTSQDTSRSQVVLSLTNVDPVDTATYYCARVGLYD-IN 125

Qy  127 MVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 186
Db  126 AYYLYYLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 185

Qy  187 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP 246
Db  186 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP 245

Qy  247 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 306
Db  246 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 305

Qy  307 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 366
Db  306 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 365

Qy  367 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 426
Db  366 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 425

Qy  427 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db  426 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
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RESULT 14
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163

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; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-216

Query Match              83.2%;   Score 2120.5;  DB 9;  Length 450;
Best Local Similarity    87.3%;   Pred. No. 1.9e-106;
Matches 400;  Conservative  18;  Mismatches  31;  Indels  9;  Gaps  3;

Qy    20  QVQLQESGPGLVKPSETLSLTCAVSGGSIS-GGYGWGWIRQPPGKGLEWIGSFYSSSGNT  78
              ||:|||||:||||: :||:|:||||:         ::|||||||||: |||| : :
Db     1  QVTLRESGPALVKPTQTLTLTCTFSGFSLSTPGMSVGWIRQPPGKALEWLADIW-WDGKK  59

Qy    79  YYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMYNNWFDVWGP  138
              :||||||:: ::|:|||||:::|:|:: :||:|||  ::|    :|||:|:|||||
Db    60  HYNPSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD------MIFNWYFDVWGQ  112

Qy   139  GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  198
              | :|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113  GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  172

Qy   199  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC  258
              ||||||||||||||||||||||||||||||||||||||||||:|||:|||||||||||
Db   173  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC  232

Qy   259  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  292

Qy   319  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  352

Qy   379  TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK  438
              ||||||:: ||||||||||||||||||||||||||||||||||||||||||||||||
Db   353  TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK  412

Qy   439  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
              ||||||||||||||||||||||||||||||||||||||
Db   413  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  450

Search completed: March 29, 2003, 09:38:44
Job time : 19.2478 secs
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; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table
US-09-925-179-68

Query Match    83.2%;    Score 2121;  DB 9;  Length 451;
Best Local Similarity  87.6%;  Pred. No. 1.8e-106;
Matches 401;  Conservative  17;  Mismatches  32;  Indels  8;  Gaps  3;

Qy    20  QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY  79
              :||||||:  ::|:||||  :  ||| :  ||| |:|||| :||  ||| : |:
Db     1  EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWMGSI-TYDGSTN  59

Qy    80  YNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMYNNW-FDVWGP  138
              |:..:|:                 :    :|||||      :|    ||||||
Db    60  YNDSLKGRITVSRDDSKNTFYLQLNSARAEDTAVYYCARGSHY-----FGHWHFAVWGQ  113

Qy   139  GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  198
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   114  GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT  173

Qy   199  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC  258
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   174  FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC  233

Qy   259  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   234  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT  293

Qy   319  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   294  KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  353

Qy   379  TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK  438
              ||||||:: ||||||||||||||||||||||||||||||||||||||||||||||||
Db   354  TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK  413

Qy   439  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
              ||||||||||||||||||||||||||||||||||||||
Db   414  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  451
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OM nucleic - nucleic search, using sw model

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Run on: April 5, 2003, 19:13:05 ; Search time 4490.25 Seconds
                                         (without alignments)
                                         9274.790 Million cell updates/sec

Title: US-09-758-173-11
Perfect score: 1431
Sequence: 1 ATGAAACACCTGTGGTTCTT..........CCCTGTCTCCGGGTAAATGA 1431
Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
     1: gb_ba:*
     2: gb_htg:*
     3: gb_in:*
     4: gb_om:*
     5: gb_ov:*
     6: gb_pat:*
     7: gb_ph:*
     8: gb_pl:*
     9: gb_pr:*
    10: gb_ro:*
    11: gb_sts:*
    12: gb_sy:*
    13: gb_un:*
    14: gb_vi:*
    15: em_ba:*
    16: em_fun:*
    17: em_hum:*
    18: em_in:*
    19: em_mu:*
    20: em_om:*
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    27: em_sts:*
    28: em_un:*
    29: em_vi:*
    30: em_htg_hum:*
    31: em_htg_inv:*
    32: em_htg_other:*
    33: em_htg_mus:*
    34: em_htg_pln:*
    35: em_htg_rod:*
    36: em_htg_mam:*
    37: em_htg_vrt:*
    38: em_sy:*
    39: em_htgo_hum:*
    40: em_htgo_mus:*
    41: em_htgo_other:*

                              SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1431	100.0	1431	6	AR108867	AR108867 Sequence
2	1315.8	91.9	1431	6	AR108863	AR108863 Sequence
3	1276.4	89.2	1567	6	AR135359	AR135359 Sequence
4	1261.2	88.1	1431	6	E10697	E10697 cDNA encodi
5	1256.8	87.8	1594	9	AK057754	AK057754 Homo sapi
6	1251.6	87.5	1596	9	AK098516	AK098516 Homo sapi
7	1236.8	86.4	1589	9	AK057775	AK057775 Homo sapi
8	1224.8	85.6	1418	6	A49389	A49389 Sequence 7
9	1213.6	84.8	1418	6	AR176296	AR176296 Sequence
10	1182.8	82.7	1566	9	AK097365	AK097365 Homo sapi
11	1181	82.5	1404	6	AR135375	AR135375 Sequence
12	1177.8	82.3	1404	6	AR135377	AR135377 Sequence
13	1176.2	82.2	1404	6	AR135376	AR135376 Sequence
14	1142.6	79.8	1630	9	BC024289	BC024289 Homo sapi
15	1134.8	79.3	1428	6	AR031184	AR031184 Sequence
16	1134.8	79.3	1428	6	AR042589	AR042589 Sequence
17	1134.8	79.3	1428	6	AR059282	AR059282 Sequence
18	1134.8	79.3	1428	6	AR076260	AR076260 Sequence
19	1134	79.2	1430	6	AX419496	AX419496 Sequence
20	1134	79.2	1673	9	HSIG1LH	Y14737 Homo sapien
21	1133.8	79.1	1507	6	BD000501	BD000501 Process f
22	1131.8	79.0	1679	9	BC018747	BC018747 Homo sapi
23	1130.6	79.0	1633	9	AK097859	AK097859 Homo sapi
24	1125.2	78.6	1428	6	AR031186	AR031186 Sequence
25	1125.2	78.6	1428	6	AR042591	AR042591 Sequence
26	1125.2	78.6	1428	6	AR059284	AR059284 Sequence
27	1125.2	78.6	1428	6	AR076262	AR076262 Sequence
28	1122.8	78.5	1599	6	AX330501	AX330501 Sequence
29	1122.8	78.5	1599	6	AX333307	AX333307 Sequence
30	1122.8	78.5	1599	6	AX334122	AX334122 Sequence
31	1122.8	78.5	1599	9	HUMIGHEPAH	M87789 Human (hybr
32	1122.8	78.5	3143	9	BC019046	BC019046 Homo sapi
33	1122	78.4	1990	9	AK098817	AK098817 Homo sapi
34	1121.2	78.4	1549	6	A21385	A21385 Plasmid DNA
35	1121.2	78.4	1617	9	A29585	A29585 H.sapiens c
36	1116.2	78.0	1624	9	HSIG1KH	Y14735 Homo sapien
37	1115.6	78.0	1359	9	MACIGHVCDR	L13307 Macaca fasc
38	1114	77.8	1631	9	AK097010	AK097010 Homo sapi
39	1112.4	77.7	1437	6	AR108865	AR108865 Sequence
40	1112	77.7	1666	9	BC006402	BC006402 Homo sapi
41	1108.2	77.4	1628	9	AK097361	AK097361 Homo sapi
42	1107.6	77.4	1633	9	AK097367	AK097367 Homo sapi
43	1106.2	77.3	1341	6	A07562	A07562 DNA sequenc
44	1103.8	77.1	1668	9	BC026038	BC026038 Homo sapi
45	1102.2	77.0	6557	6	I26929	I26929 Sequence 3

                              ALIGNMENTS

RESULT 1
AR108867
LOCUS   AR108867   1431 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6113898.
ACCESSION   AR108867
VERSION   AR108867.1 GI:12825143
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1431)
  AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE   Human B7.1-specific primatized antibodies and transfectomas
            expressing said antibodies
  JOURNAL   Patent: US 6113898-A 11 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

FEATURES   Location/Qualifiers
     source   1..1431
                  /organism="unknown"
BASE COUNT   319 a   462 c   385 g   265 t
ORIGIN

Query Match   100.0%;   Score 1431; DB 6; Length 1431;
Best Local Similarity   100.0%;   Pred. No. 4.5e-279;
Matches 1431;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy     1 ATGAAACACCTGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGAAACACCTGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60

Qy    61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGACACCCTGTCCTCACC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGACACCCTGTCCTCACC 120

Qy   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180

Qy   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGAACACCTACTAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGAACACCTACTAC 240

Qy   241 AACCCCCTCCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AACCCCCTCCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300

Qy   301 CTGAAGCTGACTCTATGACCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGAAGCTGACTCTATGACCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360

Qy   361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGAGTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGAGTC 420

Qy   421 CTGGTCACCGTCTCCTCAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGGTCACCGTCTCCTCAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 480

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGCGCCGTGCACACCTTCCCG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAACCGGTGACGGTGTCGTGGAACTCAGCGCCGTGCACACCTTCCCG 600

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGC 660

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAACAAGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAACAAGGTG 720

Qy   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
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Db   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
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Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC 1080

Qy  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1431
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RESULT 2
AR108863
LOCUS   AR108863   1431 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6113898.
ACCESSION   AR108863
VERSION   AR108863.1 GI:12825139
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1431)
  AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE   Human B7.1-specific primatized antibodies and transfectomas
            expressing said antibodies
  JOURNAL   Patent: US 6113898-A 3 05-SEP-2000;
FEATURES   Location/Qualifiers
     source   1..1431
                  /organism="unknown"
BASE COUNT   322 a   469 c   380 g   260 t
ORIGIN

Query Match   91.9%;   Score 1315.8; DB 6; Length 1431;
Best Local Similarity   95.0%;   Pred. No. 8.5e-256;
Matches 1359;   Conservative   0;   Mismatches   72;   Indels   0;   Gaps   0;

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Qy     1 ATGAAACACCTGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGAAACACCTGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60

Qy    61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
          | || || |||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTGAAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180
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Db   121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTGGTTACTACTGGAGCTGGATCAGCCAGACC 180

Qy   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGAACACCTACTAC 240
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Db   181 CCAGGGAAGGGGCTGGAGTGGATTGGGT 181
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Qy 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
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Qy 1381 CTGCACAACCACTACACGCAGAGAGAGCCTCTCCCCGTCTCCGGGTAAATGA 1431
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Db 1381 CTGCACAACCACTACACGCAGAGAGAGCCTCTCCCCGTCTCCGGGTAAATGA 1431
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RESULT 3
AR135359
LOCUS   AR135359   1567 bp   DNA   linear   PAT 16-JUN-2001
DEFINITION   Sequence 17 from patent US 6135941.
ACCESSION   AR135359
VERSION   AR135359.1 GI:14476031
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1567)
  AUTHORS   Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J.,
             Corley,N.C., Guegler,K.J. and Baughn,M.R.
  TITLE   Human immune system associated molecules
  JOURNAL   Patent: US 6135941-A 17 24-OCT-2000;
FEATURES   Location/Qualifiers
     source   1..1567
                     /organism="unknown"
BASE COUNT   346 a   503 c   428 g   289 t   1 others
ORIGIN

Query Match   89.2%; Score 1276.4; DB 6; Length 1567;
Best Local Similarity 94.7%; Pred. No. 7.8e-248;
Matches 1358; Conservative 61; Mismatches 0; Indels 15; Gaps 3;

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Qy   1 ATGAAACACCTGTTGTTCTTCCTCCTCCTGGTTGCCAGCTCCCAGATGGGTCCTGTCCCAG 60
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Db  78 ATGAAAACACCTGTTGTTCTTCCTCCTCGTGTGGGCCAGCTCCCAGATGGGTCCTGTCCCAG 137

Qy  61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 138 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 197

Qy 121 TGCGCTGTCTCTGGTGGCTCCATC---AGCGGTGGTTATGGCTGGTGGATCCGCCAGCCAG 177
       ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db 198 TGCGCTGTCTCTGGTGGCTCCATCACTAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCAG 257

Qy 178 CCCCCAGGGAAGGGGCTGGAGTGGATTGGGGTTCTATAGTAGTAGTGGGAACACCTAC 237
       ||||||||||||||||||||||||||||||||| ||| |||   ||||  ||||||
Db 258 CCCCCAGGGAAGGGGCTGGAGTGGATTGGGGTTTATCTA---TTACAGTGGGAGCACCCTC 314

Qy 238 TACAACCCCTCCCTCAAGAGTCGAGTCACCATTTCAACAGACAGTCAGTC 297
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Db 315 TACAACCCCTCCCTCAAGAGTCGAGTCAGTATCAGTAATCAGTAGACAGTC 374

Qy 298 TCCCTGAAGCTGAACTCTATGACCGCCGCGACACGGCCGTGTATTACTGTGTGAGAGAT 357
       |||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db 375 TCCCTGAAGCTGAACTCTGTGACTGCCGCGACACGGCCGTGTATTACTGTGCCAGAGA- 433

Qy 358 CGTCTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGGGGCCCGGGA 417
       |||||||||                |||||||| ||||||||||||||||||
Db 434 ------TGACGTAGTTTAAGGGGGGAACTACGGATGGGGGGCCCAGGGA 485

Qy 418 GTCCTTCGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACC 477
       |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 486 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACC 545

Qy 478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 537
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 546 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 605

Qy 538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
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TITLE      HUMAN MONOCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR
           CLONING OF GENE THEREOF
JOURNAL    Patent: JP 1996038178-A 20 13-FEB-1996;
           TANAKA HIDEYUKI, NISSHINBO IND INC
COMMENT    OS   Homo sapiens (human)
           PN   JP 1996038178-A/20
           PD   13-FEB-1996
           PF   20-FEB-1995 JP 1995010742
           PR   18-FEB-1994 JP 94P 21628
           PI   TANAKA SHIGEAKI, NIWA HIRONUKI, TANAKA HIDEYUKI PC
           C12N15/09,C07K16/08,C12N1/21,C12N15/02,C12P21/08,C12Q1/68, PC
           G01N33/53,
           PC   G01N33/531,G01N33/577,(C12N1/21,C12R1:19),(C12N1/21,C12R1:19),(C12P21/08, PC
           C12R1:19);
           CC   strandedness: Single;
           CC   topology: Linear;
           CC   hypothetical: No;
           CC   anti-sense: No;
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           FT                    antibody against human cytomegalovirus 65kD
           FT                    antigen'
           FT   mat_peptide      58..1425
           FT                    /product='heavy chain of human monoclonal  FT
                                 antibody against
           FT                    human cytomegalovirus 65kD antigen'  FT  CDS
           FT                    1..1428
           FT                    /product='heavy chain of human monoclonal  FT
                                 antibody against
           FT                    human Cytomegalovirus 65kD antigen'  FT  3'UTR
           FT                    1429..>1431
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ORIGIN

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Best Local Similarity  93.9%;  Pred. No. 9.2e-245;
Matches 1347;  Conservative 0;  Mismatches 78;  Indels 9;  Gaps 3;

Qy    1 ATGAAACACCTGTGGTTCTTCCTCCTCGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG   60
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Db    1 ATGAAGCATCTGTGTTCTTCCTCCTCGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG   60

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Qy  121 TGCGCTGTCTCTGGTGGCTCCATCAGC---GGTGGTTATGGCTGGGGCTGGATCCGCCAG  177
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Db  121 TGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTGGTTACTCCTGGGGCTGGATCCGCCAG  180

Qy  178 CCCCCAGGGAAGGGGCTGGAGTGGATTGGGTAGTAGTAGTGGAACCTAC            237
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Db  181 CCCCCGGGGAAGGGGCTGGAGTGGATTGGGACTATCA---TTATAGTGGGAGCACCTAC  237

Qy  238 TACAACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTC  297
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Qy  298 TCCCTGAAGCTGAACTCTATGACCGCCGGGACACGGCCGTGTATTACTGTGTGAGAGAT  357
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Db  298 TCCCTGAAGCTGAGCTCTGTGACCGCCGCCGCAGCAGGCGCTGTGTATTACTGTGCGAGAACC  357

Qy  358 CGTCTTTTTCAGTGTGTGGAATGGTTACAACAACTGGTTCGATGTCTGGGGCCCCGGGA  417
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Qy  598 CCGGCTGCCTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  657
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Db  666 CCGGCTGCCTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  725

Qy  658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  717
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Db  726 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  785

Qy  718 GTGGACAAGAAAGCAGAGAGCCAAATCTTGTGACAAAATCACACATGCCCACCGTGCCCA  777
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Qy  778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  837
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Qy  958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC  1017
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Db 1086 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC  1145

Qy 1078 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC  1137
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Qy 1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA  1197
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Qy 1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1257
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Db 1266 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1325

Qy 1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC  1317
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Qy 1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA       1431
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RESULT 4
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LOCUS       AK057754                1594 bp    mRNA    linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens cDNA FLJ25025 fis, clone CBL01928, highly similar to
            Ig gamma immunoglobulin heavy chain.
ACCESSION   AK057754
VERSION     AK057754.1  GI:16553681
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL01928.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
            Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M.,
            Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
            Sugano,S.
TITLE       NEDO human cDNA sequencing project
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1594)
AUTHORS     Sugano,S. and Suzuki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure, Human Genome
            Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
            (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction and 5'-end one pass sequencing: Institute of Medical
            Science, University of Tokyo, Laboratory of Genome Structure, Human
            Genome Center; 3'-end one pass sequencing: RAB; clone selection for
            full insert sequencing: RAB and Helix Research Institute.
FEATURES             Location/Qualifiers
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                     VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFL
                     FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
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                     TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
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BASE COUNT    338 a    532 c    437 g    287 t
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Query Match             87.8%;  Score 1256.8;  DB 9;  Length 1594;
Best Local Similarity   93.8%;  Pred. No. 7.1e-244;
Matches 1345;  Conservative    0;  Mismatches    0;  Indels   12;  Gaps    3;

Qy       1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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Db     358 TCGCCGCAGTATTACGATCTTTGACTGGTT---CCTTTCCCTCATACTGGGCTCAGGGA 414
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Qy     418 GTCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 477
Db     415 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCC 474

Qy     478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 537
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Db     475 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 534

Qy     538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
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Db     535 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 594

Qy     598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 657
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Db     595 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 654

Qy     658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAACCAAG 717
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Db     655 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAACCAAG 714

Qy     718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
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Db     715 GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 774

Qy     778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 837
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Qy     898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
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Qy     958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
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Db     955 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1014

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Db    1135 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1194

Qy    1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
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Db    1195 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1254

Qy    1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317
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Qy    1318 ACGGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377
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Qy    1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db    1375 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428

RESULT 5
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Db   1227 GGCTTCTATCCAGCAGCACATGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAAC 1286
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Qy   1258 TACAAGACCACGCCTCCGTGCTGGACTCCGACGGCTCCTTCCTCTCCTACACGCAAGCTC 1317
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Db   1287 TACAAGACCACGCCTCCGTGCTGGACTCCGACGGCTCCTTCCTCTCCTACACGCAAGCTC 1346
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Qy   1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377
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Db   1347 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1406
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Qy   1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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RESULT 6
AK098516
LOCUS   AK098516   1596 bp   mRNA   linear   PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ25650 fis, clone SYN01104, highly similar to
            Ig gamma =immunoglobulin heavy chain.
ACCESSION   AK098516
VERSION   AK098516.1 GI:21758543
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens synovial membrane (knee) cDNA to mRNA, clone_lib:SYN
            clone:SYN01104.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S.,
            Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
            Sugano,S.
  TITLE   NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1596)
  AUTHORS   Sugano,S. and Suzuki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure, Human Genome
            Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
            (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction and 5'-end one pass sequencing: Institute of Medical
            Science, University of Tokyo, Laboratory of Genome Structure, Human
            Genome Center; 3'-end one pass sequencing: RAB; clone selection for
            full insert sequencing: RAB and Helix Research Institute.
FEATURES   Location/Qualifiers
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                     /clone="SYN01104"
                     /tissue_type="synovial membrane (knee)"
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                     /note="cloning vector: pME18SFL3"
BASE COUNT   342 a   540 c   426 g   288 t
ORIGIN

Query Match   87.5%; Score 1251.6; DB 9; Length 1596;
Best Local Similarity 93.5%; Pred. No. 7.9e-243;
Matches 1341; Conservative   0; Mismatches   84; Indels   9; Gaps   3;

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Db   36 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCGTGTCCCAG 95
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Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Db   156 TGCAGTGTCTCTGGTGACTCCATCGCCACAACTGCCTATTTCTGGGGTGGTTCCGCCAG 215
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Qy   178 CCCCCAGGGAAGGGGCTGGAGTGGGTTCTATAGTAGTAGTGGTGGAACACCTAC 237
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Db   216 CCCCCAGGGAAGGGACTGCAATTTATAGGGAGTGTGTA---TTATACTGGACCGGCCCAC 272
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Qy   238 TACAAACCCTCCCTCAAGAGTCAAGTCAACAGACACGTCCAAGAACCAGTTC 297
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Db   273 CACAACCCGTCCCTCAAGAGCGCCGAGTCACCAGATCCGCAGACGTCCAAGGCCCAGTTC 332
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Qy   358 CGTCTTTTTCAGTTGTTGGAATGGTTTTACAACAACTGGTTCGATGTCTCGGGGCCCGGGA 417
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Qy   598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 657
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Qy   658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
          |||||||||||||||||||||||||||| |||||||||||||| |||||||||||||||
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Qy   718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
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Qy   778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 837
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Qy   838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
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Db   1047 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1106
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Qy   1078 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1137
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
          |||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||
Db   1167 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1226
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
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Db    96 GTGCAACTGACGGAGTCCGGCTCAGGACTGGTGAGGCCTTCACAGACTCGTCTCCCTCACC 155
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Qy   121 TGGCTGTCTCGTGGGTGGCTCCAT---CAGCGGTGGTTATGCGTGGGGCTGGATCCGCCAG 177

Db   156 TGGCTGTCTTCTGTGACTCCATCATCCAGTGTGCTCACTCCGGAGTCAGTAGTGGCACCTA 215
          |||||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||
Qy   178 CCCCAGGGAAGGGGCTCGAGTGGATGGGAGTTTCTATAGTAGTAGTGGGAACACCTAC 237

Db   216 CCACCAGGGAAGGGGCCTGGAGTGGATTGGCTACGTCTA---TCTCAGTGGGCACCTCT 272
          |||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Qy   238 TACAACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTC 297

Db   273 TACAATCCGTCCCTCAAGAGTCGACTGACCATCAGTAGACAGGTCCAACAACCAGTTC 332
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Qy   298 TCCCTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGAT 357

Db   333 TCCCTGAGGTTGACCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGGG 392

Qy   358 CGTCTTTTTCAGTGTTGTGGAATGGTTACAACAACTGGTTCGATGTCTGGGGCCCGGGA 417
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Qy   418 GTCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 477
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Qy   478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 537
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Qy   538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
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Qy   598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 657
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Db   630 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 689

Qy   658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
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Db   690 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 749

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Db   750 GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 809

Qy   778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 837
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Qy   898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
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Db   990 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1049

Qy  1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
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Db  1050 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1109

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Db  1170 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1229
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Qy  1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257

Db  1230 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1289
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Qy  1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317

Db  1290 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1349
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Qy  1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377

Db  1350 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1409
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Qy  1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431

Db  1410 GGTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1463
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RESULT 7
AK057775

LOCUS   AK057775   1589 bp   mRNA   linear   PRI 26-MAR-2002
DEFINITION   Homo sapiens cDNA FLJ25046 fis, clone CBL03624, highly similar to
             Ig gamma immunoglobulin heavy chain.
ACCESSION   AK057775
VERSION   AK057775.1 GI:16553709
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL03624.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
             Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M.,
             Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
             Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
             Sugano,S.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1589)
AUTHORS   Sugano,S. and Suzuki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
             University of Tokyo, Laboratory of Genome Structure, Human Genome
             Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
             (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
             Fax:81-3-5449-5416)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
             Economy, Trade and Industry of Japan; cDNA full insert sequencing:
             Research Association for Biotechnology (RAB); cDNA library
             construction and 5'-end one pass sequencing: Institute of Medical
             Science, University of Tokyo, Laboratory of Genome Structure, Human
             Genome Center; 3'-end one pass sequencing: RAB; clone selection for
             full insert sequencing: RAB and Helix Research Institute.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CBL03624"
                     /tissue_type="cerebellum"
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                     /note="cloning vector: pME18SFL3"
BASE COUNT   338 a   532 c   430 g   289 t
ORIGIN

Query Match   86.4%; Score 1236.8; DB 9; Length 1589;
Best Local Similarity   93.0%; Pred. No. 7.8e-240;
Matches 1334; Conservative 0; Mismatches 82; Indels 18; Gaps 3;

Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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Db   38 ATGAAGCAGATGTGGTTCTTCCTCCTGCTGCTGGCGGCTCCCAGATGGGTCCTGTCCCAG 97
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Qy   1138  CTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA  1197
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Db   1163  CTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA  1222

Qy   1198  GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1257
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Db   1223  GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1282

Qy   1258  TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC  1317
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Db   1283  TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC  1342

Qy   1318  ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG  1377
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Db   1343  ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG  1402

Qy   1378  GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
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Db   1403  GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1456
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RESULT 8
A49389

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LOCUS       A49389                  1418 bp    DNA         linear   PAT 07-MAR-1997
DEFINITION  Sequence 7 from Patent WO9607740.
ACCESSION   A49389
VERSION     A49389.1    GI:2302866
KEYWORDS    .
SOURCE      unidentified.
ORGANISM    unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1418)
  AUTHORS   Edelman,L., Margaritte,C., Kaczorek,M. and Chaabihi,H.
  TITLE     MONOCLONAL RECOMBINANT ANTI-RHESUS D (D7C2) ANTIBODY
  JOURNAL   Patent: WO 9607740-A 7 14-MAR-1996;
            PASTEUR INSTITUT (FR)
COMMENT     Other publication FR 2724182 960308.
FEATURES             Location/Qualifiers
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BASE COUNT      333 a    458 c    378 g    249 t
ORIGIN

Query Match     85.6%;  Score 1224.8;  DB 6;  Length 1418;
Best Local Similarity   93.0%;  Pred. No. 2.1e-237;
Matches 1319;  Conservative    0;  Mismatches   87;  Indels  12;  Gaps   3;

Qy     13  TGGTTCTTCCTCCTCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGCTGCAGCTGCAG  72
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Db     13  TGTATCATCCTCTTCTTGGTGGCAACAGCTACAGGTGTCCCACTCCCAACTGCAG  72

Qy     73  GAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCT  132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73  CAGTCGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTAT  132
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Qy     61  GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120
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Db     98  CTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  157

Qy    121  TGCGCTGTCTGTGGTGGCTCCAT---CAGCGGTGGTTATGGCTGGAGCTGGATCCGCCAG  177
           ||||||||| |||||||||||||   |||||||||||||||||||||||||||||||||
Db    158  TGCGCTGTGTGTGGTGGCTCCATTCCATTACCAGCAATGATTACTGCTGGAGCTGGATCCGCCAG  217

Qy    178  CCCCCAGGGAAGGGGCTGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGAACACCTAC  237
           |||||||||||||              |||||||||
Db    218  CCCCCAGGGAAGGGGCTGGAGTGGTGTTTGGATGTCTC------AATGACGGGGCCACCTAC  271

Qy    238  TACAACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTC  297
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Db    272  TACGAGCCGTCCCTCGGGAGTCGAGTCGAGTCCACATATCCGCAGAGACGTCCAAGAACCAATTC  331

Qy    298  TCCCTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGAT  357
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Db    332  TCCCTGAGGCTGAACTCCGTGCGGCTGCGGGACACGGCCGTGTATTATTGTGCGAGTCTC  391

Qy    358  CGTCTTTTTTCAGTTGTTGTGAATGTTTACAACAACTGGTTCGATGTCTCGGGCCCGGGA  417
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Db    392  CGTGTTTTCCAGGGGTTCGGGAGTCCCTTTC-------TTTGACTTCTGGGGCCAGGGG  442

Qy    418  GTCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  477
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Db    443  ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  502

Qy    478  TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  537
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Db    503  TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  562

Qy    538  CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  597
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Db    563  CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  622

Qy    598  CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  657
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Db    623  CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  682

Qy    658  AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  717
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Db    683  AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  742

Qy    718  GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA  777
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Qy    778  GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  837
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Db    803  GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  862

Qy    838  CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  897
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Db    863  CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  922

Qy    898  CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG  957
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Db    923  CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG  982

Qy    958  CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC  1017
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Db    983  CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC  1042

Qy   1018  CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC  1077
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Db   1043  CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC  1102

Qy   1078  CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC  1137
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Db   1103  CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC  1162
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Db  1201  GACATGCCCTGGAGTGGGAGGAGCAATGGCAGCCGGAGAACAACTACAAGACCACGCCT 1260
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Qy  1273  CCCGTGCTGACTCCGACGCGCTCCTTCCTTCTTCCTCTACAGCAAGCAAGCTCACCGTGACAAGAGC 1332
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Qy  1393  TACACGCAGAAGAGCCTCTCCCGTCTCCGGTAAATG 1430
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Matches 1312;  Conservative    0;  Mismatches   94;  Indels   12;  Gaps    3;

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Qy   73  GAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCTGGGGGCTGAATCCGCAGTCCCCAGGGAAGGGG 132
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Qy  253  AAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACACCAGTTCTCCCTGAAGTTGAAC 312
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Qy  313  TCTATGACCGCCGGACAGGCCCGTGTATTACTGTGCGAGAGATCGTCTTTTTTCAGTT 372
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Qy  373  GTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCAAGGGACCCCGGTC 432
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Qy  193  CTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACTACAACCCCTCCTG 252
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Qy  733  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGCTCCTG 792
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Qy  793  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 852
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Qy  853  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 912
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ORGANISM   cDNA to mRNA, clone_lib:SYNOV clone:SYNOV2001300.
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS   Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
              Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
              Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
              Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
              Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
              Kimura,K., Yamashita,H., Matsuo,K., Sekine,M.,
              Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
              Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
              Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1566)
AUTHORS   Isogai,T. and Yamamoto,J.
TITLE   Direct Submission
JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
              Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
              (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
              Economy, Trade and Industry of Japan; cDNA full insert sequencing:
              Research Association for Biotechnology (RAB); cDNA library
              construction: Helix Research Institute (HRI) (supported by Japan
              Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
              HRI, and Biotechnology Center, National Institute of Technology and
              Evaluation; clone selection for full insert sequencing: HRI and
              RAB; annotation: HRI and RAB.
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                     ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
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Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Qy   121 TGGCTGTCTTGGTGGCTCCATCAGCCGGTGGTTAT---GGCTGGGCGTGACTCCGCCAG 177
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Qy   553 GTGTCGTGGAACTCAGGCGCCTGGCGCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG 612
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Qy   613 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 672
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RESULT 11
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VERSION     AR135375.1   GI:14476047
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
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AUTHORS     Hanna,N., Newman,R.Anthony. and Reff,M.Elliot.
TITLE       Recombinant anti-CD4 antibodies for human therapy
JOURNAL     Patent: US 6136310-A 7 24-OCT-2000;
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Matches 1294;  Conservative  0;  Mismatches 110;  Indels 27;  Gaps  2;
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 539

Qy    538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 599

Qy    598 CCGGCTGTCCTACAGTCTCCTACAGTCTCCTCAGCAGCGTGTGACCGTGCCCTCC 657
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 CCGGCTGTCCTACAGTCTCCTACAGTCTCCTCAGCAGCGTGTGACCGTGCCCTCC 659

Qy    658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 719

Qy    718 GTGGACAAGAAAGCAGAGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 GTGGACAAGAAAGTTGAGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 779

Qy    778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTTCCCCCCAAAACCCAAGGACACC 837
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTTCCCCCCAAAACCCAAGGACACC 839

Qy    838 CTCATGATCTCCCGGACCCCTGAGGTCACATCGTGGTGGTGGACGTGAGCCACGAAGAC 897
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 899

Qy    898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 959

Qy    958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1019

Qy   1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1079

Qy   1078 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1137
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1139

Qy   1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1199

Qy   1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1259

Qy   1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317
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FEATURES             Location/Qualifiers
     source          1..1404
                     /organism="unknown"
BASE COUNT      313 a      447 c      379 g      265 t
ORIGIN

Query Match            82.3%;   Score 1177.8; DB 6;  Length 1404;
Best Local Similarity  90.3%;   Pred. No. 6.6e-228;
Matches 1292;  Conservative   0;  Mismatches 112;  Indels 27;  Gaps 2;

Qy    1 ATGAAACACCTGGTTCTCCTCCTCCGGTGGCAGCTCCCAGATGGGTCGTGTCCCAGCA  60
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    1 ATGAAACACCTGGTTCTTCCTCCTCCTCCGGTGGCAGCCCCCAGATGGGTCTTGTGCCCAG  60

Qy   61 GTGCAGTGCACGAGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120

Qy  121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGTTATGGCTGGGGCTGGATCCGCCAGTCC  180
         | |||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db  121 TGCAGTGTCTCTGGTGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC  180

Qy  181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  181 CCAGGGAAGGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGGGGCACCAATTAC  240

Qy  241 AACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGGCCGTGTATTACTTCTCC  300
         || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AATCCCTCCCTCAACAATCAGTCTCCATTCAATCAAGACACGTCCAAGAACCTCTCTCC  300

Qy  301 CTGAAGCTGAACTCTATGACCGCGCGGACAGCCGTGTATTACTGTGTGAGAGATCGT  360
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||  --
Db  301 CTGAAACTGAGTGTCTGTGACCGCCGCGCGGACACGGCCGTGTATTACTGTGCGAGTAATA--  358

Qy  361 CTTTTTCAGTTGTTGGAATGGTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC  420
         ||||                    -TATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTC  402
Db  359 ------------------------TATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTC  402

Qy  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCCACCCTC  480
         ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGC  462

Qy  481 TCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  463 TCCAAGAGCACCTCCGGAGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  522

Qy  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  582

Qy  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  642

Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  643 AGCTTGGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG  702

Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
         ||||||| ||||||||||||||||||||||||||||||| ------TCCCCATGCCCACCGTGCCCAGCA  753
Db  703 GACAAGAGAGTTGAGTCCAAAATATGG------TCCCCATGCCCACCGTGCCCAGCA  753

Qy  781 CCTGAACTCCTGGGGGGACCGTCAGTTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
         |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  754 CCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC  813

Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  814 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCC  873

Qy  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
         |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACACAAGCCG  933

Db  523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  582

Qy  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  642

Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
         ||||| |||||||||||||||||||||| ------TCCCCATGCCCATCATGCCCAGCA  753
Db  703 GACAAGAGAGTTGAGTCCAAATATGG------TCCCCATGCCCATCATGCCCAGCA  753

Qy  781 CCTGAACTCCTGGGGGGACCGTCAGTTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  754 CCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC  813

Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC  873

Qy  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
         ||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACACAAGCCG  933

Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  993

Qy 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC  1053

Qy 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG  1113

Qy 1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1114 CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1173

Qy 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1233

Qy 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
         |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db 1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTAACC  1293

Qy 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
         ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db 1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT  1353

Qy 1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1404
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RESULT 12
AR135377
LOCUS       AR135377        1404 bp    DNA        linear     PAT 16-JUN-2001
DEFINITION  Sequence 11 from patent US 6136310.
ACCESSION   AR135377
VERSION     AR135377.1  GI:14476049
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1404)
  AUTHORS   Hanna,N., Newman,R.Anthony. and Reff,M.Elliot.
  TITLE     Recombinant anti-CD4 antibodies for human therapy
  JOURNAL   Patent: US 6135310-A 11 24-OCT-2000;
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Qy    241 AACCCCTCCCTCCCCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC  300
          ||  ||||||||||||| |||   ||||| ||||||||| ||||||||||||||  |  |||||
Db    241 AATCCCTCCCTCCCCAACAATGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC   300

Qy    301 CTGAAGCTGAACTCTATGACCGTGGCCGGGACACGGCCGGTGTATTACTGTGTGAGAGATCGT  360
          ||||| |||| |||||||||| | ||| ||||||| |||||| |||||||||| | |||  |
Db    301 CTGAAACTGAGGTCTGTGACCGCCGCGGGGACACGGCCGGTCTATTACTGTGCGGAGTAATA--  358

Qy    361 CTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTGTCGGGGCCCCGGAGTC   420
                         |||| |||||||| ||  ||||   ||  |||||  ||||||| ||||||||
Db    359 -------------TATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGAGGTC       402

Qy    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGC   462

Qy    481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540
          ||||||||||||||||||||||||||| |||||||||| ||||||||||||| |||||||
Db    463 TCCAAGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   522

Qy    541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   600
          ||||| |||||||||||||||||||||| |||||||||||||| |||||||||||||||||
Db    523 GAACCCGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   582

Qy    601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   660
          |||||||| ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   642

Qy    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720
          |||||||||||| |||||||||| ||||||   |||  |||  ||  |
Db    643 AGCTTGGGCACGCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   702

Qy    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780
          ||  ||  ||||  ||||||||||  ||||||  ||               ||||||||||
Db    703 GACAAGAGAGTTGAGTCCAAATATGG-------------TCCCCCATGCCCATGCCCAGCA   753

Qy    781 CCTGAACTCCTGGGGGGACCGTCAGTCTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840
          ||||| ||||| |||||||||||||||||||||||||||||||| |||||| ||| |||
Db    754 CCTGAGTTCGAGGGGGGACCATCAGTCTTCTCTTCCCCCCAAAACCCAAGGACACTCTC   813

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT   900
          |||||||||||||||||||||||||| ||||||||||||||||||||||||| ||||||||
Db    814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCC   873

Qy    901 GAGGTCAAGTTCAACTGGTACGTGACGGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960
          ||||||||||||||||||||||  |||| ||||||||||||||||||||||| |||||||
Db    874 GAGGTCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   933

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG   993

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
          |||||||||| ||||||||||||||||||||||||||||||||||| |||||||||| ||
Db    994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC  1053

Qy   1081 ATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Db   1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1113

Qy   1141 CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1200
          |||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1114 CCCCATCCCGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC    1173

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
          |||||||||||||  ||||||||||||||||||||||||||| ||||||||||||||||||
Db   1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1233

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTTAACC  1293

Qy   1321 CGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1380
Db   1294 CGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1353

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA          1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA           1404
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RESULT 13
AR135376

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LOCUS       AR135376                1404 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 9 from patent US 6136310.
ACCESSION   AR135376
VERSION     AR135376.1  GI:14476048
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1404)
  AUTHORS   Hanna,N., Newman,R.Anthony, and Reff,M.Elliot.
  TITLE     Recombinant anti-CD4 antibodies for human therapy
  JOURNAL   Patent: US 6136310-A 9 24-OCT-2000;
FEATURES             Location/Qualifiers
     source          1..1404
                     /organism="unknown"
BASE COUNT      313 a    446 c    379 g    266 t
ORIGIN
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Query Match   82.2%; Score 1176.2; DB 6; Length 1404;
Best Local Similarity   90.2%; Pred. No. 1.4e-227;
Matches 1291; Conservative   0; Mismatches 113; Indels 27; Gaps 2;

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Qy      1 ATGAAACAACCTGTCGTTCTTCCTCCTGCTGGTGGCAGCTGCAGATGGTCCTGGTCCCCAG    60
          ||||| |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      1 ATGAAACAACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTGCAGATGGGTCTTGTCCCCAG   60

Qy     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCCACC   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCCACC   120

Qy    121 TGCGCTGTCTCTGGTTGGTCCATCAGCAGTGGTTATGGCGGTTATCCGGTCGCCGCCAGC   180
          |||  ||||||||||||||| |||| |||||  |||||| |||  | ||  |||| ||
Db    121 TGCAGTGTCTCTGGTGGCTCCATCAGCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC  180

Qy    181 CCAGGAAGGGGCTGGAGTGGATTGGGTCTATTCATAGTAGTGGGAACACTACTAC        240
          ||||||||||  |||||||| |||||||||||| ||||||||||||||||||||||||
Db    181 CCAGGGAAGGGACTGGAGTGGATCGGTCATATTCATAGTAGTGGGAGCACCTATTAC      240
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Qy  1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
                ||||||||||||||||| |||||||||||||||||||| |||||||||||||||||||
Db  1294  GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT  1353

Qy  1381  CTGGCACACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA          1431
                ||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  1354  CTGGCACACCACTACACGCAGAAGAGCCTCTCCCTGTCTCTGGGTAAATGA          1404
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RESULT 14

BC024289

LOCUS   BC024289   1630 bp   mRNA   linear   PRI 28-FEB-2002
DEFINITION   Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA, complete cds.
ACCESSION   BC024289
VERSION   BC024289.1 GI:18999464
KEYWORDS   MGC.
SOURCE   Homo sapiens.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1630)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (26-FEB-2002) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Genome Sequence Centre,
             BC Cancer Agency, Vancouver, BC, Canada
             info@bcgsc.bc.ca
             Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
             Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
             Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
             Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
             Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
             Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
             Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
             George Yang, Scott Zuyderduyn, Marco Marra.

             Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRAL Plate: 42 Row: o Column: 20
             This clone was selected for full length sequencing because it
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Job time : 4493.25 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 65.1566 Seconds
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Title: US-09-758-173-11
Perfect score: 1431
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1315.8	91.9	1431	3	US-08-487-550-3	Sequence 3, Appli
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4	1213.6	84.8	1418	3	US-08-793-450-7	Sequence 7, Appli
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6	1177.8	82.3	1404	3	US-08-523-894-11	Sequence 11, Appl
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17	1125.2	78.6	1428	2	US-08-634-223-19	Sequence 19, Appl
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26	1112.4	77.7	1437	3	US-08-487-550-7	Sequence 7, Appli
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28	1102.2	77.0	6557	1	US-08-286-740-3	Sequence 3, Appli
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42	1069	74.7	1655	3	US-09-049-672A-21	Sequence 21, Appl
43	1051.2	73.5	6285	1	US-08-467-420A-49	Sequence 49, Appl
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45	1051.2	73.5	6285	1	US-08-667-769A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-11
; Sequence 11, Application US/08487550
; Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1431
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1431
US-08-487-550-11

Query Match 100.0%; Score 1431; DB 3; Length 1431;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CTTTTTCAGTTGTTGTGGAATGGTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC  420

Qy  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480

Qy  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660

Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720

Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780

Qy  781 CCTGAACTCCTGGGGGGACCGGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCTGAACTCCTGGGGGGACCGGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900

Qy  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
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Db  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
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Db  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
        |||
Db 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy 1141 CCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 CCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy 1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTCTCCCGGGTAAATGA      1431
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTCTCCCGGGTAAATGA      1431
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RESULT 2
US-08-487-550-3
; Sequence 3, Application US/08487550
; Patent No. 6113898
GENERAL INFORMATION:
  APPLICANT: Anderson, Darrell R.
  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22314
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/487,550
    FILING DATE: 07-JUN-1995
    CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: Teskin, Robin L.
    REGISTRATION NUMBER: 35,030
    REFERENCE/DOCKET NUMBER: 012712-131
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 703-836-6620
    TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1431 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: not relevant
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..1431
  FEATURE:
    NAME/KEY: mat_peptide

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;
US-08-487-550-3
  LOCATION: 1..1431

Query Match      91.9%;  Score 1315.8;  DB 3;  Length 1431;
Best Local Similarity   95.0%;  Pred. No. 4.4e-308;
Matches 1359;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 ATGAAACACCTGTGGTTCTCCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAG    60
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCGACC  60

Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120
        |||   |||||| |||  |||||  |||||||||| || |||||||  ||| |||||||||
Db   61 TGCGTGTCTCTGTGGCTCCATCAGCGGGTTACTACTGACCTGGATCTGCGTCCCGCCAGACC  120

Qy  121 TGCGTGTCTCTGTGGCTCCATCAGCGGTGTTATGGCGTTGGGCTGGATCCGCCAGCCC  180
        |||  ||||||||||||||||||||||  |||| | ||| || |||||| || ||
Db  121 TGCGTGTCTCTGTGGCTCCATCAGCGGGTTACTACTGACCTGGATCTGCGTCCCAGACC  180

Qy  181 CCAGGGAAGGGCGTGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGAACACCTACTAC  240
        ||||||||||||||||||||||| ||| ||  ||||  |||||||| | ||||| ||||
Db  181 CCAGGGAGGGGACTGGAGTGGATTGGCCATATTATGGTAATGGTGACAACACAACTAC  240

Qy  241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC  300
        ||  |||||||||||||| || |||||| |||  |||||  |||||||||||||| |  |
Db  241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC  300

Qy  301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT  360
        |||||||||||| | |||| || |||| ||||| |  |||||||||||||||| | |
Db  301 CTGAACTTGAATTCTGTGACCGCGGACACGGCCGTCTATTACTGTGTGCGAGAGGGCCCT  360

Qy  361 CTTTTTCAGTTGTTGGAATGGTTACAACAACTGGTTCGGGGCCCGGGAGTC  420
        |          ||||||  ||||| ||||||| |||| ||||| |||||| ||
Db  361 CGCCCCTGATTGCACAACCATTTGTTATGGCGGTCGGTGGGCCCGGGGGAGAC  420

Qy  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480
        ||||||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||
Db  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480

Qy  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660

Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720

Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780

Qy  781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900

Qy  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
        ||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||||
Db 1021 GACTGGCTGAATGGCGAAGGAGTACAAGTGCAAGGTCTTCAACAAAGCCCTCCCAGCCCCC 1080

Qy 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy 1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCGGAGAACAACTAC 1260
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCGGAGAACAACTAC 1260

Qy 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
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Db 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy 1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTGTCTCCGGGTAAATGA 1431
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Db 1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTGTCTCCGGGTAAATGA 1431
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; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1567 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;     LIBRARY: PANCTUT01
;     CLONE: 1513264
US-09-049-672A-17

Query Match          89.2%;    Score 1276.4;  DB 3;  Length 1567;
Best Local Similarity  94.7%;   Pred. No. 1.4e-299;
Matches 1358;  Conservative    0;  Mismatches   61;  Indels  15;  Gaps    3;

Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGCAGCTGCCAGATGGGTCCTGTCCCAG 60
            ||||||||||||||||||||||||||||||| ||||||||||||||| |||||||||||
Db     78 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGCAGCTGCCAGATGGGTCCTGTCCCAG 137

Qy     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTGGAGACCCTGTCCCTCACC 120
            ||||| |||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db    138 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTGGAGACCCTGTCCCTCACC 197

Qy    121 TGGCGTGTCTCGTGGTGGCTCCATC--AGCCGGTGGTTATGGCTGGGCTGGATCGGCCAG 177
            ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db    198 TGGCGTGTCTCGTGGTGGCTCCATCACTAGTGGTGGTTACTACTGGAGCTGGATCGGCCAG 257

Qy    178 CCCCCAGGAAGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTAC 237
            ||||||||||||||||||||||||||||||| ||||| |||  || |||||||||||
Db    258 CCCCCAGGAAGGGCTGGAGTGGATTGGGTACTA---TTACAGTGGGAGCACCCCTC 314

Qy    238 TACAACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTC 297
            ||||||||||||||||||||||||| |||||||||||||  ||||||||||||||||
Db    315 TACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCCAAGAACCAGTTC 374

Qy    298 TCCCTGAAGCTGAACTCTATGACCGCGGACACGTCCGTGTATTACTGTGTGAGAGAT 357
            |||||||||||    ||  |||||||||| ||||||  ||||||||||||
Db    375 TCCCTGAAGCTGAGCTCTGTGACTGCGGACACGTCCGTGTATTACTGTGTGAGAGA- 433

Qy    358 CGTCTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGA 417
            |||||||                  |||||||||||| |||||||||||||||||||
Db    434 ------TGACGTAGGTTTAAGGGGGGAACTACCGTATGGACGTCTGGGGCCCAGGGA 485

Qy    418 GTCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCC 477
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Db    486 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 545

Qy    478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 537
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Db    546 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 605

Qy    538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 665

Qy    598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 657
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Db    666 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 725

Qy    658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
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Db    726 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 785

Qy    718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    786 GTGGACAAGAAAGCAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 845

Qy    778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 837
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 905

Qy    838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 897
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 965

Qy    898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
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Db    966 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 1025

Qy    958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
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Db   1026 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1085

Qy   1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1145

Qy   1078 CCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1137
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Db   1146 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1205

Qy   1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   1206 CTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1265

Qy   1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1325

Qy   1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1326 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1385

Qy   1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTTTTCTCATGCTCCGTGATGCATGAG 1445

Qy   1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1499
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RESULT 4
US-08-793-450-7
; Sequence 7, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
;   APPLICANT: EDELMAN, LENA
;   APPLICANT: MARGARITTE, CHRISTEL
;   APPLICANT: KACZOREK, MICHEL
;   APPLICANT: CHAABIHI, HASSAN
;   TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
;   TITLE OF INVENTION:
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE: P.C.
;   STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;   CITY: ARLINGTON
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/793,450
;   FILING DATE: 03-MAR-1997
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: FR 94/10566
;   FILING DATE: 02-SEP-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: OBLON, NORMAN F.

```
;      REGISTRATION NUMBER: 24,618
;      REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 703-413-3000
;      TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 7:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 1418 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: other nucleic acid
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 1..1418
;      FEATURE:
;      NAME/KEY: sig_peptide
;      LOCATION: 1..57
;      FEATURE:
;      NAME/KEY: mat_peptide
;      LOCATION: 58..1418
;      OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY
;      OTHER INFORMATION: CHAIN"
US-08-793-450-7

Query Match      84.8%;   Score 1213.6;  DB 4;  Length 1418;
Best Local Similarity  92.5%;   Pred. No. 1.8e-283;
Matches 1312;  Conservative  0;  Mismatches  94;  Indels  12;  Gaps  3;
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Qy    13  TGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTGCAG  72
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Db    13  TGTATCATCCTCTTCTTGTAGCAACAGCTACAGGTGTCCACTCCCAGGTCCAACTGGAG  72

Qy    73  GAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCTCCTCACCTGCGTCTGTCT 132
              ||| |||||||||||||||||||||| |||| |||||||||||||||||||| |||||
Db    73  CAGTGGGGCGCAGGACTGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTAT 132

Qy   133  GGTGGCTCCATCAGCGGTGGTTATGGCTGGTGGCTGGATCCGCCAGCCCCAGGGAAGGGG 192
              ||| || ||||| |||     ||||||   |   |||||||||||||||||||||||
Db   133  GGTGGGTCCTTCA---GTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGG 189

Qy   193  CTGGAGTGGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTACAACCCCTCCCTC 252
              |||||||||||||||||| |||| |||   |     |      ||||| |||||||
Db   190  CTGGAGTGGGATTGGGGAAATC---AATCATAGTGGAAGCACCAACTACAACCCGTCCCTC 246

Qy   253  AAGAGTCAAGTCACCATTTCACACAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAAC 312
              |||||| ||| |||||||| |   ||| || ||  ||   ||||||||||||||||||
Db   247  AAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAACTGAAC 306

Qy   313  TCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTT 372
              ||  |  |||| ||| ||||   |||||||||||||| |||||||||||    |||
Db   307  TCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGGGCCCCAGAGTATAAA-- 363

Qy   373  GTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTCCTGGTCACCGTC 432
              |   |  |  ||| |||||| |||||||||||||||||||||||||| ||||||||||||
Db   364  ---TGGAAGTATCATGGGGACTTGGTTCGACCCCTGGGGCCAAGGTACCACTGTCACCGTC 420

Qy   433  TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 492
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   421  TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 480

Qy   493  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG 552
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Db   481  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG 540

Qy   553  GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG 612
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Qy   613  TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 672
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Db   661  CAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTGGACAAGAAAGCA 720

Qy   733  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 792
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 780

Qy   793  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 852
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 840

Qy   853  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 912
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 900

Qy   913  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAG 972
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAG 960

Qy   973  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1032
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TACAACAGCACTTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1020

Qy  1033  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1092
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATTGAGAAAACC 1080

Qy  1093  ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCGG 1152
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCGG 1140

Qy  1153  GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1212
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Qy  1273  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1332
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Db  1261  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1320

Qy  1333  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1392
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 5
US-08-523-894-7
; Sequence 7, Application US/08523894
; Patent No. 6136310
;    GENERAL INFORMATION:
;    APPLICANT: Hanna, Nabil
;    APPLICANT: Newman, Roland A.
;    APPLICANT: Reff, Mitchell E.
;    TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;    TITLE OF INVENTION: Therapy
;    NUMBER OF SEQUENCES: 59
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;       STREET: 699 Prince Street
;       CITY: Alexandria
;       STATE: VA
;       COUNTRY: USA
;       ZIP: 22314-3187
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
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;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/523,894
;   FILING DATE: 06-SEP-1995
;   CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1404 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   POSITION IN GENOME:
;     CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
;     CHROMOSOME/SEGMENT: 4
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..1404
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 1..1404
US-08-523-894-7

  Query Match         82.5%;  Score 1181;  DB 3;  Length 1404;
  Best Local Similarity  90.4%;  Pred. No. 1.3e-275;
  Matches 1294;  Conservative  0;  Mismatches 110;  Indels  27;  Gaps  2;

Qy      1 ATGAAACACCTGGTTCTTCCTCCTCCGGTGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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Qy     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Db     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy    121 TGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTTATGCTGGGGCGTGGTTATCCGCCAGCCC 180
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Db    121 TGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTTCTGGATTAGTTCTGGATCCGCCAGTCC 180

Qy    181 CCAGGGAAGGGGCTGGAGTGGATTGGAGTTTCTATAGTAGTGGGAACACCTACTAC 240
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Db    181 CCAGGGAAGGGGCTGGAGTGGATTGGGGTTACATCTATGCAGTGGGGGCCACCAATTAC 240

Qy    241 AACCCCTCCCAAGAGTCAAGTGCAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300
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Db    241 AATCCCTCCCACAACATCGAGTCTCATTTCATTCAATAGACACGTCCCTATTACTGTGCCGAGTAATA-- 358

Qy    301 CTGAAGCTGAACTCTATGACCGCGGCGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
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Db    301 CTGAAACTGAGGTCTGTGACCGCCGCGGCACAGGCCGTGTATTACTGTGCCGAGTAATA- 358

Qy    361 CTTTTTTCAGTTGTTGGAATGGTTACAACAACTGGTTCGATGTCTGGGGCCCCGGGAGTC 420
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Db    359 ----------TATTGAAATATCTTCACTGGTTATTATATACTGGGGCCCAGGGACGGAGTC 402

Qy    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
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Db    403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGC 462

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Db    523 GAACCGGTGACGTGTCTGTGAACTCAGGCGCCCTGACCAGCAGCGGCGTGCACACCTTCCCG 582
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Db    754 CCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC 813

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGGACCCT 900
          ||||||||||||||||||||||||||| |||||||||||||||||||||||| |||||||
Db    814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCC 873

Qy    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          |||||| ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 933

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 993

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
          |||||||||||  |||||||||||||||||||||||||||||||||| |||||| ||| ||
Db    994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC 1053

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG 1113

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
          |||||||||| ||| || ||||||||||||||||||||||||||||||||||||||||||
Db   1114 CCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1173

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1233

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db   1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC 1293

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db   1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1404
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RESULT 6
US-08-523-894-11
; Sequence 11, Application US/08523894
; Patent No. 6135310
; GENERAL INFORMATION:
;   APPLICANT: Hanna, Nabil
;   APPLICANT: Newman, Roland A.
;   APPLICANT: Reff, Mitchell E.
;   TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;   TITLE OF INVENTION: Therapy
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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;     STREET: 699 Prince Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314-3187
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/523,894
;     FILING DATE: 06-SEP-1995
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin, Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-165
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1404 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   ORIGINAL SOURCE:
;     ORGANISM: Homo sapiens
;   POSITION IN GENOME:
;     CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E
;     CHROMOSOME/SEGMENT: mutation
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..1404
;   FEATURE:
;     NAME/KEY: mat peptide
;     LOCATION: 1..1404

US-08-523-894-11

Query Match             82.3%;  Score 1177.8;  DB 3;  Length 1404;
  Best Local Similarity   90.3%;  Pred. No. 7.8e-275;
  Matches 1292;  Conservative    0;  Mismatches  112;  Indels   27;  Gaps   2;

Qy       1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCAGATGGGTCCTGTGTCCCAG   60
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Db       1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCCCCAGATGGGTCTTGTGTCCCAG   60

Qy      61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120
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Db      61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120

Qy     121 TGCGCTGTCTCTGGTGGCTCCATCAGCAGCGGTGGTTATGGCGTCGGGATCCGGCCAGCCC  180
           ||| || ||||||||||||||||||||||||||||||  ||| || |||||||||||| |
Db     121 TGCAGTGTCTCTGGTGGCTCCATCAGCAGCGGTGGTTATTGGTTCTGGATCCGGCCAGTCC  180

Qy     181 CCAGGGAAGGGGCTGGAGTGGATTGGAGTTCTATAGTAGTAGCACCACTTACTAC      240
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Db     181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTCCATCTATTACAGTGGGAGCACCAATTAC   240

Qy     241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACAGTCCAAGAACCAGTTCTCC   300
           ||||||||| ||| | |||||| |||||||||| | |||||| |||| || |||||||||
Db     241 AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGTCCAAGAACCTCTTCTCC   300

Qy     301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT  360
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Db     301 CTGAAACTGAGGTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGTGGGAGAGTC   358

Qy     361 CTTTTTTCAGTTGTTGGGAATGGTTTACAACAACTGGTTCACTGGTTATTAAAGGCCGGGGAGTC  420
                   ||                 ||||||||||||||||||||||||||||||||||||
Db     359 ------------------TATTGAAATATCTTCACTGGTTATTATTACTGTGCGAGTC  402
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Qy     421 CTGGTCACCGTCTCCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCTCC      480
           ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     403 CTGGTCACCGTCTCCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCTGGCGCCCTGC      462

Qy     481 TCCAAGAGCACCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC     540
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Qy     541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG     600
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Db     523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG     582

Qy     601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC     660
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Db     583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC     642

Qy     661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG     720
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Db     643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG     702

Qy     721 GACAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA     780
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Db     703 GACAGAGAGTTGAGTCCAAATATGG-------TCCCCATGCCCACCATGCCCAGCA     753

Qy     781 CCTGAACTCCTGGGGGGACCCTCAGTCTTCTTCCCCCCAAAACCCAAGGACACCCTC     840
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Db     754 CCTGAGTTCGAGGGGGGACCCTCAGTCTTCTTCCCCCCAAAACCCAAGGACACTCTC     813

Qy     841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT     900
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Db     814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCG     873

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Db     874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG     933

Qy     961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG    1020
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG    993

Qy    1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC    1080
           ||||||||||||||||||||||||| |||||||||||||||||||||| ||||||| ||
Db     994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC    1053

Qy    1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG    1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG    1113

Qy    1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC    1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1114 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC    1173

Qy    1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC    1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC    1233

Qy    1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC    1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC    1293

Qy    1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT    1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT    1353

Qy    1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCGGTAAATGA                    1431
           |||||||||||||||||||||||||||||||||||||| ||||
Db    1354 CTGCACAACCACTACACAGAGAAGAGCCTCTCCGTCTCTGGGTAAATGA             1404
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RESULT 7
US-08-523-894-9
; Sequence 9, Application US/08523894
; Patent No. 6136310
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GENERAL INFORMATION:
  APPLICANT: Hanna, Nabil
  APPLICANT: Newman, Roland A.
  APPLICANT: Reff, Mitchell E.
  TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
  TITLE OF INVENTION: Therapy
  NUMBER OF SEQUENCES: 59
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22314-3187
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/523,894
    FILING DATE: 06-SEP-1995
    CLASSIFICATION: 424
  ATTORNEY/AGENT INFORMATION:
    NAME: Teskin, Robin L.
    REGISTRATION NUMBER: 35,030
    REFERENCE/DOCKET NUMBER: 012712-165
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 703-836-6620
    TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1404 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  ORIGINAL SOURCE:
    ORGANISM: Homo sapiens
  POSITION IN GENOME:
    CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..1404
  FEATURE:
    NAME/KEY: mat peptide
    LOCATION: 1..1404

US-08-523-894-9

Query Match   82.2%;   Score 1176.2;   DB 3;   Length 1404;
Best Local Similarity   90.2%;   Pred. No. 1.9e-274;
Matches 1291;   Conservative 0;   Mismatches 113;   Indels 27;   Gaps 2;

Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGGTCCTGTCCCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGGTCTTGTCCCAG   60

Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC   120

Qy   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC   180
           ||||||||||||||||||||||||| || |||| |||||||||||||||||||||||||
Db   121 TGCAGTGTCTCTGGTGGCTCCATCAGCAGTGGTGTCTATTATTGTTCTGGATCCGCCAGTCC   180

Qy   181 CCAGGGAAGGGGCTGGAGTGGGTTGGAGTTTCTATAGTAGTAGGGGACCACCTACTAC   240
           |||||||||||||||||||||||||| |||| ||| | | |||||||| ||||||
Db   181 CCAGGGAAGGGGGACTGGAGTGGATCGGCTACATCATGGCAGTGGTGTGGGGCCACCAATTAC   240

Qy   241 AACCCCTCCCTCAAGAGTCAAGTCACCATTCAACACGACACGTCCAAGAACCAGTTCTCC   300
           ||||||||||||||||||||||||||| ||||| || |||||||||||||||||||||||
Db   241 AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCCTTCTCTCC   300

Qy   301 CTGAAGCTGAACTTCTATGACCGGCCGCCGGCACGCGCCGTGTATTACTGTGTGAGAGATCGT   360
           |||| |||| || ||| |||||||||||| || |||| |||||||||| |||||||
Db   301 CTGAAACTGAGGTCTGTGACCGGCCGCCGGCGTCTTATTACTGTGCGAGTAATA--   358

Qy   361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCGGGGCCCGGGAGTC   420
                   -------TATTGAAATATCTTCACTGTGTTATTATACTGGGGCCAGGGAGTC   402
Db   359

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC   480
           ||||||||||||||||||||||||||||||||||| |||| |||||||||||||||||
Db   403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGC   462

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   463 TCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   522

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   582

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   642

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG   702

Qy   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780
           |||||||||||||| ||||||| |||||||| --------TCCCCATGCCCATCCCCAGCA   753
Db   703 GACAAGAGAGTTGAGTCCAAATATGG

Qy   781 CCTGAACTCCTGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   754 CCTGAGTTCGAGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC   813

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT   900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCC   873

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960
           ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   874 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   933

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTGCACCAG 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG   993

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
           |||||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||
Db   994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGGCTCCCGTCCTCC 1053

Qy   1081 ATCGAAAAACCATCTCCAAAGGGGCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCCTG 1140
           |||||||||||| |||||||||||||||||||||||||||||||||||||| |||||||
Db   1054 ATCGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG 1113

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
           ||||||||||||| |||||||||||| |||||||||||||||||||||||||||||||
Db   1114 CCCCCATCCCGAGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1173

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1233

Qy   1261 AAGACCACAGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC 1293

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431

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Db  1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAAATGA 1404
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RESULT 8
US-08-488-376-17
; Sequence 17, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Burns, Doane, Swecker & Mathis
;     STREET: P.O. Box 1404
;     CITY: Alexandria
;     STATE: Virginia
;     COUNTRY: United States
;     ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/488,376
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin, Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-150
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (703) 836-6620
;     TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1428 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..1428
US-08-488-376-17

Query Match             79.3%;  Score 1134.8;  DB 1;  Length 1428;
Best Local Similarity   89.0%;  Pred. No. 1.8e-264;
Matches 1262;  Conservative  0;  Mismatches 147;  Indels  9;  Gaps  3;

Qy   17 TCTTCCTCCTCCTGGTGGCAGCTTCCCAGATGGGTCCTCCAGGTGCAGCTGCAGGAGT  76
         ||||  ||| |||| ||  ||  ||| ||  |   ||||  |||||||| | |||||||
Db   17 TCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTTGCTGTCCCAGGTGCAGTTGCAGGAGT  76

Qy   77 CGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTGCACCGTCTCTGGT 136
         | |  ||  | ||||||||| || |  |||||||| | |||||||||||||||
Db   77 CTGTCCTGTGGTGGTGAAACCCACAGAGACCCTCACGCTGACCTGCACCGTCTCTGGT 136

Qy  137 GCTC---CATCAGCGGTGTTATGGCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGC 193
         | ||      |  | |  |  |  | |||  ||  | ||||| ||||| |||||   |
Db  137 TCTCACTCAGCAACCCTAGAATGGGTGTGACCTGGGTGGCTCGTCAGCCCCCGGGGAAGGCCC 196

Qy  194 TGGAGTGGATTGGGAGTTCTATAGTAGTAGTAGTACCTACTACAACACTTACAACCCCTCCCTCA 253
         | || |||| ||| ||| |    || |      |  | |   |    |   |||   ||| ||
Db  197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAA--GTCCTTCAGTCCTTCTCTGA 253

Qy  254 AGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAACT 313
         |||| |  | ||||| ||| |||||||| |||||| |||| | | ||| ||| || ||
Db  254 AGAGCAGACTCACCACCTCCAGAGACACCTCCAAGAGCCAGGTGGTCCTAAGCTTGACCA 313

Qy  314 CTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATGTCTTTTTCAGTTG 373
         | ||||| |   ||||| ||||   |||||||||| |  |   ||| |   |  ||
Db  314 ACGTGGACCCTGTGACACAGCCACCATATTACTGTGCACGGTAGGACTGTATGACATCA 373

Qy  374 TTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCGGGAGTCCTGGTCTCACCGTCT 433
            | |  |   |  | || |   |      || ||||| |||||   |||||  ||||||
Db  374 ATGCTT---ATTACCTATACTACCTGGATTATTGGGGTCAGGGAACCCTGGTCACCGTCT 430

Qy  434 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT 493
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Db  431 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT 490

Qy  494 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 553
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Db  491 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 550

Qy  554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 613
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Db  551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 610

Qy  614 CCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 673
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Db  611 CCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 670

Qy  674 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGCAG 733
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Db  671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGCAG 730

Qy  734 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 793
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Db  731 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 790

Qy  794 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 853
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Db  791 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 850

Qy  854 CCCCTGAGGTCACATCGTGTGGTGGTGGACGTGAGCCAGAAGACCCTGAGGTCAAGTTCA 913
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  851 CCCCTGAGGTCACATCGTGTGGTGGTGGACGTGAGCCAGAAGACCCTGAGGTCAAGTTCA 910

Qy  914 ACTGTGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 973
         |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 970

Qy  974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1033
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1030

Qy 1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCCGAGAAACCA 1093
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCCGAGAAACCA 1090

Qy 1094 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1153
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1091 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1150

Qy 1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1213
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1151 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1210

Qy 1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1270

Qy 1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1333
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1271 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1330
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Qy   1334 GGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 GGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTCCGTGATGCATGAGGCTCTGCACAACCACT 1390

Qy   1394 ACACGCAGAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
           |||||||||||||||||||||||||||||||||||||||
Db   1391 ACACGCAGAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428

RESULT 9
US-08-634-223-17
; Sequence 17, Application US/0863423
; Patent No. 5840298
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaima Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
US-08-634-223-17

Query Match   79.3%; Score 1134.8; DB 2; Length 1428;
Best Local Similarity 89.0%;
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;   Pred. No. 1.8e-264;

Qy   17 TCTTCCTCCTCCTGTGGCAGCTCCAGATGGGTCCTGTCCCAGTGCAGTCAGGTGCAGGAGT   76
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Db   17 TCTTGCTCCTCCTTGTCGCTGTGTTGCTACGCGGTGTCCTGTCCCAGTGCAGTTGCAGGAGT   76

Qy   77 CGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTG 136
           | || ||| ||| ||||| || ||||||||| || |||||||||| || ||||| |
Db   77 CTGTGCTCCTGTGGTGGTGAAACCCAGAGACCCTGACCTGCACCGTCTCTGGGT 136

Qy   137 GCTC--CATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCCCAGGGAAGGGGGC 193
           ||| || ||||| || | | ||| | ||||||| |||||||| || |||| | |
Db   137 TCTCACTCAGCAACCCTAGAGATGGGTGTGACCTGGATCCGTCAGCCCCCGGAAGGAGGCCC 196

Qy   194 TGGAGTGGATTGGAGTTCTATAGTAGTAGTGGAACACTACTACAACCCCTCCTCA 253
           | ||||||| || | | | ||||| | |||| ||| || | ||| |||
Db   197 TAGAATGGCTGGAAACATTTTTCGAGTGACGAGAA---GTCCTTCAGTCCTTCTCTGA 253

Qy   254 AGAGTCAAGTCACCATTTCAACGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAACT 313
           |||| | | ||||| | ||| ||||| ||||| ||||||| | ||| ||||||| |
Db   254 AGAGCAGACTCACCACCACCTCCAGGACACCTCCAGGAGCCAGTGGTCCTAAGCTGACCA 313

Qy   314 CTATGACCGCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTTG 373
           | |||||| || |||ac| ||| | ||||||||| | |||| | | ||| ||
Db   314 ACGTGGACCCCTGTGGACACAGCCACCACATATTACTGTGTACGGTAGGACTGTATGACATCA 373

Qy   374 TTGGAATGGTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTCTCGTGTCACCGTCT 433
           | | ||||| | || | || | | |||||||| |||| | | |||||||||||
Db   374 ATGCTT--ATTACCTATACTACCTGGATTATTGGGGGCAGGGAACCCTGGTCACCGTCT 430

Qy   434 CCTCAGTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT 493
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT 490

Qy   494 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 550

Qy   554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 610

Qy   614 CCTCAGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 673
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 CCTCAGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 670

Qy   674 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG 733
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Db   671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG 730

Qy   734 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 793
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 790

Qy   794 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 853
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 850

Qy   854 CCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA 913
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 CCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA 910

Qy   914 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 973
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 970

Qy   974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCAACCAGGACTGGCTGAATG 1033
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCAACCAGGACTGGCTGAATG 1030

Qy   1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA 1093
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACCA 1090

Qy   1094 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1153
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Db   1091 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1150

Qy   1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1210

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Qy    17 TCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTCGTCTCCCAGGTGCAGCTGCAGGAGT   76
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Db    17 TCTTGCTCTTCCTTGTCTGTTGCTCGCGGTGTTGCTACGGCGTGTCCTGCAGGTGCAGCTGCAGGAGT   76

Qy    77 CGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGTCTCTGGTG   136
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Db    77 CTGGTCCTGGTGGTGGTGAAACCCACAGAGACCCTCACGCTGACTGACTGCCGTCTGGGT   136

Qy   137 GCTC---CATCAGCGGTGGTTATGCTGCGTGGGCTGGATCGGCAGCCCCAGGGAAGGGGC   193
         ||||   || |||||||||||||  |||||||| |||||||||||||||||||||||
Db   137 TCTCACTCAGCAACCCTAGAATGGGTGACCTGGATCGTCAGCCCCAGCCCCCGGGAAGGGCCC   196

Qy   194 TGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGAACACTACTACAACCCCTCCCTCA   253
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Db   197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAA---GTCCTTCAGTCCTTCTCTGA   253

Qy   254 AGAGTCAAGTCACCATTTCAACAGACACGTCAAGAACCAGTTCTCCCTGAAGCTGAACT   313
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Qy   314 CTATGACCGCCGCGACACGGCCGTGTATTACTGTGTATGAGATCGTCTTTTTCAGTTG   373
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Qy   374 TTGGAATGGTTTACAACAACTGGTTCGATGTCTCGGGGCCCGGGAGTCCTGGTCACCGTCT   433
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Db   374 ATGCTT---ATTACCTATACCTGGGATTATTGGGGCAGGGAACCCTGGTCACCGTCT   430

Qy   434 CCTCAGCTAGCACCAAGGGCCCATGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT   493
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Db   431 CCTCAGCTAGCACCAAGGGCCCATGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT   490

Qy   494 CTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAACTACTTCCCCGAACGGTGACGG   553
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Db   491 CTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAACTACTTCCCCGAACGGTGACGG   550

Qy   554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT   613
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Db   551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT   610

Qy   614 CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGTTGGGCACCC   673
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGTTGGGCACCC   670

Qy   674 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGCAG   733
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Db   671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG   730

Qy   734 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG   793
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG   790

Qy   794 GGGGACCGTCAGTCTTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA   853
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Db   791 GGGGACCGTCAGTCTTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA   850

Qy   854 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA   913
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   851 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA   910

Qy   914 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT   973
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Db   911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT   970

Qy   974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG   1033
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Db   971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG   1030

Qy  1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA   1093
         |||| ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA   1090
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Qy  1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC   1273
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Db  1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC   1270

Qy  1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA   1333
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Qy  1334 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT   1393
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Db  1331 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT   1390

Qy  1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1431
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Db  1391 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1428
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RESULT 10
US-08-634-224-17
; Sequence 17, Application US/08634224
; Patent No. 586125
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/634,224
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/488,376
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-150
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 836-6620
;   TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1428 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1428
US-08-634-224-17

Query Match   79.3%; Score 1134.8; DB 2; Length 1428;
Best Local Similarity   89.0%; Pred. No. 1.8e-264;
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

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Qy  1094  TCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGTGTACACCCTGCCCCATCCCGGG  1153
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Db  1091  TCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGTGTACACCCTGCCCCATCCCGGG  1150

Qy  1154  ATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTCGTCAAAGGCTTCTATCCCAGCG  1213
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Db  1151  ATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTCGTCAAAGGCTTCTATCCCAGCG  1210

Qy  1214  ACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCCGAGAACAACTACACAGAGACCACGCCCTC  1273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1211  ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGAGACCACGCCCTC  1270

Qy  1274  CGGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1333
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Db  1271  CGGTGCTGGACTCCGACGGGTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGACA  1330

Qy  1334  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1393
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Db  1331  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1390

Qy  1394  ACACGCAGAAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
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Db  1391  ACACGCAGAAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1428
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RESULT 11
US-08-634-400-17
; Sequence 17, Application US/08634400
; Patent No. 5939068
GENERAL INFORMATION:
    APPLICANT: BRAMS, Peter
    APPLICANT: CHAMAT, Soulaima Salim
    APPLICANT: PAN, Li-Zhen
    APPLICANT: WALSH, Edward E.
    APPLICANT: HEARD, Cheryl Janne
    APPLICANT: NEWMAN, Roland Anthony
    TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
    TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
    TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
    NUMBER OF SEQUENCES: 19
    CORRESPONDENCE ADDRESS:
       ADDRESSEE: Burns, Doane, Swecker & Mathis
       STREET: P.O. Box 1404
       CITY: Alexandria
       STATE: Virginia
       COUNTRY: United States
       ZIP: 22313-1404
    COMPUTER READABLE FORM:
       MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible
       OPERATING SYSTEM: PC-DOS/MS-DOS
       SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/08/634,400
       FILING DATE:
       CLASSIFICATION:
    PRIOR APPLICATION DATA:
       APPLICATION NUMBER: US 08/488,376
       FILING DATE: 07-JUN-1995
    ATTORNEY/AGENT INFORMATION:
       NAME: Teskin, Robin L.
       REGISTRATION NUMBER: 35,030
       REFERENCE/DOCKET NUMBER: 012712-150
    TELECOMMUNICATION INFORMATION:
       TELEPHONE: (703) 836-6620
       TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
    SEQUENCE CHARACTERISTICS:
       LENGTH: 1428 base pairs
       TYPE: nucleic acid
       STRANDEDNESS: single
       TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
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;
;    FEATURE:
;        NAME/KEY: CDS
;        LOCATION: 1..1428
US-08-634-400-17

Query Match   79.3%;   Score 1134.8;   DB 2;   Length 1428;
Best Local Similarity   89.0%;   Pred. No. 1.8e-264;
Matches 1262;  Conservative   0;  Mismatches 147;   Indels   9;   Gaps   3;
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Qy   17  TCTTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGTCGCAGGAGT  76
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Db   17  TCTTGCTCTTCCTTGTCCGCTGTTGCTACGGGTCGTCCCAGGTGCAGTTGCAGGAGT  76

Qy   77  CGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTG  136
         ||||| ||||||||  |||||  ||||||||||| |  ||||||||||||||||||||
Db   77  CTGGTCCTGGTGGTGAAACCCACAGACCCACGCTGACCTGCACCGTCTCTGGT  136

Qy  137  GCTC---CATCAGCGGTGGTTATGGCTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGC  193
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Db  137  TCTCACTCAGCAACCCTAGAATGGGTGTGACCTGGATCAGCCGTCAGCCCCCGGGAAGGGCC  196

Qy  194  TGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGAACACATTCTCCCTGAAGCTGAACT  253
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Db  197  TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAA---GTCCTTCAGTCCTTCTCTGA  253

Qy  254  AGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAACC  313
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Db  254  AGAGCAGATCACCACCTCCCAGAGCACACTCCCAGAAGCAGGTGGTCTCAAGCTTGACCA  313

Qy  314  CTATGACCGCCGCGGACACGGCCGTGTATTACTGTGAGAGATCGTCTTTTTCAGTTG  373
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Db  314  ACGTGACCCTGTGGACACAGCCACATATTACTGTGCACGGGTAGGACTGTGATGACATCA  373

Qy  374  TTGGAATGGTTTACAAACAACTGGTTCGATGTCGGGGCCCCGGGAGTTCTGCGTCACCGTCT  433
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Db  374  ATGCTT---ATTACCTATACACCTGGATTATTGGGGCCAGGGGCAGGGAACCCTGGTCACCGTCT  430

Qy  434  CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCTGCCCTGCTCCTGAAGAGCACCT  493
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Db  431  CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCTCCAAGAGCACCT  490

Qy  494  CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG  553
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Db  491  CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG  550

Qy  554  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCGGGCTGTCCTACAGT  613
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Db  551  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCGGGCTGTCCTACAGT  610

Qy  614  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  673
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Db  611  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  670

Qy  674  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  733
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Db  671  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  730

Qy  734  AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG  793
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Db  731  AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG  790

Qy  794  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCTCATGATCTCCCGGA  853
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Db  791  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA  850

Qy  854  CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  913
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Db  851  CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  910

Qy  914  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  973
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Db  911  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  970
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;      TELEFAX:  (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 1428 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
;      FEATURE:
;        NAME/KEY: CDS
;        LOCATION: 1..1428
US-08-635-878-17

Query Match       79.3%;    Score 1134.8;  DB 2;  Length 1428;
Best Local Similarity  89.0%;   Pred. No. 1.8e-264;
Matches 1262;  Conservative  0;  Mismatches 147;  Indels 9;  Gaps 3;
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Qy    17  TCTTCCTCCTCCTGGTGCCAGCTCCCAGATGGGTCCTGTCCCAGTGCAGCTGCAGGAGT  76
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Qy    77  CGGGCCCAGGACTGGTGAAGCCTTGGAGACCCTGTCCCTCACCTGCGCTGCGTCTCTCGGTG  136
              |||| |||||||||||||| |||||||||  ||| |||||||||||||| | |||||||||
Db    77  CTGGTCCTGGTGGTGTGGAGTGTGAAACCCACAGAGACCCTCACGGTGACCTGCACCGTCTCTGGGT  136

Qy   137  GCTC---CATCAGCGGTGGTTATGGCTGGGGCTGGGGTGACCTGGATCCGCCAGGAGGGC  193
              ||||      |||||  ||  | ||||||| |||||  |||| || |||||||||
Db   137  TCTCACTCAGCAACCCTAGAATGGTGTGACCTGGATCCGCCAGCCCCCGGGAAGGGCCC  196

Qy   194  TGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGAACACTACTACACCCCTCCCTCA  253
              ||||||||||||||||||     |||||||||||||||||||||||||||||
Db   197  TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAA---GTCCTTCAGTCCTTCTCTGA  253

Qy   254  AGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACACCAGTTCTCCCTGAAGCTGAACT  313
              |||| | ||||||||||||||||||||||| || |||||||||||||||||||||||||
Db   254  AGAGCAGACTCACCACCTTCACCACCTCCAGGACACCCAGAAGAGCCAGGTCGTCCTGACCA  313

Qy   314  CTATGACCGCCGGACACGGCCGTGTATTACTGTGTGGATGACATCGTCTTTTTTCAGTTG  373
              ||  ||||||||| ||| ||||| |||||||||| |||||||| ||| |||||||||||
Db   314  ACGTGGACCCTGTGACACAGCCACCACATATTACTGTGCACGGGTAGGACTGTATGACATCA  373

Qy   374  TTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCCGGGAGTCCTGGTCACCGTCT  433
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Db   374  ATGTT---ATTACCTATCTACCTGATTATTGGGGCAGGAACCCTGGTCTCGGTCACCGTCT  430

Qy   434  CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT  493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431  CCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT  490

Qy   494  CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG  553
              ||||||||||||| |||||||||||||||||||||||||||||||| |||||||||||||
Db   491  CTGGGGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG  550

Qy   554  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT  613
              ||||||||||| |||| |||||||||||||||||||||||||||||||||||| |||||||
Db   551  TGTCGTGGAACTTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT  610

Qy   614  CCTCAGCAGACTCTACTCCCTCAGCAGCGTGGGCACCC  673
              |||||||||||||||||||||||||||||||||||||||
Db   611  CCTCAGCAGACTCTACTCCCTCAGCAGCGTGGGCACCC  670

Qy   674  AGACCTACACCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671  AGACCTACACCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  730

Qy   734  AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG  793
              ||||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   731  AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG  790

Qy   794  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA  853
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Db   791  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA  850

Qy   974  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1033
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Db   971  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1030

Qy  1034  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1031  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1090

Qy  1094  TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1091  TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1150

Qy  1154  ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1151  ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1210

Qy  1214  ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC  1273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1211  ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC  1270

Qy  1274  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1333
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Db  1271  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1330

Qy  1334  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1393
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Db  1331  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1390

Qy  1394  ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
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Db  1391  ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1428
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RESULT 12
US-08-635-878-17
; Sequence 17, Application US/08635878
; Patent No. 5955364
GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/635,878
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/488,376
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-150
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 836-6620

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APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1428
US-08-770-057-17
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Query Match          79.3%;   Score 1134.8;   DB 2;   Length 1428;
Best Local Similarity 89.0%;   Pred. No. 1.8e-264;
Matches 1262;  Conservative    0;  Mismatches 147;   Indels   9;   Gaps   3;

Qy     17 TCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGAGCTGCAGGAGT  76
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Db     17 TCTTGCTTCCTTGTGTCGCTGTTGCTACGCGTGTCCCAGGTCCTCCGTGCAGTTGCAGGAGT  76

Qy     77 CGGGCCCAGGACTGGTGAAGCCTTCGGAGACCTGGTCCTCCACCGTGCGTGTCTCCGGTG  136
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Qy    137 GTCTC---CATCAGCGGTGGTTATGGCTGTCGGGCTGGAATGGGGCTGGATCCCGCAGCCCCCAGGGAAGGGGC  193
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Db    137 TCTCACTCAGCACCCTAGAATGGGGTGTGACCTGGATCCGTCAGCCGCCCGGGAAGGGCC  196

Qy    194 TGGAGTGGAGTGGAGTTCTATAGTAGTAGTAGTGGGAACAACTACTACACCCTCCCTCA  253
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Db    197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAA---GTCCTTCAGTCCTTCTCTGA  253

Qy    254 AGAGTCAAGTCACCATTCAACAGACACGTCAAGAACAGTTCTCCCTGAAGCTGAACT  313
          ||||  |||||||||||||||  |||||||||||||||||||
Db    254 AGAGCAGACTCACCACTCCCCAGGACACCTCCAGAAGCCAGGTGGTCCTAAGCTTGACCA  313

Qy    314 CTATGACCGCCGCGACACGGCCGTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTTG  373
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Db    314 ACGTGGACCCTGTGGACACAGCCACATATTACTGTGCACGGGTAGGACTGTATGACATCA  373

Qy    374 TTGGAATGGTTACAACAACTGGTTCGATGTCGGGGCTCTGGGGCAGGGAAGCCCTGGT  433
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Db    374 ATGCTT---ATTACCTATACCTTGGATTATTGGGGCCAGGGAACCCTGGTCACCGTCT  430

Qy    434 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCTTCCCCTGGCACCTC  493
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Db    431 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTGGCACACCT  490

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Db    491 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG  550

Qy    554 TGTCGTGGAACTCAGGCGCCTGAGCCAGCGGTGCACACCTTCCCGGCTGTCCTACAGT  613
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Db    551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT  610

Qy    614 CCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCCTCAGCAGCTTGGGCACCC  673
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Db    611 CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  670

Qy    674 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  733
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Db    671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  730
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Qy    854 CCCTGAGGTCACATGCCTGGTGGTGAGCGTGAGCAGCGTGAGGTCAAGTTCA  913
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Db    851 CCCTGAGGTCACATGCCTGGTGGTGAGCGTGAGCAGCGTGAGGTCAAGTTCA  910

Qy    914 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  973
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  970

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Db    971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAGTGGCTGAATG  1030

Qy   1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1093
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Db   1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1090

Qy   1094 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1153
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Db   1091 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1150

Qy   1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1213
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Db   1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC  1270

Qy   1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1333
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Qy   1334 GGTGGCAGCAGGGGAAGTCTTCTCATGATGCATGAGGCTCTGCACAACCACT  1393
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Db   1331 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1390

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Db   1391 ACACGCAGAAGAGCCCTCCCGTGTCCCGGGTAAATGA  1428
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RESULT 13
US-08-770-057-17
; Sequence 17, Application US/08770057
; Patent No. 5958765
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Burns, Doane, Swecker & Mathis
;     STREET: P.O. Box 1404
;     CITY: Alexandria
;     STATE: Virginia
;     COUNTRY: United States
;     ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/770,057
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
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                    COMPUTER: IBM PC compatible
                    OPERATING SYSTEM: PC-DOS/MS-DOS
                    SOFTWARE: PatentIn Release #1.0, Version #1.30
           CURRENT APPLICATION DATA:
                    APPLICATION NUMBER: US/09/335,697B
                    FILING DATE: 06-Jul-2000
                    CLASSIFICATION: <Unknown>
           PRIOR APPLICATION DATA:
                    APPLICATION NUMBER: 08/770,057
                    FILING DATE: <Unknown>
           ATTORNEY/AGENT INFORMATION:
                    NAME: Teskin, Robin L.
                    REGISTRATION NUMBER: 35,030
                    REFERENCE/DOCKET NUMBER: 012712-150
           TELECOMMUNICATION INFORMATION:
                    TELEPHONE: (703) 836-6620
                    TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
           SEQUENCE CHARACTERISTICS:
                    LENGTH: 1428 base pairs
                    TYPE: nucleic acid
                    STRANDEDNESS: single
                    TOPOLOGY: linear
           MOLECULE TYPE: DNA (genomic)
           FEATURE:
                    NAME/KEY: CDS
                    LOCATION: 1..1428
           SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-335-697B-17

Query Match             79.3%;   Score 1134.8;  DB 4;  Length 1428;
Best Local Similarity   89.0%;   Pred. No. 1.8e-264;
Matches 1262;  Conservative   0;  Mismatches 147;  Indels   9;  Gaps   3;

Qy     17 TCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGTCTGTCCCAGGTGCAGCTGCAGGAGT     76
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Db     17 TCTTGCTCTTCCTTGTCGCTGTTGCTACCGGTGTCCTGTCCCAGGTGCAGTTGCAGGAGT     76

Qy     77 CGGGGCCCAGAGCTGGTGAAGCCTTCGGAGACCCTGTCTCACCTGCGCTGTCTCTGGTG    136
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Db     77 CTGGTCCTGGTGGTGTGAAACCCACCAGAGACCCTCACGCTGACCTGCACCGTCTCTGGGT    136

Qy    137 GCTC---CATCAGCGGTGGTTATGGCTGGGGTGGATCGGCGTCCGCAGCCCCAGGGAAGGGGC    193
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Db    137 TCTCACTCAGCAACCCTAGAATGGGTGACCGGTGACCGTCAGCCCCCGGGAAGCCC    196

Qy    194 TGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGAACAACCTACTACAACCCTCCCTCA    253
          |||| |||| ||||||| ||||||||||||| |||| ||| |||||||||| ||||||||
Db    197 TAGAATGGCTGGAAACATTTTTTCGAGTGACGAGAA--GTCCTTCAGTCCTTCTCTGA    253

Qy    254 AGAGTCAAGTCACCATTTCAACAGACACGTCCAAGACACCAGTTCTCCCTGAAGCTGAACT    313
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Db    254 AGAGCAGACTCAACCACCTCCAGGACACCTACTTCCCGACGTGGTCCTAAGCTTGACCA    313

Qy    314 CTATGACCCGCCGGACACGGCCGTGTATTACTGTGTGAGAGATCGGTCTTTTTCAGTTG    373
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Db    314 ACGTGGACCCCGTGTGGACACAGCCACATATTACTGTGCACGGGTAGGACTGTATGACATCA    373

Qy    374 TTGGAATGGTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTCTGGTCACCGTCT    433
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Db    374 ATGCTT---ATTACCTATACTACCTGGATTATTGGGGGCAGGGAACCCCTGGTCACCGTCT    430

Qy    434 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT    493
          |||||||||||| |||| |||| |||| |||||||||| |||||||||||||| ||||||||
Db    431 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT    490

Qy    494 CTGGGGCACAGCAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG    553
          || ||||||||||||| |||||||| |||||||||||||||||||||||| |||||||||||
Db    491 CTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG    550

Qy    554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT    613
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Db    551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT    610

Qy    734 AGCCCAAATCTTGTGACAAAACTCACACATGCCACGTGCCCAGCACCTGAACTCCTGG    793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731 AGCCCAAATCTTGTGACAAAACTCACACATGCCACGTGCCCAGCACCTGAACTCCTGG    790

Qy    794 GGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA    853
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Db    791 GGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA    850

Qy    854 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA    913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA    910

Qy    914 ACTGTACGTGGACGGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT    973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 ACTGTACGTGGACGGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT    970

Qy    974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG   1033
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Db    971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG   1030

Qy   1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACCA   1093
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACCA   1090

Qy   1094 TCTCCAAAGCCAAAGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG   1153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 TCTCCAAAGCCAAAGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG   1150

Qy   1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG   1213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG   1210

Qy   1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC   1273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC   1270

Qy   1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA   1333
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Db   1271 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA   1330

Qy   1334 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT   1393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT   1390

Qy   1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1431
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Db   1391 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1428
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RESULT 14
US-09-335-697B-17
; Sequence 17, Application US/0935697B
; Patent No. 6200804
; GENERAL INFORMATION:
           APPLICANT: BRAMS, Peter
           CHAMAT, Soulaima Salim
           PAN, Li-Zhen
           WALSH, Edward E.
           HEARD, Cheryl Janne
           NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
           MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
           METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

```
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Burns, Doane, Swecker & Mathis
    STREET: P.O. Box 1404
    CITY: Alexandria
    STATE: Virginia
    COUNTRY: United States
    ZIP: 22313-1404
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/335,697B
    FILING DATE:
    CLASSIFICATION:
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/770,057
    FILING DATE:
ATTORNEY/AGENT INFORMATION:
    NAME: Teskin, Robin L.
    REGISTRATION NUMBER: 35,030
    REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (703) 836-6620
    TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
    LENGTH: 1428 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..1428
US-09-335-697B-17
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Best Local Similarity  89.0%;  Pred. No. 1.8e-264;
Matches 1262;  Conservative  0;  Mismatches 147;  Indels  9;  Gaps  3;

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Db    17  TCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTCCCAGGTCAGTTGCAGGAGT   76

Qy    77  CGGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACCTGCGCTGTCTCGGTG  136
          |||||||  ||||||||||||||||||||||| ||||||||||||||||||||||||||
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Qy   137  GCTC---CATCAGGCGGTGGTTATGGCTGGTGGGCTGGATCCGCCAGCCCCAGGGAAGGGGC  193
          |||    |||  ||||||||||||||||||||||  ||||||||  ||||||||||||||
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Qy   194  TGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGGAACACCTACTACAACCCCTCCCTCA  253
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Db   254  AGAGCAGACTCACCACCTCACCAGGCAGACACCTCCAGAGCAGCCAGTGCCTAAGCTTGACCA  313

Qy   314  CTATGACCCGCCGGACACGGCCGTGTATTACTGTGCAGATCGTCTTTTCAGTTG  373
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Qy   374  TTGGAATGTTTACAACACTGTTCGATGTCTGGGGCCCGGGAGTCTCGTCACCGTCT  433
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Qy   434  CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT  493
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Qy   734  AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG   793
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Qy   794  GGGGACCGTCAGTCTTCTCTTCCCCCCAAAACCCAAGGACACACCCTCATGATCTCCCGGA   853
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Db   791  GGGGACCGTCAGTCTTCTCTTCCCCCCAAAACCCAAGGACACACCCTCATGATCTCCCGGA   850

Qy   854  CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA   913
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Qy   914  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT   973
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Qy   974  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1033
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Qy  1034  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1093
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Qy  1154  ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1213
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RESULT 15
US-09-335-697B-17
; Sequence 17, Application US/09335697B
; Patent No. 6413771
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
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Qy   674  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  733
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Qy   1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACA  1093
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Qy   1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1333
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Qy   1334 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1393
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               GenCore version 5.1.4 p5 4578
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      March 29, 2003, 09:06:23 ; Search time 48.9575 Seconds
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Title:          US-09-758-173-12
Perfect score:  2549
Sequence:       1 MKHLWFFLLLVAAPRWVLSQ........MHEALHNHYTQKSLSLSPGK 476

Scoring table:  BLOSUM62
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Searched:       908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:    908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2549	100.0	476	18	AAW01822	Primatised anti-hu
2	2549	100.0	476	19	AAW63765	Macaque primatized
3	2549	100.0	476	23	AAU11646	Protein sequence o
4	2342.5	91.9	473	22	AAB36206	Human immune syste
5	2309	90.6	476	18	AAW01818	Primatised anti-hu
6	2309	90.6	476	19	AAW63761	Macaque primatized
7	2309	90.6	476	23	AAU11539	Protein sequence o
8	2296.5	90.1	475	17	AAR93553	Monoclonal antibod
9	2278	89.4	470	21	AAY44721	Human immune syste
10	2217	87.0	472	17	AAR93166	Anti-rhesus D reco
11	2162.5	84.8	467	13	AAR22759	Reshaped CD4 antib
12	2159.5	84.7	467	13	AAR22758	Reshaped CD4 antib
13	2148	84.3	470	13	AAR22757	Reshaped CAMPATH-1
14	2145.5	84.2	467	18	AAW14927	Human gamma-4PE he
15	2144.5	84.1	467	18	AAW14925	Human gamma-4 heav
16	2138.5	83.9	446	17	AAW05829	Humanised 1D10 ant
17	2137.5	83.9	467	18	AAW14926	Human gamma-4E hea
18	2134.5	83.7	581	22	AAB81972	Ganglioside GD2 sp
19	2126.5	83.4	475	18	AAW11639	Human anti-RSV mon
20	2126.5	83.4	475	22	AAG63640	Amino acid sequenc
21	2126	83.4	451	20	AAY50031	Human E27 anti-IgE
22	2126	83.4	451	20	AAW95663	Mus musculus anti-
23	2126	83.4	451	21	AAB07473	Amino acid sequenc
24	2126	83.4	451	22	AAB74212	E27 anti-IgE antib
25	2126	83.4	451	22	AAB76952	Full length heavy
26	2124	83.3	451	20	AAW95659	Mus musculus anti-
27	2124	83.3	451	21	AAW95661	Mus musculus anti-
28	2124	83.3	451	21	AAY85201	Light chain amino
29	2124	83.3	451	22	AAB47088	Anti-IgE antibody,
30	2124	83.3	451	22	AAB76948	Full length heavy
31	2124	83.3	451	22	AAB76950	Full length heavy
32	2122.5	83.3	450	22	AAE10515	Humanised high pot
33	2121	83.2	462	21	AAB26884	Human immunoglobul
34	2120.5	83.2	450	22	AAE10521	Humanised high pot
35	2119.5	83.2	450	22	AAE10511	Humanised high pot
36	2119.5	83.2	450	22	AAE10513	Humanised high pot
37	2118.5	83.1	450	22	AAE10509	Humanised high pot
38	2117.5	83.1	450	22	AAE10517	Humanised high pot
39	2115.5	83.0	450	22	AAE10523	Humanised high pot
40	2115.5	83.0	450	22	AAE10525	Humanised high pot
41	2114.5	83.0	450	22	AAE10519	Humanised high pot
42	2094.5	82.2	475	18	AAW11641	Human anti-RSV mon
43	2094.5	82.2	477	22	AAU14288	Human novel protei
44	2094	82.1	476	22	AAB49243	Chimeric 4H6 anti-
45	2093	82.1	453	14	AAR33311	Humanised MaE11 Ve

ALIGNMENTS

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RESULT 1
AAW01822
ID   AAW01822 standard; Protein; 476 AA.
XX
AC   AAW01822;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
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DR   N-PSDB; AAT62513.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 14; Fig 10B; 81pp; English.
XX
CC   2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 16C10.  Cloned 16C10 light and
CC   heavy variable genes (see also AAT62512 and AAT62513) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells.  Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   476 AA;

Query Match             100.0%;  Score 2549;  DB 18;  Length 476;
Best Local Similarity   100.0%;  Pred. No. 6e-149;
Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy        181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy        241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy        301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

Qy        361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy        421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 2
AAW63765
ID   AAW63765 standard; Protein; 476 AA.
XX
AC   AAW63765;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 16C10 heavy chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;  97WO-US19906.
XX
PR   08-NOV-1996;  96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35489.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 16C10 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence   476 AA;

Query Match             100.0%;  Score 2549;  DB 19;  Length 476;
Best Local Similarity   100.0%;  Pred. No. 6e-149;
Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60

Qy         61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISDTSKNQFSLKLNSMTAADTAVYYCVRDR 120

Qy        121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy        181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy        241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy        301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
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```
SQ    Sequence   476 AA;

Query Match             100.0%;  Score 2549;  DB 23;  Length 476;
Best Local Similarity   100.0%;  Pred. No. 6e-149;
Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60

Qy     61 PGKGLEWIGSFYSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PGKGLEWIGSFYSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120

Qy    121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy    181 EPVTVSWNSGALTSGVHTFPAVLQSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EPVTVSWNSGALTSGVHTFPAVLQSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy    241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy    301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

Qy    361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy    421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
```

```
RESULT 3
AAU11646
ID    AAU11646 standard; Protein; 476 AA.
XX
AC    AAU11646;
XX
DT    12-MAR-2002  (first entry)
XX
DE    Protein sequence of primatised form of the heavy chain of 16C10 antibody.
XX
KW    Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW    neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW    B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW    tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW    graft-vs-host disease; immunosuppression; organ rejection;
KW    interleukin-2; IL-2; mutant; mutein.
XX
OS    Chimeric - Homo sapiens.
OS    Chimeric - Macaca sp.
OS    Synthetic.
XX
PN    WO200189567-A1.
XX
PD    29-NOV-2001.
XX
PF    22-MAY-2001; 2001WO-US16364.
XX
PR    22-MAY-2000; 2000US-0576424.
XX
PA    (IDEC-) IDEC PHARM CORP.
XX
PI    Anderson DR,  Hanna N,  Brams P;
XX
DR    WPI; 2002-089895/12.
DR    N-PSDB; AAS17247.
XX
PT    Use of monoclonal antibody which specifically binds to B7.1 antigen
PT    CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT    treating cancer, graft-vs-host disease and autoimmune disease such as
PT    allergy -
XX
PS    Example 8; Fig 5b; 89pp; English.
XX
CC    The present invention relates to a new use of a monoclonal antibody
CC    which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC    (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC    useful for treating diseases such as B cell cancer, lymphoma, a
CC    cancer where B cells promote the growth and/or metastasis of tumours,
CC    B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC    idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC    type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC    anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC    or graft-vs-host disease. The antibody is useful for immunosuppression
CC    in a human or animal and for treating or preventing resistance to or
CC    rejection of transplanted organ or tissue for treating proliferative
CC    and hyperproliferative diseases, for treating reversible obstructive
CC    airways disease, intestinal inflammations and allergies e.g. Crohn's
CC    disease and ulcerative colitis, food-related allergies e.g. migraine,
CC    rhinitis and eczema, and other types of allergies. The present protein
CC    sequence represents the heavy chain of 16C10, a primatised antibody
CC    used in the invention to induce apoptosis and inhibit production of
CC    interleukin-2 (IL-2).
XX
```

```
RESULT 4
AAB36206
ID    AAB36206 standard; protein; 473 AA.
XX
AC    AAB36206;
XX
DT    15-FEB-2001  (first entry)
XX
DE    Human immune system associated protein HISAP-4.
XX
KW    Human; immune system associated protein; HISAP-4;  immune disorder;
KW    infection; autoimmune disease; cancer.
XX
OS    Homo sapiens.
XX
PN    US613541-A.
XX
PD    24-OCT-2000.
XX
PF    27-MAR-1998;   98US-0049672.
XX
PR    27-MAR-1998;   98US-0049672.
XX
PA    (INCY-) INCYTE PHARM INC.
XX
PI    Tang YT,  Yue H,  Lal P,   Corley NC,  Guegler KJ,   Baughn MR;
PI    Hillman JL,  Au-Young J;
XX
DR    WPI; 2001-030926/04.
DR    N-PSDB; AAC66522.
XX
PT    New human immune system associated proteins (HISAP) and polynucleotides
PT    encoding the HISAP, useful for diagnosing, treating or preventing
PT    immune or cell proliferative disorders or infections -
```

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XX
PS   Claim 1; Column 53-56; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ   Sequence  473 AA;

Query Match        91.9%;    Score 2342.5;  DB 22;  Length 473;
Best Local Similarity  93.3%;  Pred. No. 3e-136;
Matches 446;   Conservative  9;  Mismatches 16;  Indels  7;  Gaps  4;

Qy    1  MKHLWFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSI-SGGYGWGWIRQ  59
         |||||||||||||||||||||||||||||||||||||||||||||||| |||| |||||
Db    1  MKHLWFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQ  60

Qy   60  PPGKGLEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRD  119
         |||||||||||||||||||||||||||||||:::|:|||||:|:||:||||||||||||
Db   61  PPGKGLEWIGYIY-YSSGTLYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARD  119

Qy  120  RLFSVVGMVYNNW-FDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  178
         |:||   |:  | |||||||||||||||||||||||||||||||||||||||||||||||
Db  120  D---VGLRGGNYGMDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  175

Qy  179  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  238
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  176  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  235

Qy  239  KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  298
         |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  236  KVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  295

Qy  299  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  358
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  296  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  355

Qy  359  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  418
         |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db  356  APIEKTISKAKGQPREPQVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  415

Qy  419  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  416  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  473

RESULT 5
AAW01818
ID   AAW01818 standard; Protein; 476 AA.
XX
AC   AAW01818;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macacque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
```

```
PD   19-DEC-1996.
XX
PF   06-JUN-1996;    96WO-US10053.
PR   07-JUN-1995;    95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT62510.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 6; Fig 8B; 81pp; English.
XX
CC   2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 7C10.  Cloned 7C10 light and heavy
CC   variable genes (see also AAT62509 and AAT62510) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells.  Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence  476 AA;

Query Match        90.6%;    Score 2309;  DB 18;  Length 476;
Best Local Similarity  91.2%;  Pred. No. 3.5e-134;
Matches 434;   Conservative  9;  Mismatches 33;  Indels  0;  Gaps  0;

Qy    1  MKHLWFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60
         |||||||||||||||||||||||||:::|:|||||||||||||||||||| |||||||||
Db    1  MKHLWFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT  60

Qy   61  PGKGLEWIGSFYSSSGNTYNPSLKSQVIISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120
         |||:||| ||||:|||||||||||:|:||| |||||||||||:|||||||||||||||||
Db   61  PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP  120

Qy  121  LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPP  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180

Qy  181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240

Qy  241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP  300

Qy  301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  360

Qy  361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY  420

Qy  421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476

RESULT 6
AAW63761
ID   AAW63761 standard; Protein; 476 AA.
XX
```

```
Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 EVKLFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

Qy  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
```

RESULT 7
AAU11539
ID   AAU11539 standard; Protein; 476 AA.
XX
AC   AAU11539;
XX
DT   12-MAR-2002 (first entry)
XX
DE   Protein sequence of primatised form of the heavy chain of 7C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   N-PSDB; AAS17243.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 3b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis

---

AC   AAW63761;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 7C10 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
PN   WO981706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35485.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7C10 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions. Particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 476 AA;

Query Match   90.6%; Score 2309; DB 19; Length 476;
Best Local Similarity 91.2%; Pred. No. 3.5e-134;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

Qy   1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
          |||||||||||||||||||||| :::||:::|::||||||||||||::|||||||||||
Db   1 MKHLWFPLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT 60

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
          |||||||||:|::.: ||||||||||||||:|:||||||:||||::|||||||||||
Db   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120

Qy 121 LFSVVGMVYNNWFDVWGQGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 RPDCTTICYGGWVDWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
```

```
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present protein
CC   sequence represents the heavy chain of 7C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 476 AA;

Query Match         90.6%;  Score 2309;  DB 23;  Length 476;
Best Local Similarity 91.2%;  Pred. No. 3.5e-134;
Matches 434;  Conservative 9;  Mismatches 33;  Indels 0;  Gaps 0;

Qy  1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP  60
       |||||||||||||||||||||    ||  ||:||||||||||| |||||||  |  |||||
Db  1  MKHLWFFLLLVAAPRWVLSQVKLQQWEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT   60

Qy 61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
       | :|||||                        ||||||      |||||||||||
Db 61  PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120

Qy 121 LFSVVGMYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
             :|||||||||||||||||||||||||||||||||||||||
Db 121 RPDCTTICYGGWDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

Qy 181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240

Qy 241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Qy 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

Qy 361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Qy 421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 8
AAR93553
ID   AAR93553 standard; Protein; 475 AA.
XX
AC   AAR93553;
XX
DT   20-AUG-1996 (first entry)
XX
DE   Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
XX
KW   Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW   65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..19
FT                  /note= "Signal peptide"
FT   Protein        20..475
FT                  /note= "Mature heavy chain"
XX
PN   JP08038178-A;
```

```
PD   13-FEB-1996.
XX
PF   20-FEB-1995;  95JP-0030742.
XX
PR   18-FEB-1994;  94JP-0021628.
XX
PA   (NISN ) NISSHINBO IND INC.
PA   (TANA/) TANAKA H.
XX
DR   WPI; 1996-154852/16.
DR   N-PSDB; AAT18059.
XX
PT   Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT   produced by primer amplification, used in the diagnosis of hCMV
PT   infection
XX
PS   Claim 4; Page 16-18; 22pp; Japanese.
XX
CC   The sequences given in AAR93553-54 represent the heavy and light chains
CC   respectively of a monoclonal antibody against a 65 kD antigen of human
CC   cytomegalovirus (hCMV). The DNA's encoding these sequences were
CC   amplified using the sequences given in AAT18040-58. The monoclonal
CC   antibody may be used in the diagnosis of hCMV.
XX
SQ   Sequence 475 AA;

Query Match         90.1%;  Score 2296.5;  DB 17;  Length 475;
Best Local Similarity 91.6%;  Pred. No. 2e-133;
Matches 437;  Conservative 10;  Mismatches 27;  Indels 3;  Gaps 3;

Qy   1  MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSIS-GGYGWGWIRQ  59
        |||||||||||||||||||  ||||||||||||||||||| |||| |||   |  | |||
Db   1  MKHLWFFLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGDSISRSSYSWGCIRQ  60

Qy  60  PPGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRD 119
        |||||||||  |  | ||| ||||||||                ||||||||||||||
Db  61  PPGKGLEWIGTIY-YSGSTYNPSLKSRVTISVDASNNQFSLKLSSVTAADTAVYYCART  119

Qy 120  RLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
          : ::          |  | |||||||||||||||||||||||||||||||||||||||
Db 120  SP-QYYDLLTGSFPSVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 178

Qy 180  PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179  PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 238

Qy 240  VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
        ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 239  VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 298

Qy 300  PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 299  PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 358

Qy 360  PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 359  PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 418

Qy 420  YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 419  YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475

RESULT 9
AAY44721
ID   AAY44721 standard; Protein; 470 AA.
XX
AC   AAY44721;
XX
DT   25-APR-2000 (first entry)
XX
DE   Human immune system molecule, ISMO-2.
XX
```

KW   Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW   treatment; prevention; cell proliferation; immune system disorder.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /label= Signal_peptide
FT   Protein   20..470
FT   /label= Mature_ISMO-2
FT   Modified-site   120
FT   /note= "N-glycosylated"
FT   Modified-site   320
FT   /note= "N-glycosylated"
FT   Modified-site   105
FT   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   232
FT   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   290
FT   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   377
FT   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   47
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   81
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   92
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   98
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   142
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   154
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   322
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   347
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   460
FT   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   69
FT   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   319
FT   /note= "Tyrosine kinase phosphorylation site"
FT   Region   387..409
FT   /note= "conserved Ig/MHC protein block"
FT   Region   446..463
FT   /note= "conserved Ig/MHC protein block"
FT   Domain   34..116
FT   /note= "shows similarity to Ig superfamily protein
FT   domain"
FT   Domain   160..225
FT   /note= "shows similarity to Ig superfamily protein
FT   domain"
FT   Domain   383..450
FT   /note= "shows similarity to Ig superfamily protein
FT   domain"
XX
PN   WO200000608-A2.
XX
PD   06-JAN-2000.
XX
PF   21-JUN-1999; 99WO-US13995.
XX
PR   30-JUN-1998; 98US-0107223.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
PI   Baughn MR;
XX
DR   WPI; 2000-170916/15.
DR   N-PSDB; AAZ50012.

Query Match   89.4%; Score 2278; DB 21; Length 470;
Best Local Similarity   91.4%; Pred. No. 2.7e-132;
Matches 435; Conservative   9; Mismatches   26; Indels   6; Gaps   3;

Qy   1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
           ||||||||||||||||||||||||:|||||||||||||||||||||| | |:|:||||||
Db   1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSIR-SYYNWIRLP 59

Qy   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
           |||||||||:| :|:||||||||||| | |:||||||||||:|:|:||||||||||
Db   60 PGKGLEWIGYIY-TSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARPP 118

Qy   121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
           |: :.   :||||||||||||||||||||||||||||||||||
Db   119 PNATTTTVWTS---GAKGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 174

Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   175 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 234

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   235 DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294

Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   295 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354

Qy   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   355 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 414

Qy   421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           |||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   415 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 470

```
Qy    368  AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  427
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364  AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  423

Qy    428  DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    424  DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  472
```

RESULT 11
AAR22759
ID   AAR22759   standard; Protein; 467 AA.
XX
AC   AAR22759;
XX
DT   20-OCT-1992 (first entry)
XX
DE   Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.
XX
KW   Antigen; CDR; complementarity determining region; graft rejection;
KW   autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS   Rattus rattus.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /note= "signal peptide"
FT   Peptide   20..467
FT   /note= "mature peptide"
FT   Region   50..54
FT   /note= "Complementarity determining region 1"
FT   Region   69..85
FT   /note= "Complementarity determining region 2"
FT   Region   118..126
FT   /note= "Complementarity determining region 3"
XX
PN   WO9205274-A.
XX
PD   02-APR-1992.
XX
PF   16-SEP-1991; 91WO-GB01578.
XX
PR   17-SEP-1990; 90GB-0020282.
XX
PA   (GORM/) GORMAN S D.
XX
PI   Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX
DR   WPI; 1992-132139/16.
DR   N-PSDB; AAQ23581.
XX
PT   Humanisation of antibodies binding to human CD4 antigen - by
PT   mutation of framework-encoding regions of DNA encoding variable
PT   domain of rat or mouse antibody chain
XX
PS   Disclosure; Fig 7; 74pp; English.
XX
CC   The sequence is that of the reshaped CD4 antibody heavy chain
CC   CD4VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance
CC   against an antigen. It can also be used to alleviate autoimmune diseases
CC   such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC   to a graft, e.g. an organ graft or a bone marrow transplantation can
CC   also be useful to alleviate allergies. Tolerance to allergens could
CC   also be achieved. See also AAR22753-R22763.
XX
SQ   Sequence 467 AA;

Query Match   84.8%; Score 2162.5; DB 13; Length 467;
Best Local Similarity   87.6%; Pred. No. 3.4e-125;
Matches 411; Conservative 18; Mismatches 31; Indels 9; Gaps 3;

```
Qy      8  LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW  67
           | ||||||||||||||||||||||| |||||  |:|||||||   ||||||||||
Db      8  LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW  67
```

```
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= signal peptide
FT                   /note= "mouse VH signal peptide sequence encoded by
FT                   synthetic linker"
FT   Protein         20..472
FT                   /label= heavy_chain
FT                   /note= "human-gamma 1 chain constant region
FT                   and the variable region from anti-rhesus D
FT                   antibody D7C2"
XX
FR2724182-A1.
XX
PD   08-MAR-1996.
XX
PF   02-SEP-1994;  94FR-0010566.
PR   02-SEP-1994;  94FR-0010566.
XX
PA   (INSP ) INST PASTEUR.
PA   (PROT-) PROTEINE PERFORMANCE.
XX
PI   Chaabihi H, Edelman L, Kaczorek M, Margaritte C;
XX
DR   WPI; 1996-162018/17.
DR   N-PSDB; AAT26889.
XX
PT   Recombinant anti-rhesus D monoclonal antibody - expressed by
PT   baculovirus-transformed insect cells and useful for preventing
PT   haemolysis in new-born babies
XX
PS   Example 2; Page 35-37; 46pp; French.
XX
CC   The human monoclonal antibody D7C2, of isotype IgM, recognises a
CC   30-32 kD polypeptide on the membrane of rhesus positive red blood
CC   cells. The antibody agglutinates rhesus positive cells but not
CC   rhesus negative cells and is useful diagnostically and also for
CC   preventing haemolysis in new-born rhesus positive babies.
CC   Recombinant IgM-D7C2 can be produced by insect cells which have
CC   been transformed by a baculoviral vector comprising a D7C2
CC   expression cassette. The present sequence is that of a recombinant
CC   IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
XX
SQ   Sequence 472 AA;

Query Match             87.0%;  Score 2217;  DB 17;  Length 472;
Best Local Similarity   90.4%;  Pred. No. 1.6e-128;
Matches 424;  Conservative  9;  Mismatches 32;  Indels  4;  Gaps 3;
```

```
Qy      8  LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW   67
           | |:|| ||:|||||||||||||  |||||||||||||||||: --|||||||||||||||
Db      8  LFLVATATGVHSQVQLQQWGAGLLKPSETLSLTCTVYGGSFS--GYYWSWIRQPPGKGLEW   66

Qy     68  IGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGM  127
           |||| || |||||||||| ||:||  |||| | |||| | ||| ||||||||
Db     67  IGEI-NHSGSTNYNPSLKSRVTISVDTSKNQFSLKLNSVTAADTAVYYCARAPEYK--WK  123

Qy    128  VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW  187
           |||| |||| |||| |||||||||||||||||||||||||||||||||||||||||||||
Db    124  YHGDWFDPWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW  183

Qy    188  NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK  247
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db    184  NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK  243

Qy    248  SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY  307
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244  SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY  303

Qy    308  VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK  367
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304  VDGVEVHNAKTKPREEQYNSTYRVVSVLKVLHQDWLNGKEYKCKVSNKALPAPIEKTISK  363
```

```
PT   Humanisation of antibodies binding to human CD4 antigen - by
PT   mutation of framework-encoding regions of DNA encoding variable
PT   domain of rat or mouse antibody chain
XX
PS   Disclosure; Fig 6; 74pp; English.
XX
CC   The sequence is that of the reshaped CD4 antibody heavy chain
CC   CD4VHNEW-Thr30. Reshaped CD4 antibody can be used to induce tolerance
CC   against an antigen. It can also be used to alleviate autoimmune diseases
CC   such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC   to a graft, e.g. an organ graft or a bone marrow transplantation can
CC   also be useful to alleviate allergies. Tolerance to allergens could
CC   also be achieved. See also AAR22753-R22763.
XX
SQ   Sequence    467 AA;

Query Match             84.7%;  Score 2159.5;  DB 13;  Length 467;
Best Local Similarity   87.4%;  Pred. No. 5.3e-125;
Matches  410;  Conservative   19;  Mismatches   31;  Indels    9;  Gaps    3;

Qy          8 LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSLSGGYGWGWIRQPPGKGLEW 67
                ||| :|:::::||||||||||||||:.|| ||||||:.||  |:  ||.||||||.|||
Db          8 LFLVATATGVHSQVQLQESGPGLVRPSQTLSLTCTVSGFTFT-NYGMAWVRQPPGRGLEW 66

Qy         68 IGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGM 127
                ||:.: :.|.||    ||:|| .:|:||||||| |.|:.|||||||||||||: ::||
Db         67 IGTISHDGSDTYFRDSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARQG--TIAGI 124

Qy        128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 187
               :        |.||:||||||||||||||||||||||||||||||||||||||||||||||
Db        125 RH------WGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 178

Qy        188 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||.|||
Db        179 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK 238

Qy        248 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 298

Qy        308 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 358

Qy        368 AKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 AKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 418

Qy        428 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 13
AAR22757
ID   AAR22757 standard; Protein; 470 AA.
XX
AC   AAR22757;
XX
DT   20-OCT-1992  (first entry)
XX
DE   Reshaped CAMPATH-1 antibody heavy chain.
XX
KW   Antigen; CDR; complementarity determining region; graft rejection;
KW   autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   Region          50..54
FT                   /note= "Complementarity determining region 1"
FT   Region          69..87
FT                   /note= "Complementarity determining region 2"
```

```
Db          8 LFLVATATGVHSQVQLQESGPGLVRPSQTLSLTCTVSGFTFS-NYGMAWVRQPPGRGLEW 66

Qy         68 IGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGM 127
Db         67 IGTISHDGSDTYFRDSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARQG--TIAGI 124

Qy        128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 187
Db        125 RH------WGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 178

Qy        188 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
Db        179 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK 238

Qy        248 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 307
Db        239 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 298

Qy        308 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 367
Db        299 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 358

Qy        368 AKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 427
Db        359 AKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 418

Qy        428 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db        419 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 12
AAR22758
ID   AAR22758 standard; Protein; 467 AA.
XX
AC   AAR22758;
XX
DT   20-OCT-1992  (first entry)
XX
DE   Reshaped CD4 antibody heavy chain CD4VHNEW-Thr30.
XX
KW   Antigen; CDR; complementarity determining region; graft rejection;
KW   autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Peptide         20..467
FT                   /note= "mature peptide"
FT   Region          50..54
FT                   /note= "Complementarity determining region 1"
FT   Region          69..85
FT                   /note= "Complementarity determining region 2"
FT   Region          118..126
FT                   /note= "Complementarity determining region 3"
XX
PN   WO9205274-A.
XX
PD   02-APR-1992.
XX
PF   16-SEP-1991; 91WO-GB01578.
XX
PR   17-SEP-1990; 90GB-0020282.
XX
PA   (GORM/) GORMAN S D.
XX
PI   Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX
DR   WPI; 1992-132139/16.
DR   N-PSDB; AAQ23571.
XX
```

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FT   Region          101..110
FT                   /note= "Complementarity determining region 3"
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Peptide         20..470
FT                   /note= "mature peptide"
XX
PN   WO9205274-A.
XX
PD   02-APR-1992.
XX
PF   16-SEP-1991;
PR   17-SEP-1990;
XX
PA   (GORM/) GORMAN S D.
XX
PI   Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX
DR   WPI; 1992-132139/16.
DR   N-PSDB; AAQ23570.
XX
PT   Humanisation of antibodies binding to human CD4 antigen - by
PT   mutation of framework-encoding regions of DNA encoding variable
PT   domain of rat or mouse antibody chain
XX
PS   Disclosure; Fig 5; 74pp; English.
XX
CC   The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.
CC   Reshaped CD4 antibody can be used to induce tolerance against an
CC   antigen. It can also be used to alleviate autoimmune diseases such
CC   as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC   to a graft, e.g. an organ graft or a bone marrow transplantation can
CC   also be useful to alleviate allergies. Tolerance to allergens could
CC   also be achieved. See also AAR22754-R22763.
XX
SQ   Sequence     470 AA;

Query Match             84.3%;  Score 2148;  DB 13;  Length 470;
Best Local Similarity   87.3%;  Pred. No. 2.7e-124;
Matches  411;  Conservative   16;  Mismatches   34;  Indels   10;  Gaps  3;

Qy    8  LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW   67
Db    8  LFLVATATGVHSQVQLEESGPGLVRPSQTLSLTCTVSGFTFTDFY-MNWVRQPPGRGLEW   66

Qy   68  IGSFYSSSG--NTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVV  125
Db   67  IGFIRDKAKGYTTEYNPSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCAREGHTAAP  126

Qy  126  GMYYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV  185
Db  127  ------FDYWGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV  179

Qy  186  SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAE  245
Db  180  SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE  239

Qy  246  PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN  305
Db  240  PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN  299

Qy  306  WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI  365
Db  300  WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI  359

Qy  366  SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP  425
Db  360  SKAKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP  419

Qy  426  VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
Db  420  VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  470
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RESULT 14
AAW14927
ID   AAW14927 standard; Protein; 467 AA.
XX
AC   AAW14927;
XX
DT   18-OCT-1997 (first entry)
XX
DE   Human gamma-4PE heavy chain.
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9 gamma 4PE.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 248
FT                   /note= "site of S229P mutation"
FT   Misc-difference 255
FT                   /note= "site of L236E mutation"
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996;  96WO-US14324.
PR   06-SEP-1995;  95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   N-PSDB; AAT62870.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Claim 6; Page 91-93; 155pp; English.
XX
CC   3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
CC   regions of human gamma-4, gamma-4E carrying an L236E mutation in
CC   the hinge region, and gamma-4PE carrying L236E and S229P mutations.
CC   They can be incorporated into novel monoclonal and chimeric
CC   antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
CC   which the human IgG4 Fc binding domain framework is combined with
CC   the antigen binding domains (see also AAW14922-23) of macaque anti-
CC   human CD4 monoclonal antibody E9.1.  These antibodies show high
CC   affinity to human CD4, have little or no immunogenicity in humans
CC   and show reduced or absence of effector function. The gamma-4E and
CC   -4PE mutations confer activity enhanced stability and eliminate
CC   depleting activity. The antibodies can be used to treat autoimmune
CC   diseases such as rheumatoid arthritis.
XX
SQ   Sequence     467 AA;

Query Match             84.2%;  Score 2145.5;  DB 18;  Length 467;
Best Local Similarity   85.9%;  Pred. No. 3.8e-124;
Matches  409;  Conservative   19;  Mismatches   39;  Indels   9;  Gaps  2;

Qy    1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP   60
Db    1  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQS   60

Qy   61  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR  120
Db   61  PGKGLEWIGFYSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR    :
```

CC   human CD4 monoclonal antibody E9.1. These antibodies show high
CC   affinity to human CD4, have little or no immunogenicity in humans
CC   and show reduced or absence of effector function. They can be used
CC   to treat autoimmune diseases such as rheumatoid arthritis.
XX
SQ   Sequence   467 AA;

Query Match   84.1%; Score 2144.5; DB 18; Length 467;
Best Local Similarity   85.9%; Pred. No. 4.4e-124;
Matches 409; Conservative   19; Mismatches   39; Indels   9; Gaps   2;

Qy   1 MKGHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP   60
           ||||| ||||||||||||||||||||||||||||||||| :|||||||: :|||||| |||
Db   1 MKGHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCSVSGGSISGDYWFWIRQS   60

Qy   61 PGKGLEWIGSFYSSSGNTYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
           ||||||||| |||| |||||||||||||| :::|||||||||| :||||||||||||||::
Db   61 PGKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCASNI 120

Qy   121 LFSVGMVYNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                :| ||||| ||||||||||||||||||||||||| |:||||||||||||||
Db   121 L------KYLHWLLYWQGGVLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP 174

Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
           ||||||||||||||||||||||||||||||||||||||||||||| :||::||||||||||
Db   175 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKV 234

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
           ||:|| | || ||: : |||| ||||||||||||||||||||||||||||||||||: |
Db   235 DKRVESK---YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDP 291

Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
           || :|||||||||||||||||||||||:||||||||||||||||||||||||||||||| :
Db   292 EVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS 351

Qy   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
           |||||||||||||||||||||||:: :|||||||||||||||||||||||||||||||||
Db   352 IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411

Qy   421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ||||||||||||||||| |||||||:||||||||||||||||||||||||||| ||
Db   412 KTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 467

Search completed: March 29, 2003, 09:10:22
Job time : 49.9575 secs

Db   61 PGKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCASNI 120
           ||||||||| |||| |||||||||||||| :::|||||||||| :||||||||||||||::
Qy   121 LFSVGMVYNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                :| ||||| ||||||||||||||||||||||||| |:||||||||||||||
Db   121 L------KYLHWLLYWQGGVLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP 174

Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
           ||||||||||||||||||||||||||||||||||||||||||||| :||::||||||||||
Db   175 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKV 234

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
           ||:|| | || ||: : |||| ||||||||||||||||||||||||||||||||||: |
Db   235 DKRVESK---YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDP 291

Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
           || :|||||||||||||||||||||||:||||||||||||||||||||||||||||||| :
Db   292 EVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS 351

Qy   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
           |||||||||||||||||||||||:: :|||||||||||||||||||||||||||||||||
Db   352 IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411

Qy   421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ||||||||||||||||| |||||||:||||||||||||||||||||||||||| ||
Db   412 KTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 467

RESULT 15
AAW14925
ID   AAW14925 standard; Protein; 467 AA.
XX
AC   AAW14925;
XX
DT   18-OCT-1997 (first entry)
XX
DE   Human gamma-4 heavy chain.
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9 gamma 4.
XX
OS   Homo sapiens.
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996; 96WO-US14324.
XX
PR   06-SEP-1995; 95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   N-PSDB; AAT62868.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Claim 6; Page 82-84; 155pp; English.
XX
CC   3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
CC   regions of human gamma-4, gamma-4E carrying an L236E mutation in
CC   the hinge region, and gamma-4PE carrying L236E and S229P mutations.
CC   They can be incorporated into novel monoclonal and chimeric
CC   antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
CC   which the human IgG4 Fc binding domain framework is combined with
CC   the antigen binding domains (see also AAW14922-23) of macaque anti-

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                    GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:        March 29, 2003, 09:14:52 ; Search time 9.04722 Seconds
                                          (without alignments)
                                          1531.829 Million cell updates/sec

Title:         US-09-758-173-10
Perfect score: 1232
Sequence:      1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:      237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters:     237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications_AA:*
          1:   /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
          2:   /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
          3:   /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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          5:   /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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          7:   /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
          8:   /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
          9:   /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
         10:   /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
         11:   /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
         12:   /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
         13:   /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	1232	100.0	236	9	US-10-124-905-10	Sequence 10, Appl	
2	1232	100.0	236	9	US-09-948-429B-10	Sequence 10, Appl	
3	1006	81.7	235	10	US-09-747-669-6	Sequence 6, Appl	
4	999.5	81.1	221	9	US-10-001-857-202	Sequence 202, App	
5	973	79.0	234	9	US-10-124-905-2	Sequence 2, Appli	
6	973	79.0	234	9	US-09-948-429B-2	Sequence 2, Appli	
7	950.5	77.2	219	10	US-09-974-449-38	Sequence 38, Appl	
8	885	71.8	235	10	US-09-852-797-70	Sequence 70, Appl	
9	885	71.8	235	9	US-09-853-161-70	Sequence 70, Appl	
10	885	71.8	235	9	US-09-852-659A-70	Sequence 70, Appl	
11	882	71.6	235	10	US-09-853-161-88	Sequence 88, Appl	
12	882	71.6	235	10	US-09-852-797-88	Sequence 88, Appl	
13	882	71.6	235	10	US-09-852-659A-88	Sequence 88, Appl	
14	854.5	69.4	244	10	US-09-925-301-1424	Sequence 1424, Ap	
15	826	67.0	239	9	US-09-828-955B-26	Sequence 26, Appl	
16	815	66.2	216	10	US-09-736-371B-19	Sequence 19, Appl	
17	762.5	61.9	246	9	US-09-909-567B-49	Sequence 49, Appl	
18	683.5	55.5	216	10	US-09-291-299A-8	Sequence 8, Appli	
19	673	54.6	217	10	US-09-291-299A-7	Sequence 7, Appli	
20	639.5	51.9	216	10	US-09-291-299A-9	Sequence 9, Appli	
21	635.5	51.6	216	10	US-09-291-299A-10	Sequence 10, Appl	
22	569.5	46.2	147	9	US-09-988-115A-57	Sequence 57, Appl	
23	567	46.0	109	9	US-09-925-664-51	Sequence 51, Appl	
24	562	45.6	139	9	US-09-796-692-901	Sequence 901, App	
25	549	44.6	143	9	US-09-796-692-742	Sequence 742, App	
26	548	44.5	105	10	US-09-811-384-6	Sequence 6, Appli	
27	548	44.5	123	9	US-09-796-692-931	Sequence 931, App	
28	547	44.4	125	9	US-09-796-692-843	Sequence 843, App	
29	546	44.3	123	9	US-09-796-692-683	Sequence 683, App	
30	546	44.3	123	9	US-09-796-692-838	Sequence 838, App	
31	546	44.3	123	9	US-09-796-692-859	Sequence 859, App	
32	546	44.3	123	9	US-09-796-692-896	Sequence 896, App	
33	546	44.3	123	9	US-09-796-692-993	Sequence 993, App	
34	546	44.3	123	9	US-09-796-692-1011	Sequence 1011, Ap	
35	546	44.3	123	9	US-09-796-692-1021	Sequence 1021, Ap	
36	546	44.3	123	9	US-09-796-692-1041	Sequence 1041, Ap	
37	546	44.3	123	9	US-09-796-692-1138	Sequence 1138, Ap	
38	546	44.3	123	9	US-09-796-692-1142	Sequence 1142, Ap	
39	546	44.3	154	9	US-09-796-692-706	Sequence 706, App	
40	545	44.2	105	10	US-09-864-761-41920	Sequence 41920, A	
41	545	44.2	123	9	US-09-796-692-1105	Sequence 1105, Ap	
42	543	44.1	106	9	US-09-935-868-14	Sequence 14, Appl	
43	542	44.0	127	9	US-09-796-692-836	Sequence 836, App	
44	541	43.9	123	9	US-09-796-692-982	Sequence 982, App	
45	541	43.9	123	9	US-09-796-692-991	Sequence 991, App	

ALIGNMENTS

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RESULT 1
US-10-124-905-10
; Sequence 10, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
;;  APPLICANT:  Anderson, Darrell R.
;;  TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;;  TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;;  TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;;  TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;;  NUMBER OF SEQUENCES:  12
;;  CORRESPONDENCE ADDRESS:
;;  ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;;  STREET:  699 Prince Street
;;  CITY:  Alexandria
;;  STATE:  VA
;;  COUNTRY:  USA
;;  ZIP:  22314
;;  COMPUTER READABLE FORM:
;;  MEDIUM TYPE:  Floppy disk
;;  COMPUTER:  IBM PC compatible
;;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;;  SOFTWARE:  PatentIn Release #1.0, Version #1.30
;;  CURRENT APPLICATION DATA:
;;  APPLICATION NUMBER:  US/10/124,905
;;  FILING DATE:
;;  CLASSIFICATION:
;;  PRIOR APPLICATION DATA:
;;  APPLICATION NUMBER:  09/383,916
;;  FILING DATE:
;;  APPLICATION NUMBER:  US 08/487,550
;;  FILING DATE:  07-JUN-1995
;;  ATTORNEY/AGENT INFORMATION:
;;  NAME:  Teskin, Robin L.
;;  REGISTRATION NUMBER:  35,030
;;  REFERENCE/DOCKET NUMBER:  012712-131
;;  TELECOMMUNICATION INFORMATION:
;;  TELEPHONE:  703-836-6620
;;  TELEFAX:  703-836-2021
;;  INFORMATION FOR SEQ ID NO:  10:
;;  SEQUENCE CHARACTERISTICS:
;;  LENGTH:  236 amino acids
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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-10-124-905-10

Query Match           100.0%;   Score 1232;  DB 9;  Length 236;
Best Local Similarity 100.0%;   Pred. No. 5.6e-52;
Matches 236; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL  60

Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 2
US-09-948-429B-10
; Sequence 10, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
;      APPLICANT: Anderson, Darrell R.
;      TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;      TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;      TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;      TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;      NUMBER OF SEQUENCES: 12
;      CORRESPONDENCE ADDRESS:
;         ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;         STREET: 699 Prince Street
;         CITY: Alexandria
;         STATE: VA
;         COUNTRY: USA
;         ZIP: 22314
;      COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/948,429B
;         FILING DATE:
;         CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: 09/383,916
;         FILING DATE:
;         APPLICATION NUMBER: US 08/487,550
;         FILING DATE: 07-JUN-1995
;      ATTORNEY/AGENT INFORMATION:
;         NAME: Teskin, Robin L.
;         REGISTRATION NUMBER: 35,030
;         REFERENCE/DOCKET NUMBER: 012712-131
;      TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 703-836-6620
;         TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
;      SEQUENCE CHARACTERISTICS:
;         LENGTH: 236 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-09-948-429B-10
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Query Match           100.0%;   Score 1232;  DB 9;  Length 236;
Best Local Similarity 100.0%;   Pred. No. 5.6e-52;
Matches 236; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL  60

Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 3
US-09-747-669-6
; Sequence 6, Application US/09747669
; Patent No. US20020122807A1
; GENERAL INFORMATION:
;      APPLICANT: Dan, Michael D.
;      APPLICANT: Saleh, Mansoor
;      TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
;      TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
;      TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
;      TITLE OF INVENTION: AND DETECTION OF CANCERS
;      FILE REFERENCE: 316082001001
;      CURRENT APPLICATION NUMBER: US/09/747,669
;      CURRENT FILING DATE: 2002-04-08
;      PRIOR APPLICATION NUMBER: US 09/111,286
;      PRIOR FILING DATE: 1998-07-07
;      NUMBER OF SEQ ID NOS: 7
;      SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;      LENGTH: 235
;      TYPE: PRT
;      ORGANISM: Artificial Sequence
;      FEATURE:
;      OTHER INFORMATION: Synthetic construct
US-09-747-669-6

Query Match            81.7%;   Score 1006;  DB 10;  Length 235;
Best Local Similarity  83.9%;   Pred. No. 2.5e-41;
Matches 193; Conservative 14; Mismatches 23; Indels  0; Gaps  0;

Qy    7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK  66
          ||| ||:: ||||||||||||||||||||||||||||||||  ::||||||||||||||
Db    6 LLLTLLTHCAGSWAQSVLTQPPSAASGTPGQRVTISCSGSNSNIGSKTVNWYQQLPGTAPK  65

Qy   67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
          |||||||||||||||||||||||||||| |: :||||||||||| : :||||||||||||
Db   66 FLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSBDEADYYCAAWDDSLNGWVFGGGTK 125

Qy  127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
          |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db  126 LTVLGQPKAAPSVTLFPPSSEELQANKPTLVCLISDFYPGAVTVAWKAGVETT 185

Qy  187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 4
US-10-001-857-202
; Sequence 202, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
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;  APPLICANT: Macina, Roberto
;  APPLICANT: Recipon, Herve
;  APPLICANT: Chen, Sei-Yu
;  APPLICANT: Sun, Yongming
;  APPLICANT: Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
;  FILE REFERENCE: DEX-0273
;  CURRENT APPLICATION NUMBER: US/10/001,857
;  CURRENT FILING DATE: 2001-11-20
;  PRIOR APPLICATION NUMBER: 60/252,054
;  PRIOR FILING DATE: 2000-11-20
;  NUMBER OF SEQ ID NOS: 208
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 202
;  LENGTH: 221
;  TYPE: PRT
;  ORGANISM: Homo sapien
US-10-001-857-202

Query Match          81.1%;  Score 999.5;  DB 9;  Length 221;
Best Local Similarity  87.4%;  Pred. No. 4.8e-41;
Matches  194;  Conservative 12;  Mismatches 13;  Indels 3;  Gaps 3;

Qy   17 GARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYD-LHWYQQLPGTAPKLLIYDINK 74
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Db    1 GSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDYVHWYQQLPGTAPKLMIYEVAK 60

Qy   75 RPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPK 134
         ||:||:||||| |||:||| ||||||| |||||||||||:|||  |||||||||||||
Db   61 RPSGVSDRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSY-TWFGGGTKLTVLGQPK 119

Qy  135 AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN 194
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  120 AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN 179

Qy  195 KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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Db  180 KYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 221

RESULT 5
US-10-124-905-2
; Sequence 2, Application US/10124905
; Patent No. US2002016136A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;  STREET: 699 Prince Street
;  CITY: Alexandria
;  STATE: VA
;  COUNTRY: USA
;  ZIP: 22314
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/10/124,905
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 09/383,916
;  FILING DATE:
;  APPLICATION NUMBER: US 08/487,550
;  FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
```

```
;  NAME: Teskin, Robin L.
;  REGISTRATION NUMBER: 35,030
;  REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 703-836-6620
;  TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 234 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-10-124-905-2

Query Match          79.0%;  Score 973;  DB 9;  Length 234;
Best Local Similarity  80.1%;  Pred. No. 8.9e-40;
Matches  189;  Conservative 13;  Mismatches 32;  Indels 2;  Gaps 1;

Qy    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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Db    1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58

Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
         | :||||||||  ||||| :|||||||| |||| || |  ||||||||| :|  |
Db   59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118

Qy  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178

Qy  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 6
US-09-948-429B-2
; Sequence 2, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;  STREET: 699 Prince Street
;  CITY: Alexandria
;  STATE: VA
;  COUNTRY: USA
;  ZIP: 22314
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/948,429B
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 09/383,916
;  FILING DATE:
;  APPLICATION NUMBER: US 08/487,550
;  FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Teskin, Robin L.
;  REGISTRATION NUMBER: 35,030
;  REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 703-836-6620
```

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;    TELEFAX:  703-836-2021
; INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH: 234 amino acids
;    TYPE: amino acid
;    TOPOLOGY: linear
;    MOLECULE TYPE: protein
US-09-948-429B-2

Query Match             79.0%;  Score 973; DB 9; Length 234;
Best Local Similarity   80.1%;  Pred. No. 8.9e-40;
Matches 189; Conservative 13; Mismatches 32; Indels  2; Gaps  1;

Qy    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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Db    1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58

Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
          |||||||||||||||||||||||||||||||||   :|: : |
Db   59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLITNGVEAGDEADYYCQWDRASDHPV 118

Qy  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178

Qy  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234


RESULT 7
US-09-974-449-38
; Sequence 38, Application US/09974449
; Patent No. US2002014198941
; GENERAL INFORMATION:
;    APPLICANT: Kricek, Franz
;    APPLICANT: Stadler, Beda
;    APPLICANT: Vogel, Monique
;    TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST
;    TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO
;    TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR
;    FILE REFERENCE: 4-30888A
;    CURRENT APPLICATION NUMBER: US/09/974,449
;    CURRENT FILING DATE: 2001-10-10
;    PRIOR APPLICATION NUMBER: PCT/EP00/03288
;    PRIOR FILING DATE: 2000-04-12
;    NUMBER OF SEQ ID NOS: 62
;    SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;    LENGTH: 219
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-974-449-38

Query Match             77.2%;  Score 950.5; DB 10; Length 219;
Best Local Similarity   83.1%;  Pred. No. 9.7e-39;
Matches 182; Conservative 16; Mismatches 18; Indels  3; Gaps  2;

Qy   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
          |:|||||||||:|||||||||||||||||:  : ||||||||:|||||||||||||||
Db    1 ELVVTQPASVSGSPGQSITISCTGTRSDVGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGV 60

Qy   80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLG--QPKAAP 137
          :|||||||||||||||||||||||||||| :|:||||||||||||:| ||  ||||||
Db   61 SNRFSGSKSGNTASLTIGLQAEDEADYYCSSYTSSTLGVFGGGTKLTVLGQPQPKAAP 120

Qy  138 SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYA 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYA 180

Qy  198 ASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||:|||||||||||||||||||||||
Db  181 ASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 219
```

```
RESULT 8
US-09-852-797-70
; Sequence 70, Application US/09852797
; Patent No. US2002017299441
; GENERAL INFORMATION:
;    APPLICANT: Rosen et al.
;    TITLE OF INVENTION: 28 Human Secreted Proteins
;    FILE REFERENCE: PZ003P2
;    CURRENT APPLICATION NUMBER: US/09/852,797
;    CURRENT FILING DATE: 2001-05-11
;    PRIOR APPLICATION NUMBER: 60/265,583
;    PRIOR FILING DATE: 2001-02-02
;    PRIOR APPLICATION NUMBER: 09/152,060
;    PRIOR FILING DATE: 1998-09-11
;    PRIOR APPLICATION NUMBER: PCT/US98/04858
;    PRIOR FILING DATE: 1998-03-12
;    PRIOR APPLICATION NUMBER: 60/040,762
;    PRIOR FILING DATE: 1997-03-14
;    PRIOR APPLICATION NUMBER: 60/040,710
;    PRIOR FILING DATE: 1997-03-14
;    PRIOR APPLICATION NUMBER: 60/050,934
;    PRIOR FILING DATE: 1997-05-30
;    PRIOR APPLICATION NUMBER: 60/048,100
;    PRIOR FILING DATE: 1997-05-30
;    PRIOR APPLICATION NUMBER: 60/048,357
;    PRIOR FILING DATE: 1997-05-30
;    PRIOR APPLICATION NUMBER: 60/048,189
;    PRIOR FILING DATE: 1997-05-30
;    PRIOR APPLICATION NUMBER: 60/057,765
;    PRIOR FILING DATE: 1997-09-05
;    PRIOR APPLICATION NUMBER: 60/048,970
;    PRIOR FILING DATE: 1997-06-06
;    PRIOR APPLICATION NUMBER: 60/068,368
;    PRIOR FILING DATE: 1997-12-19
;    NUMBER OF SEQ ID NOS: 118
;    SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
;    LENGTH: 235
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-852-797-70

Query Match             71.8%;  Score 885; DB 9;  Length 235;
Best Local Similarity   77.1%;  Pred. No. 1.2e-35;
Matches 178; Conservative 11; Mismatches 38; Indels  4;  Gaps  1;

Qy   10 LLLLWLPGARCESV---LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP 65
          |||||:|||||||    ||||||||| |::|:|: :|:|
Db    5 LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLLTCTGNNNNVGDQGAAWLQQHQGHPP 64

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
          ||||||||||||||:|||||||||||:|:  ||||:|||||| :|||||||||:|||||
Db   65 KLLSYRNNNRPSGISERLSASRSGATSSLIITGLQPEDEADYYCAAYDSSLAVMFGGGT 124

Qy  126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
          :||||||||||||:||||||||||||||||||||||||||||:|||||||||||||||
Db  125 KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 184

Qy  186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||:|||||||||||||||||||||||
Db  185 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235


RESULT 9
US-09-853-161-70
; Sequence 70, Application US/09853161
; Patent No. US200200767566A1
; GENERAL INFORMATION:
;    APPLICANT: Rosen et al.
;    TITLE OF INVENTION: 28 Human Secreted Proteins
;    FILE REFERENCE: PZ003P3
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CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 70
  LENGTH: 235
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-853-161-70

Query Match             71.8%;  Score 885;  DB 10;  Length 235;
Best Local Similarity   77.1%;  Pred. No. 1.2e-35;
Matches  178;  Conservative  11;  Mismatches 38;  Indels  4;  Gaps  1;

Qy   10 LLLLWLPGARCESV---LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP 65
            ||||||     :|||||  |||||||||||| :|:|  ||||||||||||
Db    5 LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCGNNNNVGDQGAAWLQQHQGHPP 64

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSLNAQVFGGGT 125
           ||||||||||||  |||||| :|:||||||||||||||||||   :||||:||||||
Db   65 KLLSYRNNNRPSGISERLSASRGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGT 124

Qy  126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  125 KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 184

Qy  186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  185 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235


RESULT 10
US-09-852-659A-70
Sequence 70, Application US/09852659A
Patent No. US20020077287A1
GENERAL INFORMATION:
  APPLICANT: Rosen et al.
  TITLE OF INVENTION: 28 Human Secreted Proteins
  FILE REFERENCE: PZ003P4
  CURRENT APPLICATION NUMBER: US/09/852,659A
  CURRENT FILING DATE: 2001-05-11
  PRIOR APPLICATION NUMBER: 60/265,583
  PRIOR FILING DATE: 2001-02-02
  PRIOR APPLICATION NUMBER: 09/152,060
  PRIOR FILING DATE: 1998-09-11
  PRIOR APPLICATION NUMBER: PCT/US98/04858
  PRIOR FILING DATE: 1998-03-12
  PRIOR APPLICATION NUMBER: 60/040,762
  PRIOR FILING DATE: 1997-03-14
```

```
  PRIOR APPLICATION NUMBER: 60/040,710
  PRIOR FILING DATE: 1997-03-14
  PRIOR APPLICATION NUMBER: 60/050,934
  PRIOR FILING DATE: 1997-05-30
  PRIOR APPLICATION NUMBER: 60/048,100
  PRIOR FILING DATE: 1997-05-30
  PRIOR APPLICATION NUMBER: 60/048,357
  PRIOR FILING DATE: 1997-05-30
  PRIOR APPLICATION NUMBER: 60/048,189
  PRIOR FILING DATE: 1997-05-30
  PRIOR APPLICATION NUMBER: 60/057,765
  PRIOR FILING DATE: 1997-09-05
  PRIOR APPLICATION NUMBER: 60/048,970
  PRIOR FILING DATE: 1997-06-06
  PRIOR APPLICATION NUMBER: 60/068,368
  PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 70
  LENGTH: 235
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-852-659A-70

Query Match             71.8%;  Score 885;  DB 10;  Length 235;
Best Local Similarity   77.1%;  Pred. No. 1.2e-35;
Matches  178;  Conservative  11;  Mismatches 38;  Indels  4;  Gaps  1;

Qy   10 LLLLWLPGARCESV---LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP 65
            ||||||     :|||||  |||||||||||| :|:|  ||||||||||||
Db    5 LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCGNNNNVGDQGAAWLQQHQGHPP 64

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSLNAQVFGGGT 125
           ||||||||||||  |||||| :|:||||||||||||||||||   :||||:||||||
Db   65 KLLSYRNNNRPSGISERLSASRGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGT 124

Qy  126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  125 KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 184

Qy  186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  185 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235


RESULT 11
US-09-852-797-88
Sequence 88, Application US/09852797
Patent No. US20020172994A1
GENERAL INFORMATION:
  APPLICANT: Rosen et al.
  TITLE OF INVENTION: 28 Human Secreted Proteins
  FILE REFERENCE: PZ003P2
  CURRENT APPLICATION NUMBER: US/09/852,797
  CURRENT FILING DATE: 2001-05-11
  PRIOR APPLICATION NUMBER: 60/265,583
  PRIOR FILING DATE: 2001-02-02
  PRIOR APPLICATION NUMBER: 09/152,060
  PRIOR FILING DATE: 1998-09-11
  PRIOR APPLICATION NUMBER: PCT/US98/04858
  PRIOR FILING DATE: 1998-03-12
  PRIOR APPLICATION NUMBER: 60/040,762
  PRIOR FILING DATE: 1997-03-12
  PRIOR APPLICATION NUMBER: 60/040,710
  PRIOR FILING DATE: 1997-03-14
  PRIOR APPLICATION NUMBER: 60/050,934
  PRIOR FILING DATE: 1997-05-30
  PRIOR APPLICATION NUMBER: 60/048,100
  PRIOR FILING DATE: 1997-05-30
  PRIOR APPLICATION NUMBER: 60/048,357
  PRIOR FILING DATE: 1997-05-30
  PRIOR APPLICATION NUMBER: 60/048,189
  PRIOR FILING DATE: 1997-05-30
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-88

```
Query Match            71.6%;  Score 882;  DB 10;  Length 235;
Best Local Similarity  76.6%;  Pred. No. 1.7e-35;
Matches  177;  Conservative  12;  Mismatches  38;  Indels  4;  Gaps  1;

Qy     10  LLLLWLPGARCESV----LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP   65
               ||||| |       |  ||||| ::|:: ::||: : :
Db      5  LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP   64

Qy     66  KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT  125
               |:|: |||||||||||||:|:|||: ||||||||||:|: :|||||
Db     65  KLLSYRNNNRPSGISERLSASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGT  124

Qy    126  RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET  185
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125  KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET  184

Qy    186  TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185  TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS  235
```

RESULT 13
US-09-852-659A-88
; Sequence 88, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-88

```
Query Match            71.6%;  Score 882;  DB 10;  Length 235;
Best Local Similarity  76.6%;  Pred. No. 1.7e-35;
Matches  177;  Conservative  12;  Mismatches  38;  Indels  4;  Gaps  1;

Qy     10  LLLLWLPGARCESV----LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP   65
               ||||| |       |  |:::||: :|::
```

; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-88

```
Query Match            71.6%;  Score 882;  DB 9;  Length 235;
Best Local Similarity  76.6%;  Pred. No. 1.7e-35;
Matches  177;  Conservative  12;  Mismatches  38;  Indels  4;  Gaps  1;

Qy     10  LLLLWLPGARCESV----LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP   65
               ||||| |       |  ||||| ::|:: ::||: : :
Db      5  LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP   64

Qy     66  KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT  125
               |:|: |||||||||||||:|:|||: ||||||||||:|: :|||||
Db     65  KLLSYRNNNRPSGISERLSASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGT  124

Qy    126  RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET  185
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125  KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET  184

Qy    186  TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185  TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS  235
```

RESULT 12
US-09-853-161-88
; Sequence 88, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19

```
Db    5  LLẹLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP  64
            |  ||||  | ||||||  :||  ||| |  :|||    ::||||
Qy   66  KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT  125
            |||| ||||||||   |  ||  ||:| :|||||  |||||||||| :|||| :||||
Db   65  KLLSYRNNNRPSGISERLSASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGT  124

Qy  126  RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET  185
            :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  125  KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET  184

Qy  186  TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
            |||||||||||||||||||||||||||:|||||||||||||||||||||
Db  185  TTPSKQSNNKYAASSYLSLTPEQWKSHSYSCQVTHEGSTVEKTVAPTECS  235
```

RESULT 14
US-09-925-301-1424
; Sequence 1424, Application US/09925301
; Patent No. US2002052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1424
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (62)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (221)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1424

Query Match   69.4%; Score 854.5; DB 10; Pred. No. 3.5e-34;
Best Local Similarity 70.7%;
Matches 174; Conservative 15; Mismatches 44; Indels 13; Gaps 3;

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Qy    2  RVPAQLLG-LLLLWLP--------GARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG  50
            :|| :     |::|:|          ||:||||||||| :| | |:|||:| |:
Db    1  RVRRQSSGNLTMAWTPLLLPLLITFCTVSEASYELTQPPSVSPGQTARITCSGDA--LP  58

Qy   51  GYDLHWYQQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQ  110
            |||||||| :| ||:|:||   |||:  | |||:  || : |:||  || |||||||||:
Db   59  XKYXYWYQQKSGQAPVLVIYEDTRRPSAIPERFSASSGTMATLTISGAQVEDEADYYCY  118

Qy  111  SYDSSLNAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV  170
            | |||   | |||||:||||||||||||||||||||||||||||||||||||||||||||
Db  119  STDSSSYYRVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV  178

Qy  171  AWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV  230
            |||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db  179  AWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHXSYSCQVTHEGSTVEKTV  238

Qy  231  APTECS  236
            ||||||
Db  239  APTECS  244
```

RESULT 15

US-09-828-995B-26
; Sequence 26, Application US/09828995B
; Patent No. US20020161351A1
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: The 'Xaa' at location 147 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (148)..(148)
; OTHER INFORMATION: The 'Xaa' at location 148 stands for Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: The 'Xaa' at location 149 stands for Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (169)..(169)
; OTHER INFORMATION: The 'Xaa' at location 169 stands for Ser, or Asn.
US-09-828-995B-26

Query Match   67.0%; Score 826; DB 9; Length 239;
Best Local Similarity 70.0%; Pred. No. 7.6e-33;
Matches 161; Conservative 21; Mismatches 48; Indels 0; Gaps 0;

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Qy    7  LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK  66
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Db   10  LLLTLLAHCTGSWAQAVLNQPASVSGALGQKVTISCSGDTNDIDIFGVNWYQQLPGKAPT  69

Qy   67  LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR  126
            :|   | :||||| |||||| ||: ||| ||||| |||||||||:| :| |  | ||||:
Db   70  VLVDSDGDRPSGVPDRFSGSSGNSGTLTITGLQAEDEADYYCQSVDSTLGVYVFGSGTQ  129

Qy  127  LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT  186
            |||||||||:||||||| ::|||| |||||||||||||||:||||||||| |||:|||||
Db  130  LTVLGQPKASPSVTLFPXXKEELGANKATLVCLISDFYPXGVTVAWKADGSPVTQGVETT  189

Qy  187  TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
            ||||||||||||||||||||:|||||:|:||:||||||| |||:|||:||
Db  190  KPSKQSNNKYAASSYLSLTPDKWKSHSSFSCLVTHEGSPVEKKVAPAKCS  239
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Search completed: March 29, 2003, 09:38:43
Job time : 10.0472 secs

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                    GenCore version 5.1.4_p5_4578
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:      March 29, 2003, 09:06:24 ; Search time 8.38523 Seconds
                                        (without alignments)
                                        828.100 Million cell updates/sec

Title:            US-09-758-173-10
Perfect score:    1232
Sequence:         1 MRVPAQLLGLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:     262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued Patents AA:*
              1: /cgn2_6/pcdata/1/iaa/5A_COMB.pep:*
              2: /cgn2_6/pcdata/1/iaa/5B_COMB.pep:*
              3: /cgn2_6/pcdata/1/iaa/6A_COMB.pep:*
              4: /cgn2_6/pcdata/1/iaa/6B_COMB.pep:*
              5: /cgn2_6/pcdata/1/iaa/PCTUS_COMB.pep:*
              6: /cgn2_6/pcdata/1/iaa/backfiles1.pep:*

              Pred. No. is the number of results predicted by chance to have a
              score greater than or equal to the score of the result being printed,
              and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	1232	100.0	236	3	US-08-487-550-10	Sequence 10, Appl
2	1052.5	85.4	236	4	US-09-049-672A-7	Sequence 7, Appli
3	973	79.0	234	3	US-08-487-550-2	Sequence 2, Appli
4	965	78.3	235	4	US-09-049-672A-10	Sequence 10, Appli
5	965	78.3	235	2	US-09-049-672A-12	Sequence 12, Appl
6	955	77.5	235	2	US-08-378-939-12	Sequence 12, Appli
7	885	71.8	235	4	US-09-152-060-70	Sequence 70, Appl
8	882	71.6	235	4	US-08-152-060-88	Sequence 88, Appl
9	857.5	69.6	233	4	US-09-049-672A-11	Sequence 6, Appli
10	836	67.9	240	4	US-08-793-450-6	Sequence 11, Appli
11	804.5	65.3	238	4	US-08-751-359-22	Sequence 6, Appli
12	634.5	51.5	229	4	US-08-907-146-22	Sequence 22, Appl
13	634.5	51.5	229	4	US-08-761-277A-51	Sequence 51, Appli
14	567	46.0	109	2	US-08-422-091-9	Sequence 9, Appli
15	548	44.5	105	1	US-08-422-092-9	Sequence 9, Appli
16	548	44.5	105	1	US-08-422-092-9	Sequence 9, Appli
17	548	44.5	105	2	US-08-788-800-6	Sequence 6, Appli
18	548	44.5	105	2	US-08-422-092-9	Sequence 9, Appli
19	548	44.5	105	3	US-08-422-093-9	Sequence 9, Appli
20	548	44.5	105	3	US-08-422-112-9	Sequence 9, Appli
21	544.5	44.2	200	6	5189147-10	Patent No. 5189147
22	535	43.4	104	6	US-09-025-769B-170	Sequence 170, App
23	522	42.4	241	2	US-07-916-098A-56	Sequence 56, Appl
24	508.5	41.3	236	1	US-08-157-101A-5	Sequence 5, Appli
25	508	41.2	235	1	US-08-276-852-153	Sequence 153, App
26	508	41.2	235	1	US-08-899-575-153	Sequence 153, App
27	508	41.2	235	1	US-08-899-575-153	Sequence 153, App
28	508	41.2	235	5	PCT-US95-08743-153	Sequence 153, App
29	502.5	40.8	235	3	US-08-812-586-16	Sequence 16, Appl
30	496.5	40.3	131	1	US-08-305-683A-4	Sequence 4, Appli
31	492.5	40.0	234	4	US-09-049-672A-6	Sequence 6, Appli
32	492.5	40.0	234	5	PCT-US94-07659-4	Sequence 4, Appli
33	492.5	40.0	310	4	US-09-079-029-11	Sequence 11, Appli
34	482.5	39.2	234	4	US-07-590-192-2	Sequence 2, Appli
35	476	38.6	112	4	US-09-025-769B-18	Sequence 18, Appl
36	475	38.6	239	1	US-08-353-400-37	Sequence 37, Appl
37	472	38.3	239	4	US-08-487-550-6	Sequence 6, Appli
38	471.5	38.3	110	4	US-09-240-274-63	Sequence 63, Appli
39	466	37.8	105	2	US-08-646-981-3	Sequence 3, Appli
40	457	37.1	111	4	US-08-983-607-35	Sequence 35, Appli
41	456.5	37.1	213	2	US-08-737-129A-4	Sequence 4, Appli
42	455.5	37.0	240	4	US-09-301-593-36	Sequence 36, Appl
43	455	36.9	235	2	US-08-303-569B-5	Sequence 5, Appli
44	455	36.9	235	2	US-08-116-247-5	Sequence 5, Appli
45	454	36.9	111	2	US-08-665-202-43	Sequence 43, Appl

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                              ALIGNMENTS

RESULT 1
US-08-487-550-10
; Patent No. 6113898
; Sequence 10, Application US/08487550
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;     STREET: 699 Prince Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/487,550
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin, Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 236 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-487-550-10

  Query Match             100.0%;  Score 1232;  DB 3;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-91;
  Matches  236;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRVPAQLLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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Db          1 MRVPAQLLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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Qy    61  PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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Db    61  PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy   121  FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy   181  AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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RESULT 2
US-09-049-672A-7
; Sequence 7, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Yue, Henry
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Baughn, Mariah R.
;   TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/049,672A
;   FILING DATE: HEREWITH
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Cerrone, Michael C
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0497 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX:
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 236 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: ADRETUT05
;   CLONE: 2492122
US-09-049-672A-7

Query Match   85.4%; Score 1052.5; DB 4; Length 236;
Best Local Similarity 88.3%; Pred. No. 3.4e-77;
Matches 204; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

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Db    6  LLLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65
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Qy    66  KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
          ||||| :||||||  ||||||||||::||||||||| :|||||||||||||||   |||||
Db    66  KLLIYGSRNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGVVFGGGT 125

Qy   126  RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
          :||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db   126  KLTVLGQPKAAPSVTLFPPSSEELQANRATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185

Qy   186  TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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RESULT 3
US-08-487-550-2
; Sequence 2, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 234 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-487-550-2

Query Match   79.0%; Score 973; DB 3; Length 234;
Best Local Similarity 80.1%; Pred. No. 7.9e-71;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

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Db    1  MRVPAQLLGLLLLWLPGARCAVELTQPPSVSVSPGTARITCGGDNSR--NEYVHWYQQK 58

Qy   61  PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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Db   59  PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118

Qy  121  FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  119  FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178

Qy  181  AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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Db   179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

Qy   184 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   183 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 4
US-09-049-672A-10
; Sequence 10, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/049,672A
;   FILING DATE: HEREWITH
;   CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Cerrone, Michael C
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX:
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: THYRNOT10
;   CLONE: 2872705
US-09-049-672A-10

Query Match   78.3%; Score 965; DB 4; Length 235;
Best Local Similarity 80.3%; Pred. No. 3.5e-70;
Matches 187; Conservative 19; Mismatches 25; Indels 2; Gaps 2;

Qy   5 AQLLGLLLLWLPLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGT 63
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Db   4 ALLFLTLLTQGTGSWAQSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQSPGT 63

Qy   64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
          |||| ||:: |||||||||||||||| |||||| || ||||||||| || | ||||
Db   64 APKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYVGN-NIVVFGG 122

Qy   124 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183
          ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 182

RESULT 5
US-09-049-672A-12
; Sequence 12, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/049,672A
;   FILING DATE: HEREWITH
;   CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Cerrone, Michael C
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX:
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 235 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: LUNGTUT13
;   CLONE: 3116314
US-09-049-672A-12

Query Match   78.3%; Score 965; DB 4; Length 235;
Best Local Similarity 80.0%; Pred. No. 3.5e-70;
Matches 184; Conservative 20; Mismatches 26; Indels 0; Gaps 0;

Qy   7 LLGLLLLWLPLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
          ||| ||||||||||||||||||: |||:|||| |||||||||| |::|| ::|||:|||||
Db   6 LLLALLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGTTSNIASNSVHWYQLVPGAAPK 65

Qy   67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
          ||| |:| |||:|||||||||||::||| |||:||||:||| ::| ||| ||||||||
Db   66 LLIYANDQRASGVPDRFSGSKSGTSASLAISGLRPEDETDYYCATWDDSVSGWMFGGGTK 125

Qy   127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

RESULT 6
US-08-378-939-12
; Sequence 12, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
.,   APPLICANT: CROWE, JAMES SCOTT
.,   APPLICANT: LEWIS, ALAN PETER
.,   TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
.,   NUMBER OF SEQUENCES: 46
.,   CORRESPONDENCE ADDRESS:
.,   ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
.,   STREET: 555 THIRTEENTH ST. N.W.
.,   CITY: WASHINGTON
.,   STATE: D.C.
.,   COUNTRY: U.S.
.,   ZIP: 20004
.,   COMPUTER READABLE FORM:
.,   MEDIUM TYPE: Floppy disk
.,   COMPUTER: IBM PC compatible
.,   OPERATING SYSTEM: PC-DOS/MS-DOS
.,   SOFTWARE: PatentIn Release #1.0, Version #1.25
.,   CURRENT APPLICATION DATA:
.,   APPLICATION NUMBER: US/08/378,939
.,   FILING DATE:
.,   CLASSIFICATION: 435
.,   PRIOR APPLICATION DATA:
.,   APPLICATION NUMBER: US 07/952640
.,   FILING DATE: 01-DEC-1992
.,   ATTORNEY/AGENT INFORMATION:
.,   NAME: ERNST, BARBARA G
.,   REGISTRATION NUMBER: 30,377
.,   REFERENCE/DOCKET NUMBER: 1808-118
.,   TELECOMMUNICATION INFORMATION:
.,   TELEPHONE: (202) 783-6040
.,   TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 12:
.,   SEQUENCE CHARACTERISTICS:
.,   LENGTH: 235 amino acids
.,   TYPE: amino acid
.,   TOPOLOGY: linear
.,   MOLECULE TYPE: protein
US-08-378-939-12

Query Match   77.5%; Score 955; DB 2; Length 235;
Best Local Similarity   79.8%; Pred. No. 2.2e-69;
Matches 186; Conservative 18; Mismatches 27; Indels 2; Gaps 2;

Qy   5 AQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDL-HWYQQLPGT 63
           | :::: :||||: : :::|||| || :|||||| |||||||| :::|: |||||||
Db   4 ALLLLTLLTQDTGSWAQSALTQPASVSGSPGQSITISCTGTNNDVGSYNLVSWYQQHPGK 63

Qy   64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
           |||::::: |||| :|||:|||||||| ||| |||||||||||||||||||||:||||
Db   64 APKIMIYEVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSYTV-VFGG 122

Qy   124 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183
           | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 182

Qy   184 ETTTPSKQSNNKYAASSYLSLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183 ETTTPSKQSNNKYAASSYLSLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 7
US-09-152-060-70
; Sequence 70, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
.,   APPLICANT: Rosen et al.
.,   TITLE OF INVENTION: 28 Human Secreted Proteins
.,   FILE REFERENCE: PZ003P1.US
.,   CURRENT APPLICATION NUMBER: US/09/152,060
.,   CURRENT FILING DATE: 1998-09-11
.,   EARLIER APPLICATION NUMBER: PCT/US98/04858
.,   EARLIER FILING DATE: 1998-03-12
.,   EARLIER APPLICATION NUMBER: 60/040,762
.,   EARLIER FILING DATE: 1997-03-14
.,   EARLIER APPLICATION NUMBER: 60/040,710
.,   EARLIER FILING DATE: 1997-03-14
.,   EARLIER APPLICATION NUMBER: 60/050,934
.,   EARLIER FILING DATE: 1997-05-30
.,   EARLIER APPLICATION NUMBER: 60/048,100
.,   EARLIER FILING DATE: 1997-05-30
.,   EARLIER APPLICATION NUMBER: 60/048,357
.,   EARLIER FILING DATE: 1997-05-30
.,   EARLIER APPLICATION NUMBER: 60/048,189
.,   EARLIER FILING DATE: 1997-05-30
.,   EARLIER APPLICATION NUMBER: 60/057,765
.,   EARLIER FILING DATE: 1997-09-05
.,   EARLIER APPLICATION NUMBER: 60/048,970
.,   EARLIER FILING DATE: 1997-06-06
.,   EARLIER APPLICATION NUMBER: 60/068,368
.,   EARLIER FILING DATE: 1997-12-19
.,   NUMBER OF SEQ ID NOS: 118
.,   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
.,   LENGTH: 235
.,   TYPE: PRT
.,   ORGANISM: Homo sapiens
US-09-152-060-70

Query Match   71.8%; Score 885; DB 4; Length 235;
Best Local Similarity   77.1%; Pred. No. 9e-64;
Matches 178; Conservative 11; Mismatches 38; Indels 4; Gaps 1;

Qy   10 LLLLWLPGARCESV---LTQPPSVSGAPGQKVTISCTGSTSNIGGVDLHWYQQLPGTAP 65
          ||| |: |:: |: :::|: :| || | | ||||| :: |:: | | |||::
Db   5 LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDGAAWLQQHQGHPP 64

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
          ||| |: |||| :: :: |: ::||: ||: ||||||| || |::|| |:|||||
Db   65 KLLSYRNNNRPSGISERLSASRGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGT 124

Qy   126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125 KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 184

Qy   186 TTPSKQSNNKYAASSYLSLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 TTPSKQSNNKYAASSYLSLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 8
US-09-152-060-88
; Sequence 88, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
.,   APPLICANT: Rosen et al.
.,   TITLE OF INVENTION: 28 Human Secreted Proteins
.,   FILE REFERENCE: PZ003P1.US
.,   CURRENT APPLICATION NUMBER: US/09/152,060
.,   CURRENT FILING DATE: 1998-09-11
.,   EARLIER APPLICATION NUMBER: PCT/US98/04858
.,   EARLIER FILING DATE: 1998-03-12
.,   EARLIER APPLICATION NUMBER: 60/040,762
.,   EARLIER FILING DATE: 1997-03-14
.,   EARLIER APPLICATION NUMBER: 60/040,710
.,   EARLIER FILING DATE: 1997-03-14
.,   EARLIER APPLICATION NUMBER: 60/050,934

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; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 88
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-152-060-88

Query Match             71.6%;  Score 882; DB 4; Length 235;
Best Local Similarity   76.6%;  Pred. No. 1.6e-63;
Matches  177;  Conservative  12;  Mismatches  38;  Indels  4;  Gaps  1;

Qy     10 LLLLWLPGARCESV---LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP 65
             |||| |     ||||   | ||||||||| |||| : |||||||||||||||||||||
Db      5 LLLLTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP 64

Qy     66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYCQSYDSSLNAQVFGGGT 125
             ||| ||||||||||| |||||||| : :||:|||||||||||||: :|||||  ||||
Db     65 KLLSYRNNNRPSGISERLSASRSGATSSLTITGLQPEDEADYCAAYDSSLAVWMFGGGT 124

Qy    126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 184

Qy    186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
           |||||||||||||||||||||||||||| |||||||||||||||||||||
Db    185 TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235


RESULT 9
US-08-523-894-6
; Sequence 6, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
;  APPLICANT: Hanna, Nabil
;  APPLICANT: Newman, Roland A.
;  APPLICANT: Reff, Mitchell E.
;  TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;  TITLE OF INVENTION: Therapy
;  NUMBER OF SEQUENCES: 59
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314-3187
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/523,894
;   FILING DATE: 06-SEP-1995
;   CLASSIFICATION: 424
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-165
```

```
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX:   703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 233 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-523-894-6

Query Match             69.6%;  Score 857.5; DB 4; Length 233;
Best Local Similarity   74.8%;  Pred. No. 1.4e-61;
Matches  172;  Conservative  16;  Mismatches  39;  Indels  3;  Gaps  2;

Qy      7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
           ||||| :   : ||||  | ||| :||| :||| : |||||||||||||||| ||||
Db      7 LLGLLAHTDSA-ASYELSQPRSVSVSPGQTAGFTCGG--DNVGRKSVQWYQQKPPQQAPV 63

Qy     67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYCQSYDSSLNAQVFGGGTR 126
           | :|||| ||||||| |||||||: :||:|:|: |||||||||| :|||: |||||||||
Db     64 LVIYADSERPSGIPARFSGSNSGNTATLTISGVEAGDEADYCQVWDSTADHWVFGGGTR 123

Qy    127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 183

Qy    187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233


RESULT 10
US-09-049-672A-11
; Sequence 11, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
;  APPLICANT: Hillman, Jennifer L.
;  APPLICANT: Lal, Preeti
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Yue, Henry
;  APPLICANT: Au-Young, Janice
;  APPLICANT: Corley, Neil C.
;  APPLICANT: Guegler, Karl J.
;  APPLICANT: Baughn, Mariah R.
;  TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;  NUMBER OF SEQUENCES: 28
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/049,672A
;   FILING DATE: HEREWITH
;   CLASSIFICATION: 536
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Cerrone, Michael C
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0497 US
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX:   650-845-4166
```

; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LNODNOT08
; CLONE: 3056213
US-09-049-672A-11

Query Match 67.9%; Score 836; DB 4; Length 240;
Best Local Similarity 70.2%; Pred. No. 7.8e-60;
Matches 172; Conservative 17; Mismatches 42; Indels 14; Gaps 4;

Qy 1 MRVPAQLLGLLLLWL----PGARCESVLTQPPSVSGAPGQKVTISC----TGSTSNIGG 51
        |||: |||||||: ||| ::|| |||| ||| |:| | ||| ||||
Db 1 MSVPTMAWMMLLLGLLAYGSGVDSQTVVTQEPSFSVSPGGTVTLTCGLSSGSVSTSNYPS 60

Qy 52 YDLHWYQQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQS 111
        |||||||| ||| | | |: | | |:||| | ||| ::| ||||||||||||
Db 61 ---WYQQTPGQAPRTLIYGTSVRSSGVPDRFSGSILGNKAGLTITGAQADDESDYYCVL 116

Qy 112 YDSSLNAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA 171
        ||: | ||||||| ||||||||||||||||||||||||||||||||||||||||||
Db 117 YRRS-GSWVFGGGTKLSVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA 175

Qy 172 WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA 231
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 176 WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVA 235

Qy 232 PTECS 236
        ||||
Db 236 PTECS 240

RESULT 11
US-08-793-450-6
; Sequence 6, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-6

Query Match 65.3%; Score 804.5; DB 4; Length 238;
Best Local Similarity 70.9%; Pred. No. 2.6e-57;
Matches 163; Conservative 10; Mismatches 40; Indels 17; Gaps 3;

Qy 17 GARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRP 76
        || | :| :|::|:||::| : ||: : ||||| || |||||||||||
Db 16 GVHSDIELTQDPAVSVALGQTVRITCQG--DSLRTYYASWYQQKPGQAPVLVIYGKNNRP 73

Qy 77 SGISDRFSGSKSGTAASLAITGLQTEDEADYYCQGYDSSLNAQVFGGGTRLTVLGQPKAA 136
        ||| ||||| |||||||||||||||||||| ||||||||||||||||||||
Db 74 SGIPDRFSGSSSGNTASLTITGAQAEDEADYFCNS----GGKVFGGGTKLTVLGQPKAA 128

Qy 137 PSVTLFPPS----------SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
        ||||||||| ||||||||||||||||||||||||||||||:||||||||
Db 129 PSVTLFPPSLEELQANKATLEELQANKATLVCLISDFYPGAVTLAWKADGRPVKAGVETN 188

Qy 187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
        ||||||||||||||||||||||||||||||||||||||||||:|||
Db 189 KPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTAEKTVAPAECS 238

RESULT 12
US-08-751-359-22
; Sequence 22, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-22

Db   4 APLLLAVLAHTSGSLVQAALTQPSSVSANPGETVKITCSGDRSYYG----WYQQKAPGS 58

Qy   64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
         || ||||| |: |:|||||||| :| ::|:||| :|:||||||| :|||||::
Db   59 APVTVIYANTNRPSDIPSRFSGSKSGSTATLTITGVQADDEAVYYCGSADSSSTAGIFGA 118

Qy 124 GTRLTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAG 182
         || ||||||||| |||||||||:|| |:| |||||||| :|||||| |||| ||||:|
Db 119 GTTLTVLGQPKVAPTITLFPPSKEELNEATKATLVCLINDFYPSPVTVDWIDGS-TRSG 177

Qy 183 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 235
         | |||||||||:||||||||||||||||||||||:||||||||||||||:||
Db 178 -ETTAPQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNGTSITKTLKRSEC 229

RESULT 14
US-08-761-277A-51
; Sequence 51, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
;   APPLICANT: Denney Jr., Dan W.
;   TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
;   TITLE OF INVENTION: Leukemia
;   NUMBER OF SEQUENCES: 80
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Medlen & Carroll, LLP
;   STREET: 220 Montgomery Street, Suite 2200
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/761,277A
;   FILING DATE: 06-DEC-1996
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/644,664
;   FILING DATE: 01-MAY-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MacKnight, Kamrin T.
;   REGISTRATION NUMBER: 38,230
;   REFERENCE/DOCKET NUMBER: GENITOPE-02406
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 705-8410
;   TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 51:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 109 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-761-277A-51

  Query Match   46.0%; Score 567; DB 2; Length 109;
  Best Local Similarity 100.0%; Pred. No. 1.1e-38;
  Matches 109; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 128 TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 187
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 60

Qy 188 PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 109

RESULT 15
US-08-422-101-9

Query Match   51.5%; Score 634.5; DB 4; Length 229;
Best Local Similarity   55.8%; Pred. No. 1e-43;
Matches 130; Conservative   32; Mismatches   62; Indels   9; Gaps   5;

Qy   5 AQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQ-LPGT 63
         | || | | | | ||||||||| |: ||||||||||:|:|:|||:| |||||| |:||
Db   4 APLLLAVLAHTSGSLVQAALTQPSSVSANPGETVKITCSGDRSYYG----WYQQKAPGS 58

Qy   64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
         || ||||| |: |:|||||||| :| ::|:||| :|:||||||| :|||||::
Db   59 APVTVIYANTNRPSDIPSRFSGSKSGSTATLTITGVQADDEAVYYCGSADSSSTAGIFGA 118

Qy 124 GTRLTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAG 182
         || ||||||||| |||||||||:|| |:| |||||||| :|||||| |||| ||||:|
Db 119 GTTLTVLGQPKVAPTITLFPPSKEELNEATKATLVCLINDFYPSPVTVDWIDGS-TRSG 177

Qy 183 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 235
         | |||||||||:||||||||||||||||||||||:||||||||||||||:||
Db 178 -ETTAPQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNGTSITKTLKRSEC 229

RESULT 13
US-08-907-146-22
; Sequence 22, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
;   APPLICANT: Michael, Nancy M
;   APPLICANT: Accavitti, Marianne
;   APPLICANT: Thompson, Craig B
;   TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/907,146
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/751,359
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Highlander, Steven L
;   REGISTRATION NUMBER: 37,642
;   REFERENCE/DOCKET NUMBER: ARSB:504
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512/418-3000
;   TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 229 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
US-08-907-146-22

Query Match   51.5%; Score 634.5; DB 4; Length 229;
Best Local Similarity   55.8%; Pred. No. 1e-43;
Matches 130; Conservative   32; Mismatches   62; Indels   9; Gaps   5;

Qy   5 AQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQ-LPGT 63
         | || | | | | ||||| | :: | ||| ||

```
;  Sequence 9, Application US/08422101
;  Patent No. 5739277
;  GENERAL INFORMATION:
;     APPLICANT:  Leonard Presta
;     APPLICANT:  Brad Snedecor
;     TITLE OF INVENTION:  Altered Polypeptides with Increased
;     TITLE OF INVENTION:  Half-Life
;     NUMBER OF SEQUENCES:  31
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Genentech, Inc.
;        STREET:  460 Point San Bruno Blvd
;        CITY:  South San Francisco
;        STATE:  California
;        COUNTRY: USA
;        ZIP:  94080
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/422,101
;        FILING DATE:  14-APR-1995
;        CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:
;        FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;        NAME:  Lee, Wendy M.
;        REGISTRATION NUMBER:
;        REFERENCE/DOCKET NUMBER:  932-3
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  415/225-1994
;        TELEFAX:  415/952-9881
;        TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  105 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
US-08-422-101-9
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Query Match          44.5%;   Score 548;  DB 1;  Length 105;
Best Local Similarity 100.0%;  Pred. No. 3.4e-37;
Matches  105;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   132  QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
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Db     1  QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 60

Qy   192  SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||
Db    61  SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 105
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Search completed: March 29, 2003, 09:17:44
Job time : 9.38523 secs
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                 Copyright  GenCore version 5.1.3
                 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     April  5, 2003, 18:12:24 ; Search time 392.719 Seconds
                                       (without alignments)
                                       8205.894 Million cell updates/sec

Title:        US-09-758-173-11
Perfect score: 1431
Sequence:     1 ATGAAACACCTGTGGTTCTT.........CCCTGTCTCCGGGTAAATGA 1431

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0

Searched:     2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:   4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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             21: /SIDS2/gcgdata/geneseq/geneseq-embl/NA2000.DAT:*
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             24: /SIDS2/gcgdata/geneseq/geneseq-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1431	100.0	1431	18	AAT62513	Primatised anti-hu
2	1431	100.0	1431	19	AAV35489	Macaque primatized
3	1431	100.0	1431	24	AAS17247	DNA sequence of a
4	1315.8	91.9	1431	18	AAT62510	Primatised anti-hu
5	1315.8	91.9	1431	19	AAV35485	Macaque primatized
6	1315.8	91.9	1431	24	AAS17243	DNA sequence of a
7	1276.4	89.2	1567	22	AAC66522	Human immune syste
8	1261.2	88.1	1431	17	AAT18059	Monoclonal antibod
9	1261	88.1	1634	21	AAZ50012	Human immune syste

```
10  1224.8  85.6  1418  17  AAT26889     Anti-rhesus D reco
11  1181    82.5  1404  18  AAT62868     Human gamma-4 heav
12  1177.8  82.3  1404  18  AAT62870     Human gamma-4PE he
13  1176.2  82.2  1404  18  AAT62869     Human gamma-4E hea
14  1151    80.4  1428  22  AAH74680     Nucleotide sequenc
15  1136.4  79.4  1428  18  AAT61241     Human anti-RSV mon
16  1134    79.2  1430  24  AAK98701     cDNA of the heavy
17  1134    79.2  1644  22  AAS22593     Human cDNA encodin
18  1133.8  79.2  1507  21  AAA09695     Human immunoglobul
19  1133.4  79.2  1798  22  AAC98220     Human colon cancer
20  1123.6  78.5  1428  18  AAT61279     Human anti-RSV mon
21  1122.8  78.5  1599  24  ABK64550     Human benign prost
22  1122.8  78.5  1599  22  ABL62673     Colon adenocarcino
23  1122.8  78.5  1599  24  ABL65479     Lung cancer relate
24  1121.2  78.4  1599  24  ABL66294     Lung cancer relate
25  1121.2  78.4  1617  19  AAQ35099     Antibody D heavy c
26  1120.8  78.3  19035 19  AAV61794     Traget plasmid Man
27  1119.6  78.2  1549  13  AAQ20066     Encodes heavy chai
28  1119    78.2  1442  22  AAC84208     Plasmid Glambda-1B
29       1118       78.1  1449  20  AAX06951     Monoclonal antibod
30       1118       78.1  1449  20  AAX06952     Monoclonal antibod
c 31  1115.8  78.0  6281  22  AAC84206     Plasmid Glambda-1A
32  1112.4  77.7  1437  19  AAV35487     Macaque primatized
33  1112.4  77.7  1437  24  AAS17245     DNA sequence of a
34  1110.8  77.6  1427  19  AAV41429     Plasmid Hu19BHcpcd
35  1110.8  77.6  1427  19  AAV41431     Plasmid Hu19CHcpcd
36  1110.8  77.6  1437  18  AAT13847     Primatised anti-hu
37  1109.8  77.6  1458  13  AAQ23571     Reshaped CD4 antib
38  1109.8  77.6  1458  13  AAQ23581     Reshaped CD4 antib
39  1109.2  77.5  1427  19  AAV41432     Plasmid Hu19DHcpcd
40  1107.8  77.4  1576  14  AAQ49944     Human anti-HBs hea
41  1102.8  77.1  6284  19  AAV41427     Plasmid Hu19AHcpcd
42  1102.2  77.0  6557  17  AAT15932     Anti-IgE VH expres
c 43  1101    76.9  1431  22  AAC91017     Chimeric 4H6 anti-
c 44  1101    76.9  1431  22  AAC91018     Chimeric 4H6 anti-
c 45  1100.8  76.9  2912  22  AAS22718     Human cDNA encodin
```

ALIGNMENTS

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RESULT 1
AAT62513
ID   AAT62513 standard; DNA; 1431 BP.
XX
AC   AAT62513;
XX
DT   25-MAY-1997 (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996; 96WO-US10053.
XX
PR   07-JUN-1995; 95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
```

DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01822.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 11; Fig 10B; 81pp; English.
XX
CC   2 DNA sequences (AAT62512 and AAT62513) respectively code for
CC   primatised forms (AAW01821 and AAW01822) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   16C10. Cloned 16C10 light and heavy variable genes are inserted
CC   into an expression vector (pref, NEOSPLA) which contains human light
CC   and heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

Query Match   100.0%; Score 1431; DB 18; Length 1431;
Best Local Similarity 100.0%; Pred. No. 8.5e-286;
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCGGAGCTGGGTCCTGTCCCAG 60
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Db   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCGGAGCTGGGTCCTGTCCCAG 60

Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

[alignment rows continue through 1431 BP]

RESULT 2
AAV35489
ID   AAV35489 standard; DNA; 1431 BP.
XX
AC   AAV35489;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 16C10 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1431
FT   /*tag= a
FT   /product= 16C10 heavy chain
XX

PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63765.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5b; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 16C10 heavy chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

      Query Match   100.0%;   Score 1431; DB 19; Length 1431;
      Best Local Similarity 100.0%;   Pred. No. 8.5e-286;
      Matches 1431 Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGAAAACCTGTGGTTCTTCCTCCTGGCAGCTCCAGATGGGTCCTGTCCCAG 60
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Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGTGGGTGGATCCGGCCAGCCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGTGGGTGGATCCGGCCAGCCC 180

Qy   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGGAACACCTACTAC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGGAACACCTACTAC 240

Qy   241 AACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTCTCC 300
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Db   241 AACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTCTCC 300

Qy   301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360

Qy   361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420
          ||||||

Db   361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480

Qy   481 TCCAAGAGCACCTCTGGGGCACAGGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAAGAGCACCTCTGGGGCACAGGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
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Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
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Db   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720

Qy   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCACCGTGCCCAGCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCACCGTGCCCAGCA 780

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
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Db   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
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Db   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
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Db   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
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Db   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
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Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431

RESULT 3
AAS17247

ID   AAS17247 standard; DNA; 1431 BP.
XX
AC   AAS17247;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the heavy chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1431
FT   /*tag= a
FT   /product= "Heavy chain of 16C10 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11646.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   useful for treating diseases such as B cell cancer, lymphoma, a
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 5b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present nucleic
CC   acid sequence encodes the heavy chain of 16C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

Query Match   100.0%;   Score 1431;   DB 24;   Length 1431;
Best Local Similarity   100.0%;   Pred. No. 8.5e-286;
Matches 1431;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60

```
Db           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG   60

Qy        61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC  120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC  120

Qy       121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGTTATGGCTGGGCTGGATCCGCCAGCCC  180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGTTATGGCTGGGCTGGATCCGCCAGCCC  180

Qy       181 CCAGGGAAGGGGCTGGAGTGGATTGGAGTTTCTATAGTAGTGGGAACACCTACTAC  240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCAGGGAAGGGGCTGGAGTGGATTGGAGTTTCTATAGTAGTGGGAACACCTACTAC  240

Qy       241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC  300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC  300

Qy       301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGCCGTGTATTACTGTGTGAGAGATCGT  360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGCCGTGTATTACTGTGTGAGAGATCGT  360

Qy       361 CTTTTTTCAGTTGTTGTTGGAATGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC  420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTTTTTTCAGTTGTTGTTGGAATGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC  420

Qy       421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480

Qy       481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy       541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy       601 GCTGTCCTACAGTCCTCAGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCCAGC  660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GCTGTCCTACAGTCCTCAGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCCAGC  660

Qy       661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAGACCACAGCCCAGCAACACCAAGGTG  720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAGACCACAGCCCAGCAACACCAAGGTG  720

Qy       721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780

Qy       781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy       841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900

Qy       901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy       961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy      1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy      1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
Qy  1141 CCCCATCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CCCCATCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
Qy  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
Qy  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
Qy  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
```

RESULT 4
AAT62510
ID AAT62510 standard; DNA; 1431 BP.
XX
AC AAT62510;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primatised anti-human B7.1 antigen antibody 7C10 heavy chain DNA.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopaenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR WPI; 1997-108638/10.
DR P-PSDB; AAW01818.
XX
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
XX
PS Claim 7; Fig 8B; 81pp; English.
XX
CC 2 DNA sequences (AAT62509 and AAT62510) respectively code for
CC primatised forms (AAW01817 and AAW01818) of the light and heavy chains
CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC 7C10. Cloned 7C10 light and heavy variable genes are inserted into
CC an expression vector (pref. NEOSPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of primatised
CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC antibody have also been produced (see also AAW01819-22). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
SQ Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

Query Match   91.9%; Score 1315.8; DB 18; Length 1431;
Best Local Similarity   95.0%; Pred. No. 4.8e-262;
Matches 1359; Mismatches 72; Conservative 0; Indels 0; Gaps 0;

```
Qy    1 ATGAAACACCTGGTTCTCCTCCTCCTGGTTCAGCTCCCAGATGGTGGTCCTGTCCCAG 60
        |||||||||||||||| ||||||||||||||||||||||||||||| |||||||||||||
Db    1 ATGAAACACCTGGTTCTTCCTCCTCCTGGTTCAGCTCCCAGATGGTCGTCCTGTCCCAG 60
Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
        ||| |||||||| ||| |||||| ||||||||||| ||||||  ||||||||||||| ||
Db   61 GTGAAGCTGCAGCAGTCTGGGGCTGGGCTGGTGCAGCCTTCGCAGCCTGTCCCTGTCGACC 120
Qy  121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTTGTTATGGCTGGTGGATCCGGCAGCCC 180
        ||||  ||||||||||||||||||||||| | |||| ||| ||||||||||||||||
Db  121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGAGCTGGATCCGGCAGCCC 180
Qy  181 CCAGGGAAGGGGCTGGAGTGGATTGGGTATATTTATTATGGTAATGGTGCGACCAACTAC 240
        |||||||||||||||||||||||||||||| |||||| ||||||||||||| |||||||||
Db  181 CCAGGGAAGGGGCTGGAGTGGATTGGTTATAGTTATAGTAGTGGTAATGGGTCGGACACCTAC 240
Qy  241 AACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTCTCC 300
        |||||||||||||||||||||||||||||||||||| ||||||||||||||||||| |||
Db  241 AATCCCTCCCTCAAGAGTCAGTCACCATTTCAAAGACACGTCCAAGAACCAGTTCTTC 300
Qy  301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
        |||||||||||| ||||||||| ||| |||| ||||||| ||||||||||||||||||
Db  301 CTGAACTTGAATTCTGTGACCGCCGACACGGCCGTCTATTACTGTGCGGAGAGGGCCCT 360
Qy  361 CTTTTTTCAGTTGTTGGAATGTTTACAAAACTGGTTCGGGGGCCCGGGAGTC 420
Db  361 CGCCCTGATTGCACAACCATTTGTATGGGCGGCTGGTCTGGGCCCGGGAGAC 420
Qy  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
Db  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
Qy  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
Db  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
Qy  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
Db  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
Qy  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
Db  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
Db  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
Db  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
Qy  781 CCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
Db  781 CCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
Db  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
Qy  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
Db  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
```

PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3b; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 7C10 heavy chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. Mab's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

Query Match   91.9%;   Score 1315.8;   DB 19;   Length 1431;
Best Local Similarity   95.0%;   Pred. No. 4.8e-262;
Matches 1359;   Conservative   0;   Mismatches   72;   Indels   0;   Gaps   0;

```
Qy      1  ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTTCCTGTCCCAG     60
           ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db      1  ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTTCCTGTCCCACC    60

Qy     61  GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC   120
           ||| ||||||| |||||||||  ||||||| ||||||||||||||||||||||||| ||||
Db     61  GTGAAGCTGCAGCAGTCGGGGGCGGAAGGACTTCTGCAGCCTTCGGAGACCCTGTCCCACC   120

Qy    121  TGCGCTGTCTCTGGTGGCTCCATCAGCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC  180
           ||||  |||||||||||||||||||||||||||    ||| ||  ||||||||||||||| | 
Db    121  TGCGTTGTCTCTGGTGGCTCCATCAGCAGCGGTTACTACTGGGACTGGATCCGCCAGACC   180

Qy    181  CCAGGGAAGGGCCTGGAGTGGCTGGGAGTTCTCATAGTAGTGGGAACACCTACTAC       240
           ||||| ||||| |||||||| |||||| |||| |||| || |||| ||| ||  |||
Db    181  CCAGGAGGGGACTGGAGTGGATGGGAGTTGATTGGGTGCGCCATATTATGGTAATGG       240

Qy    241  AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC    300
           ||  |||||||||||||||| |||||||||||||| ||||| | |||||||||||||| | 
Db    241  AATCCCTCCCTCAAGAGTCAAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC    300

Qy    301  CTGAAGCTGACTCTATGACCGCCCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT     360
           ||||| || |||||  ||  |||| ||||| |||||||| |||||||||||| ||   | 
Db    301  CTGAACTTGAATTCTGTGACCGACGGGACACGGCCGTGTCTTATTACTGTGCGAGAGAGCCCT  360

Qy    361  CTTTTTCAGTTGTTGGAATGGTTACAACAACCATTTGTTATGGGCCCCGGGAGTC      420
           | |||  || ||  ||||| |||| ||||||||||| |||| |||||||||||||
Db    361  CGCCCTGATTGCACAACCATTTGTTATGGGCCCCGGGAGGGCCGGGACTCTGGGGGAGAC   420

Qy    421  CTGGTCACCGTCTCCTCAGTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC   480
           ||||||||| |||||||||||||||||||||||||||| |||||||||||||||||||||
Db    421  CTGGTCACCGTCTCCTCAGTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCCTCC   480

Qy    481  TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy    541  GAACCGGTGACGGTGCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   600
           ||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||| |
Db    541  GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC  600

Qy    601  GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
```

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Db    961  ...||||||...CGGGAGGAGCAGTACAACAGCAGTACAGCTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020

Qy   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080

Qy   1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140

Qy   1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200

Qy   1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260

Qy   1261  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320

Qy   1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380

Qy   1381  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
```

RESULT 5
AAV35485
ID   AAV35485 standard; DNA; 1431 BP.
XX
AC   AAV35485;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 7C10 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1431
FT   /tag= a
FT   /product= 7C10 heavy chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63761.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B

```
Qy    661  AGCTTGGGCACCCAGACCTACATCTGAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AGCTTGGGCACCCAGACCTACATCTGAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720

Qy    721  GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780

Qy    781  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840

Qy    841  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT   900

Qy    901  GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960

Qy    961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTGCACCAG   1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTGCACCAG   1020

Qy   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC   1080

Qy   1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACCAGGTGTACACCCTG   1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACCAGGTGTACACCCTG   1140

Qy   1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1200

Qy   1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1260

Qy   1261  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC   1320

Qy   1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCT   1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCT   1380

Qy   1381  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1431
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1431
```

```
RESULT 6
AAS17243
ID     AAS17243 standard; DNA; 1431 BP.
XX
AC     AAS17243;
XX
DT     12-MAR-2002  (first entry)
XX
DE     DNA sequence of a primatised form of the heavy chain of 7C10 antibody.
XX
KW     Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW     neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW     B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW     tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW     graft-vs-host disease; immunosuppression; organ rejection;
KW     interleukin-2; IL-2; mutant; ds.
XX
OS     Chimeric - Homo sapiens.
OS     Chimeric - Macaca sp.
OS     Synthetic.
```

```
XX
FH     Key            Location/Qualifiers
FT
FT     CDS            1..1431
FT                    /*tag= a
FT                    /product= "Heavy chain of 7C10 antibody"
XX
PN     WO200189567-A1.
XX
PD     29-NOV-2001.
XX
PF     22-MAY-2001; 2001WO-US16364.
XX
PR     22-MAY-2000; 2000US-0576424.
XX
PA     (IDEC-) IDEC PHARM CORP.
XX
PI     Anderson DR, Hanna N, Brams P;
XX
DR     WPI; 2002-089895/12.
DR     P-PSDB; AAU11539.
XX
PT     Use of monoclonal antibody which specifically binds to B7.1 antigen
PT     CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT     treating cancer, graft-vs-host disease and autoimmune disease such as
PT     allergy -
PS     Example 8; Fig 3b; 89pp; English.
XX
CC     The present invention relates to a new use of a monoclonal antibody
CC     which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC     (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC     useful for treating diseases such as B cell cancer, lymphoma, a
CC     cancer where B cells promote the growth and/or metastasis of tumours,
CC     B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC     idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC     type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC     anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC     or graft-vs-host disease. The antibody is useful for immunosuppression
CC     in a human or animal and for treating or preventing resistance to or
CC     rejection of transplanted organ or tissue for treating proliferative
CC     and hyperproliferative diseases, for treating reversible obstructive
CC     airways disease, intestinal inflammations and allergies e.g. Crohn's
CC     disease and ulcerative colitis, food-related allergies e.g. migraine,
CC     rhinitis and eczema, and other types of allergies. The present nucleic
CC     acid sequence encodes the heavy chain of 7C10, a primatised antibody
CC     used in the invention to induce apoptosis and inhibit production of
CC     interleukin-2 (IL-2).
XX
SQ     Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;
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Query Match              91.9%;   Score 1315.8;  DB 24;  Length 1431;
Best Local Similarity    95.0%;   Pred. No. 4.8e-262;
Matches 1359;   Conservative    0;  Mismatches  72;  Indels    0;  Gaps    0;

Qy     1  ATGAAAACACCTGTTCTTCCTCCTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGAAAACACCTGTTCTTCCTCCTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG   60

Qy    61  GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GTGAAGCTGCAGCAGTCGGGGGCAGGGAGGCGAAGGACTTCTCGAGACCCTGTCCCGACC  120

Qy   121  TGCGCTGTCTCTGGTGGCTCCATCAGCAGCGGTGGTTATGGCTGGATCCGGCCAGCCCC  180
          |||||||||| ||||||||||||||||||| |||||||||||||||||||||| |||||
Db   121  TGCGGTGTCTCTGGTGGCTCCATCAGCAGCGGTTACTACTGGAGCTGGATCCGGCCAGACC  180

Qy   181  CCAGGGAAGGGGCTGGAGTGGATTGGATGTTCTATAGTAGTAGTGGAACACCTACTAC  240
          |||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||
Db   181  CCAGGGAGGGGGACTGGAGTGGATTGGGATTGGCCATATTTTATGGTAATGGTGCCACCAACTAC  240

Qy   241  AACCCCTCCCTCAAGAGTCGAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC  300
          |||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||
Db   241  AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC  300
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Qy  1381 CTGCACAACCACTACACGCAGAGAAGAGCCTCTCCCGTCTCCGGGTAAATGA 1431
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTGCACAACCACTACACGCAGAGAAGAGCCTCTCCCGTCTCCGGGTAAATGA 1431


RESULT 7
AAC66522
ID   AAC66522 standard; cDNA; 1567 BP.
XX
AC   AAC66522;
XX
DT   15-FEB-2001 (first entry)
XX
DE   Human immune system associated protein HISAP-4 coding sequence.
XX
KW   Human; immune system associated protein; HISAP-4; immune disorder;
KW   infection; autoimmune disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   US6135941-A.
XX
PD   24-OCT-2000.
XX
PF   27-MAR-1998;    98US-0049672.
XX
PR   27-MAR-1998;    98US-0049672.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI   Hillman JL, Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   P-PSDB; AAB6206.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing
PT   immune or cell proliferative disorders or infections -
XX
PS   Claim 3; Column 79-80; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ   Sequence 1567 BP; 346 A; 503 C; 428 G; 289 T; 1 other;

Query Match             89.2%;  Score 1276.4;  DB 22;  Length 1567;
Best Local Similarity   94.7%;  Pred. No. 6.4e-254;
Matches 1358;  Conservative    0;  Mismatches   61;  Indels  15;  Gaps     3;

Qy    1 ATGAAAACCCTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG   60
         ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db   78 ATGAAAACCCTGGTTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG  137

Qy   61 GTGCAGGTCGCAGGAGTCGGCGCCCAGGACTCGTGAAGCCTTCGGAGACCCTTCCCTCACC  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  138 GTGCAGGTCGCAGGAGTCGGCGCCCAGGACTCGTGAAGCCTTCGGAGACCCTTCCCTCACC  197

Qy  121 TGGCGTGCTCTGTGGCTCCATC---AGCGGTGGTTATGGCTGGGGATCCGGCAG  177
         |||||||||||||||||||||    ||||||||||||||||||||||||||||
Db  198 TGGCGTGCTCTGTGGCTCCATCACTCACTACAGTGGTGGTTACTACTGGGAACACGTG  257

Qy  178 CCCCCAGGGAAGGGGCTGGAGTTGGATTGGATTGGTACATCTA---TTACAGTGGGAGCACCCTC  237
         |||||||||||||||||||||||||||||||||||||||||||     |||||||||||||||
Db  258 CCCCCAGGGAAGGGGCTGGAGTTGGATTGGATTGGTACATCTA---TTACAGTGGGAGCACCCTC  314
```

Left column sequence alignments:

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Qy  301 CTGAAGCTGAACTCTATGACCCGCGCGACACGGCCGTGTATTACTGTGTGAGAGATCGT  360
         |||||||||   ||||  |  ||||||||||||||||||||||||||||||||||||||
Db  301 CTGAACTTGAATTCTGTCGTGACCGACGGCGACACGGCCCGTCTATTACTGTGTGAGAGATCGT  360

Qy  361 CTTTTTCAGTTGTTGTGGAATGTTTACAACAACTGGTTCGATGCTGTCTGGGGCCCGGGAGTC  420
         |      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CGCCCCTGATTGCACAACCATTTGTTATGCGGGTCGGATGTGTCTGGGGCCCGGGAGAC  420

Qy  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480

Qy  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660

Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720

Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780

Qy  781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900

Qy  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy 1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCT 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCT 1380
```

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Qy   238  TACAACCCCTCCCTCCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTC  297
          |||||||||||||| ||| |||||| ||  |  |  | |||||||||||||||||||||||
Db   315  TACAACCCGTCCCTCAAGAGTCCCTCAGTAGTCCAGTTACCATTATCAGTAGACACGTCCAAGAACCAGTTC  374

Qy   298  TCCTGAAGCTGAACTCTATGACCGGCCGGACACGGCCGTGTATTACTGTGTGAGAGAT  357
          ||||| |||||||||||||||||||||||| |||||||||||||||||||||
Db   375  TCCTCGAAGCTGAGCTCTGTGACTGACCACGGCCGTGTATTACTGTGCCAGAGA-  433

Qy   358  CGTCTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTGTGGGGCCGGGA  417
          |||                      ||||||||||||||||||||||||||||||||||
Db   434  ------TGACGTAGGTTTAAGGGGGGAACTACGGTATGGACGTCTCGGGCCAGGGA  485

Qy   418  GTCCTGGTCACCGTCTCCTCAGCTAGCAGCCAGGGCCCATCGGTCTTCCCCCTGGCACCC  477
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486  ACCCTGGTCACCGTCTCCTCAGCTCCTCCAGCGCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  545

Qy   478  TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  537
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546  TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  605

Qy   538  CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606  CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  665

Qy   598  CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  657
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666  CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  725

Qy   658  AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726  AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  785

Qy   718  GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA  777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786  GTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA  845

Qy   778  GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846  GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  905

Qy   838  CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906  CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  965

Qy   898  CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG  957
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966  CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG  1025

Qy   958  CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC  1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1026  CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC  1085

Qy  1018  CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC  1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1086  CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC  1145

Qy  1078  CCCATCGGAGAAAACCATCTCCAAAGGCAAAGGCAGCCCCGAGAACCACAGGTGTACACC  1137
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  1146  CCCATCGGAGAAACCATCTCCAAAGGCAAAGGCAGCCCCGAGAACCACAGGTGTACACC  1205

Qy  1138  CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA  1197
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1206  CTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA  1265

Qy  1198  GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1257
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  1266  GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1325

Qy  1258  TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC  1317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1326  TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC  1385

Qy  1318  ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG  1377
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Db  1386  ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG  1445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  1378  GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1446  GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAATGA  1499
```

RESULT 8
AAT18059
ID   AAT18059 standard; DNA; 1431 BP.
XX
AC   AAT18059;
XX
DT   16-AUG-1996 (first entry)
XX
DE   Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
XX
KW   Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW   65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1428
FT   /*tag= a
FT   sig_peptide   1..57
FT   /*tag= b
FT   mat_peptide   58..1425
FT   /*tag= c
FT   3'UTR   1426..1431
FT   /*tag= d
XX
PN   JP08038178-A.
XX
PD   13-FEB-1996.
XX
PF   20-FEB-1995; 95JP-0030742.
XX
PR   18-FEB-1994; 94JP-0021628.
XX
PA   (NISN) NISSHINBO IND INC.
PA   (TANA/) TANAKA H.
XX
DR   WPI; 1996-154852/16.
DR   P-PSDB; AAR93353.
XX
PT   Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT   produced by primer amplification, used in the diagnosis of hCMV
PT   infection
XX
PS   Claim 6; Page 16-18; 22pp; Japanese.
XX
CC   The sequences given in AAT18059-60 encode the heavy and light chains
CC   respectively of a monoclonal antibody against a 65 kD antigen of human
CC   cytomegalovirus (hCMV). These sequences were amplified using the
CC   sequences given in AAT18040-58. The monoclonal antibody may be used
CC   in the diagnosis of hCMV.
XX
SQ   Sequence 1431 BP; 314 A; 475 C; 379 G; 263 T; 0 other;

Query Match   88.1%; Score 1261.2; DB 17; Length 1431;
Best Local Similarity   93.9%; Pred. No. 8.6e-251;
Matches 1347; Conservative   0; Mismatches 78; Indels   9; Gaps   3;

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```
Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAAGCATCTGTGGTTCTTCCTCCTCCTGGTGGCGGCTCCCAGATGGGTCCTGTCCCAG 60

Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Qy   121 TGCCTGTCTCTGTGGCTCCATCAGC---GGTGGTTATGGCTGGGGCTGGGGCTGATCCGCCAG 177
         ||| ||||||||||||| ||||||||   | ||| ||| |  ||||||||| |  |||||||||
Db   121 TGCACTGTCTCTGTGACTCCATCAGCAGGAGTAGTTACTCCTGGGGCTGCATCCGCCAG 180

Qy   178 CCCCAGGAAGGGCTGAGTGGATTGGGAGTTTCATAGTAGTGGGAACACCTAC 237
         ||||  |||||||||||||||||||||||   |  |   ||||| |||| ||
Db   181 CCCCGGGGAAGGGCCTGAGTGGATTGGGAGTGGACTATCTA---TTATAGTGGGAGCACCTAC 237

Qy   238 TACAACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTC 297
         |||| |||||||||||||||||    ||||| ||| |  ||  ||||||| |||||||||
Db   238 TACACCCGTCCCTCAAGAGTCCCCAAGAGTCGAGTCACCATATCCGTAGACGCGTCCAACAACCAGTTC 297

Qy   298 TCCCTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGAT 357
         |||||||||||| ||||| ||||||||| |||||||| |||||||||||||| ||||
Db   298 TCCCTGAAGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGCGAGAACC 357

Qy   358 CGTCTTTTTCAGTGTGTTGGAATGGTTACAACAACTGGTTCGATGTCTCGGGGCCCGGGA 417
            ||||     || | || ||||| || |||| | |||||||   | || |||||| ||||
Db   358 TCGGCCGCAGTATTACGATCTTTTGACTGGTT---CCTTTCCCTCATACTGGGGCCAGGGA 414

Qy   418 GTCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 477
           ||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Db   415 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 474

Qy   478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 537
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   475 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 534

Qy   538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   535 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 594

Qy   598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 657
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   595 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 654

Qy   658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   655 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 714

Qy   718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
         |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   715 GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 774

Qy   778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 837
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   775 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 834

Qy   838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 897
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   835 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 894

Qy   898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   895 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 954

Qy   958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   955 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1014

Qy  1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1015 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1074

Qy  1078 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1137
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1075 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1134

Qy  1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1135 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1194

Qy  1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
         |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  1195 GGCTTCTATCCCAGGCACATCCCGTGCTGGAGTGGGAGGAGCAATGGGCAGCCGGAGAACAAC 1254

Qy  1258 TACAAGACCACCGCCTCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCCTACAGCAAGCTC 1317
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1255 TACAAGACCACCGCCTCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCCTACAGCAAGCTC 1314

Qy  1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCATGCTCCGTGATGCATGAG 1377
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1315 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCATGCTCCGTGATGCATGAG 1374

Qy  1378 GTCTGCACACCACTACACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||| |||||||||||||||||||||||||||||||||||||||||
Db  1375 GCTCTGCACAACCACTACACGCAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428
```

RESULT 9
AA250012
ID   AA250012 standard; cDNA; 1634 BP.
XX
AC   AA250012;
XX
DT   25-APR-2000 (first entry)
XX
DE   Human immune system molecule, ISMO-2 cDNA.
XX
KW   Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW   treatment; prevention; cell proliferation; immune system disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   78..1490
FT   /tag= a
FT   /product= "ISMO-2"
FT   /note= "ISMO-2 shows homology to vertebrate
FT   immunoglobulin gamma heavy-chain"
FT   sig_peptide   78..134
FT   /tag= b
FT   mat_peptide   135..1487
FT   /tag= c
FT   /product= "Mature ISMO-2 protein"
FT   misc_binding   432..473
FT   /tag= d
FT   /bound_moiety= "Hybridisation probe"
XX
PN   WO200000608-A2.
XX
PD   06-JAN-2000.
XX
PF   21-JUN-1999; 99WO-US13995.
XX
PR   30-JUN-1998; 98US-0107223.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
PI   Baughn MR;
XX
DR   WPI; 2000-170916/15.
DR   P-PSDB; AAY44721.
XX
PT   Immune system molecules used in the diagnosis, treatment and prevention
PT   of disorders associated with the immune system and cell proliferation
PT   -
XX
PS   Claim 7; Pages 64-65; 69pp; English.
XX
CC   The present sequence is a cDNA encoding an immune system molecule,
CC   ISMO-2 from an Incyte clone 2849752 isolated from the human breast
CC   tumour cDNA library (BRSTTUT13).This sequence is expressed in several
CC   libraries, generally those associated with cancer, cell
CC   proliferation, immune response or trauma.

```
CC   The present sequence is useful in the diagnosis, treatment and
CC   prevention of disorders associated with the immune system and
CC   cell proliferation.
XX
SQ   Sequence 1634 BP; 369 A; 541 C; 432 G; 292 T; 0 other;

Query Match      88.1%;  Score 1261;  DB 21;  Length 1634;
Best Local Similarity   94.2%;  Pred. No. 9.6e-251;
Matches 1348;   Conservative   0;  Mismatches 65;  Indels 18;  Gaps   3;

Qy       1 ATGAAACACCTGTTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTTCTTGTCCCAG 60
           ||||||||||||||||||||||||||||||||| || | |||||||||||||||||||||||
Db      78 ATGAAACATCTGTTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTTCTTGTCCCAG 137

Qy      61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 197

Qy     121 TGGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGTGGGGCTGATCCGGCCAGCCC 180
           |||||||||||||||||||  |||||  ||||||||||||||||||||||||
Db     198 TGCACTGTCTCTGTGTGGGCTTCCATCA--GGAGTTACTACTGGAACTGGATCCGGCCTGCC 254

Qy     181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTAGTGGAACACCTACTAC 240
           ||||||||||| | ||| |||||||||||| |||||||| | |||||||||||||| ||||||
Db     255 CCAGGGAAGGGACTGGAGTGGATTGGGTATATCTA---TACTAGTGGGAGCACCAACTAC 311

Qy     241 AACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTCTCC 300
           |||||||||||||||||||| |||||||||||| | |||||| || ||||||||||||||
Db     312 AACCCCTCCCTCAAGAGTCGAGTCAGTAGACACGTTCAGTAGACACGTCCAAGAACCAGTTCTCC 371

Qy     301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
           ||||||||||||||||||||||||||||||||||||||||||| |||| |||
Db     372 CTGAAGCTGAGCTCTGTGACCGCCGCGCGGACACGGCCGTGTATTACTGTGCGAGAGACCCCCG 431

Qy     361 CTTTTTTCAGTTGGTGTTGGAATGGTTTACAACAACTGGTTCGATGGTCTCGGGGCCCGGGAGTC 420
           |||||||  |||||
Db     432 CCCAACGCTACTACTACGGTATGGA------------CTTCTGGGGCCAAGGGACCACCGTC 479

Qy     421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 539

Qy     481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 599

Qy     541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 659

Qy     601 GCTGTCCTACAGTCCTCACTGTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GCTGTCCTACAGTCCTCACTGTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 719

Qy     661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 779

Qy     721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 GACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 839

Qy     781 CCTGAACTCCTGGGGGGACCGGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 CCTGAACTCCTGGGGGGACCGGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 899

Qy     841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 959

Qy     901 GAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     960 GAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 1019

Qy     961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1020 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1079

Qy    1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1080 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1139

Qy    1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1199

Qy    1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1259

Qy    1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1319

Qy    1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1379

Qy    1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1380 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGGT 1439

Qy    1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1440 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1490
```

RESULT 10
AAT26889
ID   AAT26889 standard; cDNA; 1418 BP.
XX
AC   AAT26889;
XX
DT   30-OCT-1996 (first entry)
XX
DE   Anti-rhesus D recombinant antibody D7C2 heavy chain cDNA.
XX
KW   Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
KW   rhesus positive; rhesus negative; haemolysis; heavy chain; gamma 1;
KW   variable region; insect host cell, baculovirus; recombinant production;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   sig_peptide   1..57
FT   /*tag= a
FT   /note= "encoded by synthetic linker corresp. to
FT   mouse VH gene signal sequence"
FT   mat_peptide   58..1416
FT   /*tag= b
FT   /product= heavy chain
FT   /note= "constructed from PCR fragments coding for
FT   human gammal heavy chain constant region
FT   and the variable region from anti-rhesus D
FT   antibody D7C2"
XX
PN   FR2724182-A1.
XX
PD   08-MAR-1996.
XX
PF   02-SEP-1994; 94FR-0010566.
XX
PR   02-SEP-1994; 94FR-0010566.
XX

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Qy  673  CAGACCTACATCTGCGAACGTGAATCACAAGCCGGCAACACCAGGTGACAAGAAAGCA  732
Db  661  CAGACCTACATCTGCGAACGTGAATCACAAGCCAGCAACACCAGGTGACAAGAAAGCA  720

Qy  733  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACTGAACTCCTG  792
Db  721  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACTGAACTCCTG  780

Qy  793  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG  852
Db  781  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG  840

Qy  853  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC  912
Db  841  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC  900

Qy  913  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG  972
Db  901  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG  960

Qy  973  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1032
Db  961  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1020

Qy 1033  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCTCCAGCCCCATCGAGAAAACC    1092
Db 1021  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCTCCAGCCCCATCGAGAAAACC    1080

Qy 1093  ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGG 1152
Db 1081  ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGG 1140

Qy 1153  GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1212
Db 1141  GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1200

Qy 1213  GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1272
Db 1201  GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1260

Qy 1273  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1332
Db 1261  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1320

Qy 1333  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1392
Db 1321  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1380

Qy 1393  TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG  1430
Db 1381  TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG  1418
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Query Match             85.6%;  Score 1224.8;  DB 17;  Length 1418;
Best Local Similarity   93.0%;  Pred. No. 2.7e-243;
Matches 1319;  Conservative    0;  Mismatches   87;  Indels   12;  Gaps    3;

Qy  13  TGGTTCTTCCTCCTCCTCGGTGCGCAGCTCCCAGATGGGTCCTGTCCCAGTGCCAGTGCAG  72
Db  13  TGTATCATCCTCCTTCTTGGTAGCAACAGCTACAGGTCCACCAGGTCCAACTGCAG       72

Qy  73  GAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCT  132
Db  73  CAGTGGGGCGCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTAT  132

Qy 133  GGTGGCTCCATCAGCGGTGGTTATGGGTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGG  192
Db 133  GGTGGGTCCTTCA--GTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGG   189

Qy 193  CTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTACAACCCCTCCCTC  252
Db 190  CTGGAGTGGATTGGGAAATC---AATCATAGTGGAAGCACCAACTACAACCCGTCCCTC   246

Qy 253  AAGAGTCAAGTCACCATTTCAACGACACGTCCAAGAACCAGTTCTCCCTGAAGTCTGAAC  312
Db 247  AAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAACTGAAC  306

Qy 313  TCTATGACCGCCGCGACACGGCCGTGTATTACTGTGCGAGAGATGTCTTTTTCAGTT     372
Db 307  TCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGGGCCCCAGAGTATAAA--- 363

Qy 373  GTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCCGGGAGTCCTGGTCACCGTC 432
Db 364  ---TGGAAGTGTATCATGGGGGACTGGTTCGACCCCTGGGGCCAAGGTACCACTGTCACCGTC 420

Qy 433  TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC  492
Db 421  TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC  480

Qy 493  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG  552
Db 481  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG  540

Qy 553  GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG  612
Db 541  GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG  600

Qy 613  TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC  672
Db 601  TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC  660
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PD   13-MAR-1997.
XX
PF   05-SEP-1996;   96WO-US14324.
XX
PR   06-SEP-1995;   95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   P-PSDB; AAW14925.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Disclosure; Page 82-84; 155pp; English.
XX
CC   DNA sequences (AAT62868-70) respectively code for the heavy chain
CC   regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC   mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC   mutation. They can be used to provide novel monoclonal and
CC   chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC   gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC   combined with the antigen binding domains (see also AAW14922-23) of
CC   macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC   show high affinity to human CD4, have little or no immunogenicity
CC   in humans and show reduced or absence of effector function. They
CC   can be used to treat autoimmune diseases such as rheumatoid
CC   arthritis.
XX
SQ   Sequence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;

Query Match   82.5%; Score 1181; DB 18; Length 1404;
Best Local Similarity   90.4%; Pred. No. 2.9e-234;
Matches 1294; Conservative   0; Mismatches 110; Indels   27; Gaps   2;

```
Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGCTCCCAGATGGGTCCTGTCCCAG    60
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Db     1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGCTCCCAGATGGGTCTTGTCCCAG    60

Qy    61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC   120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC   120

Qy   121 TGCGGTGTCTCTGGTGGCTCCATCAGCAGCGGTGGTTATGGCTGGAGCTGGATCCGCCAGCCC   180
         ||| ||||||||||||||||||||||||||||||||||| |||  |||||||||||||
Db   121 TGCAGTGTCTCTGGTGGCTCCATCAGCAGCGGTGGTTATGGCTGGAGCTGGATCCGCCAGTCC   180

Qy   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTTCATAGTAGTAGTGGGAACACCTACTAC   240
         |||||||||||||||||||||||||||  ||| ||  ||  |||||||||||||
Db   181 CCAGGGAAGGGGCTGGAGTGGATCGGCTGACTATTATTGGTTCTGGACTATTAC   240

Qy   241 AACCCCTCCCTCAAGAGTCGAGTCACCATTTCAACCAGACAGTCCAAGAACCAGTTCTCC   300
         |||||||||||||||| |||  ||||||  ||||| ||||||||||||||||||||||
Db   241 AATCCCTCCCTCAACACAATCGAGTCTCCATTTCAATACAGACAGTCCAAGAACCTCTTCTCC   300

Qy   301 CTGACAGCTGAACTCTATGACGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT   360
         |||||||||||||||||  ||| ||||||||||||||| ||||||||||| |
Db   301 CTGAAACTGAGCTCTGTTACAGCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAATGA   359

Qy   361 CTTTTTTCAGTTGTTGGAATGTCTGGGGCCCGGGACCACGGTCACCGTCTCCTCAGGGAGTC   420
         |||       |||  ||| ||  |||  |||||||||||||||||
Db   359 ---------TATTGAAATATCTTCACTGGTTATTATACGGGGCCCAGGAGTC   402

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCCTCC   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGC   462

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540
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Db   463 TCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   522

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   600
         |||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||
Db   523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   582

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   642

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG   702

Qy   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780
         ||||||| ||| |||||  ||                     |
Db   703 GACAAGAGAGTTGAGTCCAAATATGG---------TCCCCATGCCCATCATGCCCAGCA   753

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840
         ||||||| ||||||||||||||||||||||||||||||||||||  |||||| |||||
Db   754 CCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC   813

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT   900
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCC   873

Qy   901 GAGGTCCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   874 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   933

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGGTCAGCGTCAGCGTCCTCACCAG   1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGGTCAGCGTCAGCGTCCTCACCAG   993

Qy  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC   1080
         |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Db   994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC   1053

Qy  1081 ATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCGAGAACCAACAGGTGTACACCCTG   1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG   1113

Qy  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1114 CCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1173

Qy  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1233

Qy  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC   1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC   1293

Qy  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT   1380
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT   1353

Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1431
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Db  1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAATGA   1404
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RESULT 12
AAT62870
ID   AAT62870 standard; DNA; 1404 BP.
XX
AC   AAT62870;
XX
DT   18-OCT-1997   (first entry)
XX
DE   Human gamma-4PE heavy chain DNA.
XX

KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
XX
OS   Homo sapiens.
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996; 96WO-US14324.
XX
PR   06-SEP-1995; 95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   P-PSDB; AAW14927.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Disclosure; Page 91-93; 155pp; English.
XX
CC   DNA sequences (AAT62868-70) respectively code for the heavy chain
CC   regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC   mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC   mutations. They can be used to provide novel monoclonal and
CC   chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC   gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC   combined with the antigen binding domains (see also AAW14922-23) of
CC   macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC   show high affinity to human CD4, have little or no immunogenicity
CC   in humans and show reduced or absence of effector function. The
CC   gamma-4E and -4PE mutations confer activity enhanced stability and
CC   eliminate depleting activity. The antibodies can be used to treat
CC   autoimmune diseases such as rheumatoid arthritis.
XX
SQ   Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;

Query Match   82.3%; Score 1177.8; DB 18; Length 1404;
Best Local Similarity   90.3%; Pred. No. 1.3e-233;
Matches 1292; Conservative   0; Mismatches 112; Indels   27; Gaps   2;

Qy   1 ATGAAACACCTGTGGTTCTCCTCCTGGTGGCAGTCCCAGATGGGTCCTGTCCCAG   60
          ||||||||||||||||||| ||||||||||||| |||||||||||| |||||||
Db.   1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCCCCAGATGGGTCTTGTCCCAG   60

Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC   120

Qy   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGAGCTGGATCCGGCCAGCC   180
          ||| |||||||||||||||||||||| | ||| | ||| |||||||||||||
Db   121 TGCAGTGTCTCTGGTGGCTCCATCAGCAGTGACTATCAGCAGTGACTATTATTGGTTCTGGATCCGGCCAGCC   180

Qy   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGGACCACTACTAC   240
          |||||||||| ||||||||||| |||||| |||||||||||||||||
Db   181 CCAGGGAAGGGACTGGAGTGGATCGGGAGTGGTGGTGGGACCAGTGGTGGGGGCACCAATTAC   240

Qy   241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC   300
          || |||||||||||||||| | ||| ||||||| |||||||||||||||||||||||
Db   241 AATCCCTCCCTCAAGAGTCGACAATCAGTTTTCAATTCAATAGACACGTCCAAGAACCAGTTCTCC   300

Qy   301 CTGAAGCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT   360
          |||||| |||| |||||||||||||||||||||||| |||||||||| | ||| |
Db   301 CTGAAACTGAGGTCTGTGACCGCCGCGGACACGGCCGCGTTATTACTGTGCGGAGTAATA--   358

Qy   361 CTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC   420
          || |||| | ||| |||||| || |||||||| ||||||
Db   359 --------------TATTGAAATATCTTCACTGGTTATTATACTGGGGCCCAGGGAGTC   402

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCGCTCGCCCCTCC   480
          ||||||||||||||||||||||||||||||||||||| |||||||||||| ||| |||
Db   403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCGCTCGGCCCTGC   462

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540
          |||| |||||||| | |||||||||||||||||||||||||||||||||||||||||||
Db   463 TCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   522

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   582

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC   642

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720
          |||||||||| |||||||||| |||||||| ||| |||||||||||||||||||||||||
Db   643 AGCTTGGGCACGCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG   702

Qy   721 GACAAGAAGCAGAGCCCAAATTCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780
          |||||| || || |||||| | || || ||||||||||| |||||||||
Db   703 GACAAGAGAGTTGAGTCCAAATATGG--------TCCCCCATGCCCACCATGCCCAGCA   753

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840
          ||||| || |||||||||| ||||||||||| ||||||||||||||||||||||| |||
Db   754 CCTGAGTTCGAGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC   813

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT   900
          ||||||||||||||||||||||||||| ||||||||||||||||||||| |||||||||
Db   814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCC   873

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960
          |||||| |||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   933

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG   1020
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Db   934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG   993

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC   1080
          |||||||||| |||||||||||||||||||||||||||||||||| |||||| ||| |
Db   994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC   1053

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG   1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG   1113

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1173

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1260
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1233

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db   1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC   1293

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT   1380
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT   1353

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCGTCTCCGGGTAAATGA   1431
          |||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCGTCTCCGGGTAAATGA   1404

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RESULT 13
AAT62869
ID   AAT62869 standard; DNA; 1404 BP.
XX
AC   AAT62869;
XX
DT   18-OCT-1997 (first entry)
XX
DE   Human gamma-4E heavy chain DNA.
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9 gamma-4E; ss.
XX
OS   Homo sapiens.
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996; 96WO-US14324.
XX
PR   06-SEP-1995; 95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   P-PSDB; AAW14926.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Disclosure; Page 86-88; 155pp; English.
XX
CC   DNA sequences (AAT62868-70) respectively code for the heavy chain
CC   regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC   mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC   mutations. They can be used to provide novel monoclonal and
CC   chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC   gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC   combined with the antigen binding domains (see also AAW14922-23) of
CC   macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC   show high affinity to human CD4, have little or no immunogenicity
CC   in humans and show reduced or absence of effector function. The
CC   gamma-4E and -4PE mutations confer activity enhanced stability and
CC   eliminate depleting activity. The antibodies can be used to treat
CC   autoimmune diseases such as rheumatoid arthritis.
XX
SQ   Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;

Query Match         82.2%;   Score 1176.2;   DB 18;   Length 1404;
Best Local Similarity    90.2%;   Pred. No. 2.8e-233;
Matches 1291;   Conservative   0;   Mismatches  113;   Indels  27;   Gaps  2;
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Qy    1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGCTCCCAGATGGGTCCTGTCCTCCCAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGCTCCCAGATGGGTCCTGTCCTCCCAG 60

Qy   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy  121 TGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTTATGCTGGGGCGTGGATCCGCCAGCCC 180
        ||||||||||||||||||||||||||||||| ||||| ||
Db  121 TGCAGTGTCTCTGTCTGGTGGCTCCATCAGCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC 180

Qy  181 CCAGGGAAGGGACTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAAACCTACTAC 240
        ||||||||||||||||    |||| |||||||
Db  181 CC ...
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Qy   1321 GTGGACAAGAGACAGGTGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 GTGGACAAGAGACAGGTGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy   1381 CTGCACACCACTACACAGCAGAGAGCCTCTCCCTGCTCCGTGATGCATGAGGCT 1431
          |||||||||||||||||||||||||||||||||||||
Db   1354 CTGCACAACCACTACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAATGA 1404
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RESULT 14
AAH74680

```
ID   AAH74680 standard; DNA; 1428 BP.
XX
AC   AAH74680;
XX
DT   29-OCT-2001 (first entry)
XX
DE   Nucleotide sequence of a single chain antibody.
XX
KW   Complementarity determining region; CDR; single chain antibody; ScFv;
KW   hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW   envelope glycoprotein; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1428
FT                   /tag= a
FT                   /product= "single chain antibody"
XX
PN   WO200158459-A1.
XX
PD   16-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-JP00967.
XX
PR   14-FEB-2000; 2000JP-0034906.
XX
PA   (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI   Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
XX
DR   WPI; 2001-496986/54.
DR   P-PSDB; AAG63640.
XX
PT   Remedies for hepatitis C containing substances with antiviral effects
PT   e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT   compounds, by inhibiting binding of hepatitis C virus envelope
PT   glycoprotein or CD81 -
XX
PS   Claim 41; Page 105-108; 138pp; Japanese.
XX
CC   The present sequence encodes a single chain antibody of the invention.
CC   The specification describes a substance can inhibit the binding between
CC   hepatitis C virus (HCV) and cells with potential HCV infection, cells
CC   with expression of CD81, or CD81. This substance is especially an
CC   antibody with affinity towards HCV E2/NS1 protein, containing amino
CC   acid sequences based on the complementarity determining region (CDR) 1,
CC   CDR2 and CDR3 of the H and L chain variable regions. The antibody
CC   inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor.
CC   The antibodies and drugs are used for treatment and/or prevention of
CC   hepatitis C, or for diagnosis of hepatitis C.
XX
SQ   Sequence 1428 BP; 315 A; 462 C; 394 G; 257 T; 0 other;
```

```
Query Match             80.4%;  Score 1151;  DB 22;  Length 1428;
Best Local Similarity   88.3%;  Pred. No. 4.5e-228;
Matches 1263; Conservative    0; Mismatches 165;  Indels   3;  Gaps   1;

Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCAGATGGGTCCTGTCCCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCAGATGGGTCCTGTCCCAG 60
```

```
Qy     61 GTGCAGCTGCGAGGAGTCGGCGCCCAGGACTGGTGAGCCTTCGAGACCCTGTCCTCACC 120
          ||||||||| |  | | |||| || ||||||   | || |    ||||||||||||||||
Db     61 GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTC 120

Qy    121 TGCGTGTCTCGTGGCTCCATCACGCGGTGGTTATGCGGATCCGCAGCC 180
          |||| |||| |||| || ||||||| ||||||   |   |||||||||
Db    121 TGCAAGGCTTCTGGAGGCACCTACACTGACCACATCTATC--GGCTGGGTGCGGCAGGCC 177

Qy    181 CCAGGGAAGGGGCTGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGAACACCTACTAC 240
          |||| ||||| ||||||||||||||| ||| |||||||||||| |||| |||| |||||
Db    178 CCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTCTGTCCGGCCACCACTAC 237

Qy    241 AACCCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACGTCCAAGAACCAGTTCTCC 300
          || | | || ||||||| |  | ||||||||||||  ||  |||  | ||||| ||
Db    238 GCACAGAAGTTCCAGGGCAGAGTCACCGTTACCGCGGACACGAGTCCAGCACAGCTTAC 297

Qy    301 CTGAAGCTGAACTCTATGACCGCCGGACACGGCGTGTATTACTGTGTGAGAGATCGT 360
          |||||||||||||||| ||| || |||| || ||| |||||||| |||||||| |  |
Db    298 CTGGAACTGACCAGCCTCACATCTGAGGACACAGCCGTGTATTACTGTGCGAGGGTCCTT 357

Qy    361 CTTTTTCAGTTGTTGGAATGGTTTACACAACTGGTTCTGATGTCTGGGGCCCCGGGAGTC 420
          |||| ||||||||||||| ||||| ||||||||| |||||||| |||||||||||||| |
Db    358 AGGGGTTATTGTGTCGTCGTGTCCTGTATGACTGGCCACCCCTGGGGCCAGGCACC 417

Qy    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 480
          |||||||||||||||||||  ||| |||||||||| ||||| |||||||||||||||||
Db    418 CTGGTCACCGTCTCCTCAGTACTCAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 477

Qy    481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCT 537

Qy    541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 597

Qy    601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
          || || |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 657

Qy    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    658 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 717

Qy    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    718 GACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 777

Qy    781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 837

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 897

Qy    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    898 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 957

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1017

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1077

Qy   1081 ATCGAGAAAACCATCTCAAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 ATCGAGAAAACCATCTCAAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1137
```

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CC     similarly used.  The transfected host cells provide a constant,
CC     stable supply of anti-RSV F-protein hMAbs for use in the treatment
CC     or prevention of RSV infection.
XX
SQ     Sequence 1428 BP; 326 A; 465 C; 372 G; 265 T; 0 other;

       Query Match             79.4%;  Score 1136.4;  DB 18;  Length 1428;
       Best Local Similarity   89.1%;  Pred. No. 4.6e-225;
       Matches 1263;  Conservative   0;  Mismatches 146;  Indels   9;  Gaps    3;

Qy          17 TCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGCTGTCCCAGTGGCAGCTGCAGGAGT   76
               |||||| |||||||||||||||||||||||||||||| |||| |||||||||||||||
Db          17 TCTTGCTCTTCCTTGCGTGTTGCTACGGCGTCCCTGTCCCTCACCTGCGTCTGGTG   76

Qy          77 CGGGGCCAGGACTGTGGTGGTGAAACCCCAACCTGCACCCTGCACCCTGCTGTCGGTG  136
               ||||| |||||||||||||||| ||||| ||||||||| |||||||||||||||||
Db          77 CTGGTCCTGTCGTGGTGAAACCCCACCAGAGACCCCTCACCGTGACCGCCACCGTCTCTGGGT  136

Qy         137 GCTC---CATCAGCGGTGTTATGGCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGC  193
               ||| || |||||||||||||||||||||||||||||||||||||||||||||||
Db         137 TCTCACTCAGCAACCCTAGAATGGGTGGGTGACCTGGATCCGTCCGCTCAGCCCCCGGGAAGGGCCC  196

Qy         194 TGGAGTGGATTGGGAGTTTCTATAGTAGTAGTAGTGGGAACACTACTACAACCCCTCA  253
               ||  ||||  |||| |||||| ||||| ||||| |||||||      |||||| || ||
Db         197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAA---GTCCTTCAGTCCTTCTCTGA  253

Qy         254 AGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCCCTGAAGTGAACT  313
               |||| || ||||| |||  |||||||||| ||| ||||||||| || ||||||| ||||
Db         254 AGAGACAGACCCTGGACACCAGCACCACATATTACTGTGCATGCAAGAGCTGTGTCTTTTTCAGTTG  313

Qy         314 CTATGACCCGCCGGACACGGCCGTGTATTACTGTGTGAGAGATCGTCTTTTTCAGTTG  373
               |||||||||| ||| |||||||| ||| || |||||| || ||||||||
Db         314 ACGTGGACCCTGTGGACACAGCCGACATATTACTGTGCACGGGTAGGACTGTATGACATCA  373

Qy         374 TTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTCCTGGTCACCGTCT  433
               |||||||   |||||||||| |||| ||| ||||| ||||||| ||| ||||||||||||
Db         374 ATGCTT---ATTACCTATACTGGATTATTGGGGTCGAGGGCCCTGGCACCGTCACCGTCT  430

Qy         434 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT  493
               |||||||||||||||||||||||| |||| ||||||||||| ||||||||||||||||||
Db         431 CCTCAGCTAGCACCAAGGGCCCATCGGTGTTCCCCCTGGCACCCTCCTCCAAGAGCACCT  490

Qy         494 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTGAAGG  553
               ||||||||||||||||||||||||||||||||||||
Db         491 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTGAAGG  550

Qy         554 TGTCGTGGAACTCAGGCGCCGTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTCCTACAGT  613
               ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db         551 TGTCGTGGAACTCAGGCGCCGTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT  610

Qy         614 CCTCAGGACTTACTCCCTCAGCAGCGGTGGGCACCC  673
               ||||||||||||||||||||||||||||||||||||
Db         611 CCTCAGGACTTACTCCCTCAGCAGCGGTGGGCACCC  670

Qy         674 AGACCTACACTCTGACAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  733
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         671 AGACCTACACTCTGCACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  730

Qy         734 AGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCCTGG  793
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         731 AGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCCTGG  790

Qy         794 GGGGACCGTCAGTCTTCTTCCCCCCAAAACCAAGGACACACCCTCATGATCTCCCGGA  853
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         791 GGGGACCGTCAGTCTTCTTCCCCCCAAAACCAAGGACACACCCTCATGATCTCCCGGA  850

Qy         854 CCCTGAGGTCACATGCGTGGTGACGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  913
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         851 CCCTGAGGTCACATGCGTGGTGACGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  910

Qy         914 ACTGGTACGTGACGGCCTGGAGGTGCATAATGCCAAGACAAAAGCCGCGGAGGAGCAGT  973
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         911 ACTGGTACGTGACGGCCTGGAGGTGCATAATGCCAAGACAAAAGCCGCGGAGGAGCAGT  970

Qy        1141 CTCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1138 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1197

Qy        1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGCAACAACTAC  1260
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1198 TTCTATCCCAGCGACACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGCAACAACTAC  1257

Qy        1261 AAGACCACGGCCTCCCCGTGCTGGACTCCGACGCGGCTCCTTCTTCTTCCTCTACAGCAAGCTCACC  1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1258 AAGACCACGGCCTCCCCGTGCTGGACTCCGACGCGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1317

Qy        1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1318 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1377

Qy        1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCCGTGTCCCGGTAAATGA  1431
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1378 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCCGTGTCCCGGGTAAATGA  1428
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RESULT 15
AAT61241
ID   AAT61241 standard; DNA; 1428 BP.
XX
AC   AAT61241;
XX
DT   13-MAY-1997 (first entry)
XX
DE   Human anti-RSV monoclonal antibody RF-1 heavy chain DNA.
XX
KW   Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;
KW   RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;
KW   Epstein Barr virus; immortalisation; recombinant antibody; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   sig_peptide   1..57
FT   /*tag= a
FT   mat_peptide   58..1425
FT   /*tag= b
XX
PN   WO9640252-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US10070.
XX
PR   07-JUN-1995;   95US-0488376.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Brams P,   Chamat SS,   Heard CJ,   Newman RA,   Pan L;
PI   Walsh EE;
XX
DR   WPI; 1997-099892/09.
DR   P-PSDB; AAW11639.
XX
PT   Human monoclonal antibody specific for respiratory syncytial virus
PT   fusion protein - used for the prevention and treatment of RSV
PT   infection
XX
PS   Claim 9; Fig 9b-c; 85pp; English.
XX
CC   A DNA sequence (AAT61241) codes for a polypeptide (AAW11639) comprising
CC   a leader sequence, RF1 heavy chain variable region (see also
CC   AAW11637), and human gamma 1/constant region. RF1 is a human
CC   monoclonal antibody (hMAb) specific for the fusion protein of
CC   respiratory syncytial virus (RSV). The DNA sequence, in vector
CC   NEOSPLA, can be used to produce the light chain construct in
CC   transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy
CC   and light chain constructs (see also AAT61240, AAT61242, AAT61279) are

```
Qy    974 ACAACAGCACGTACCGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1033
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1030

Qy   1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCA 1093
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCA 1090

Qy   1094 TCTCCAAAGCCAAAGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGG 1153
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1150

Qy   1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1213
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1210

Qy   1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1270

Qy   1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1333
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1330

Qy   1334 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1390

Qy   1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db   1391 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428
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Search completed: April 5, 2003, 20:19:44
Job time : 395.719 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April  5, 2003, 19:13:54 ; Search time 2723.68 Seconds
                                      (without alignments)
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Title:             US-09-758-173-11
Perfect score:     1431
Sequence:          1 ATGAAACACCTGGTTCTT........CCCTGTCTCCGGGTAAATGA 1431

Scoring table:     IDENTITY.NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:   Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :      EST:*
         1:  em_estba:*
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        25:  em_gss_other:*
        26:  em_gss_pro:*
        27:  em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	902	63.0	1020	14	BQ062878	BQ062878 AGENCOURT
2	864	60.4	947	14	BQ709771	BQ709771 AGENCOURT
3	850.4	59.4	958	14	BQ706140	BQ706140 AGENCOURT
4	842.4	58.9	926	12	BG755166	BG755166 60271148
5	832	58.1	988	14	BQ708857	BQ708857 AGENCOURT
6	831.2	58.1	901	13	BM007892	BM007892 603617577
7	824.4	57.6	1029	14	BQ063185	BQ063185 AGENCOURT
8	822.8	57.5	887	14	BQ711255	BQ711255 AGENCOURT
9	822.2	57.5	918	14	BQ708022	BQ708022 AGENCOURT
10	818.6	57.2	995	14	BM914540	BM914540 AGENCOURT
11	808.8	56.5	881	14	BQ711291	BQ711291 AGENCOURT
12	800.2	55.9	1031	14	BQ064886	BQ064886 AGENCOURT
13	797.4	55.7	936	14	BQ711727	BQ711727 AGENCOURT
14	796	55.6	940	14	BQ705928	BQ705928 AGENCOURT
15	787.4	55.0	977	14	BQ710532	BQ710532 AGENCOURT
16	786.4	55.0	980	14	BM914504	BM914504 AGENCOURT
17	785.2	54.9	843	13	BM007897	BM007897 603617582
18	778.8	54.4	991	14	BQ708936	BQ708936 AGENCOURT
19	777.2	54.3	973	14	BQ706204	BQ706204 AGENCOURT
20	776	54.2	930	13	BM007597	BM007597 603616995
21	770.6	53.9	981	14	BM914528	BM914528 AGENCOURT
22	764.6	53.4	926	14	BQ710304	BQ710304 AGENCOURT
23	764.2	53.4	917	14	BQ708169	BQ708169 AGENCOURT
24	759.4	53.1	961	14	BQ710233	BQ710233 AGENCOURT
25	756.6	52.9	945	14	BQ712403	BQ712403 AGENCOURT
26	752.4	52.6	1012	14	BM914556	BM914556 AGENCOURT
27	750.4	52.5	895	14	BQ708303	BQ708303 AGENCOURT
28	750.4	52.4	783	13	BM007838	BM007838 603617519
29	748	52.3	1026	14	BM914288	BM914288 AGENCOURT
30	741.4	51.8	914	14	BQ712363	BQ712363 AGENCOURT
31	737.4	51.5	913	14	BQ707472	BQ707472 AGENCOURT
32	734.2	51.3	906	14	BQ711709	BQ711709 AGENCOURT
33	733.8	51.3	944	14	BQ712397	BQ712397 AGENCOURT
34	733.6	51.3	919	14	BQ709339	BQ709339 AGENCOURT
35	732.8	51.2	936	14	BQ707530	BQ707530 AGENCOURT
36	732.4	51.2	855	13	BM007689	BM007689 603617119
37	731.8	51.1	1014	14	BM914505	BM914505 AGENCOURT
38	730.4	51.0	973	14	BQ708902	BQ708902 AGENCOURT
39	729.6	51.0	888	12	BG757604	BG757604 602714780
40	728.8	50.9	941	14	BQ712021	BQ712021 AGENCOURT
41	728.6	50.9	925	14	BQ709853	BQ709853 AGENCOURT
42	728.4	50.9	991	14	BQ707621	BQ707621 AGENCOURT
43	726.8	50.8	870	12	BG757815	BG757815 602711335
44	726.2	50.7	925	14	BQ709152	BQ709152 AGENCOURT
45	725.8	50.7	923	14	BQ881523	BQ881523 AGENCOURT

ALIGNMENTS

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RESULT 1
BQ062878
LOCUS       BQ062878                1020 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT 6826949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
            5', mRNA sequence.
ACCESSION   BQ062878
VERSION     BQ062878.1  GI:19890085
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1020)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094 row: h  column: 21
            High quality sequence start: 21
            High quality sequence stop: 681
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source          1..1020
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5924420"
                /clone_lib="NIH_MGC_99"
                /tissue_type="lymphoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Size-selected >500bp for average insert size
                1.8kb. Library constructed by Ling Hong in the laboratory
                of Gerald M. Rubin (University of California, Berkeley)
                using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                II RT (Life Technologies). Note: this is a NIH_MGC
                Library."

BASE COUNT    239 a    344 c    269 g    166 t    2 others
ORIGIN

Query Match          63.0%;     Score 902;  DB 14;  Length 1020;
Best Local Similarity 98.0%;    Pred. No. 4.2e-219;
Matches 923;  Conservative    0;  Mismatches  17;  Indels  2;  Gaps  1;

Qy    489 CACCTCTGGGGGCACAGCGGCGCCTGGGCTGCCTGGTCAAGGACTACTTCCCGGAACCGGT 548
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Db     36 CACCTCTGGGGGCACAGCGGCGCCTGGGCTGCCTGGTCAAAGACTACTTCCCGGAACCGGT 95

Qy    549 GACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT 608
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Db     96 GACGGTGTCGTGGAACTCAAGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT 155

Qy    609 ACAGTCCTCAGAGACTCCACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG 668
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 ACAGTCCTCAAGAGACTCCACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG 215

Qy    669 CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAA 728
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAA 275

Qy    729 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 788
          |||||||||| || |||||||||||||||||||||||||||||||||||||||||||||||
Db    276 AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 335

Qy    789 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 848
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Db    336 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 395

Qy    849 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 908
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Db    396 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 455

Qy    909 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 968
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Db    456 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 515

Qy    969 GCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCTCCACCAGGACTGGCT 1028
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Db    516 GCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCTCCACCAGGACTGGCT 575

Qy   1029 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGAGCCTCCCAGCCCCCATCGAGAA 1088
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Db    576 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGAGCCTCCCAGCCCCCATCGAGAA 635

Qy   1089 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGTACACCCTGCCCCCATC 1148
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Db    636 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 695

Qy   1149 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 1208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 755

Qy   1209 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA--GAACTACAAGACC 1266
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RESULT 2
BQ709771

LOCUS   BQ709771   947 bp   mRNA   linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
            5', mRNA sequence.
ACCESSION   BQ709771
VERSION   BQ709771.1 GI:21848670
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 947)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466 row: m column: 16
            High quality sequence start: 3
            High quality sequence stop: 675.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278583"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT   225 a   320 c   252 g   150 t
ORIGIN

Query Match   60.4%;   Score 864; DB 14; Length 947;
Best Local Similarity 99.4%;   Pred. No. 2e-209;
Matches 867; Conservative   0; Mismatches 5; Indels 0; Gaps 0;

Qy   560 GGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG 619
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Db   9 GGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG 68

Qy   620 GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCT 679
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Db   69 GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCT 128

Db   756 CAGGGACCATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGGAGAAACTACTAGACC 815
Qy   1267 ACGGCCTCCCGTGCTGACCGTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 1326
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Db   816 ACGGCCTCNCGTGCTGACCGTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGGA 875
Qy   1327 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1386
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Db   876 CAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 935
Qy   1387 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1428
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Db   936 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA 977

Qy   680 ACATCTGCAACGTGAATCACACAGCCAGCAACCACCAAGGTGGACAAGAAAGCAGAGCCCA 739
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Db   129 ACATCTGCAACGTGAATCACACAGCCAGCAACCACCAAGGTGGACAAGAAAGTTGAGCCCA 188

Qy   740 AATCTTGTGACAAAACTCACACAGCCCGTGCCCAGCACCTGAACTCCTGGGGGGAC 799
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Db   189 AATCTTGTGACAAAACTCACACAGCCCGTGCCCAGCACCTGAACTCCTGGGGGGAC 248

Qy   800 CGTCAGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCGGACCCCTG 859
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Db   249 CGTCAGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCGGACCCCTG 308

Qy   860 AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 919
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Db   309 AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 368

Qy   920 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAACA 979
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Db   369 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 428

Qy   980 GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 1039
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Db   429 GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 488

Qy   1040 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1099
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Db   489 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 548

Qy   1100 AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC 1159
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Db   549 AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC 608

Qy   1160 TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG 1219
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Db   609 TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG 668

Qy   1220 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC 1279
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Db   669 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC 728

Qy   1280 TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 1339
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Db   729 TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 788

Qy   1340 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC 1399
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Db   789 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC 848

Qy   1400 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db   849 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 880

RESULT 3
BQ706140
LOCUS   BQ706140   958 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_8352177 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277512
             5', mRNA sequence.
ACCESSION   BQ706140
VERSION   BQ706140.1 GI:21845039
KEYWORDS   EST.
SOURCE   human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 958)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory

             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2464   row: a   column: 01
             High quality sequence stop: 705.

FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT   229 a   319 c   256 g   150 t   4 others
ORIGIN

Query Match   59.4%;   Score 850.4;   DB 14;   Length 958;
Best Local Similarity   99.2%;   Pred. No. 6e-206;
Matches 865;   Conservative 0;   Mismatches 6;   Indels 1;   Gaps 1;

Qy   558 GTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC 617
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Db   11 GTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC 70

Qy   618 AGGACTCTACTCCCTCCCTCCAGCAGCGTGGCCGTGCCCTCGGCAGCTTGGGCACCCAGAC 677
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Db   71 AGGACTCTACTCCCTCCCTCCAGCAGCGTGGCCGTGCCCTCGGCAGCTTGGGCACCCAGAC 130

Qy   678 CTACATCTGCAACGTGAATCACAGCCCAGCAACCAGTGGACACAGACGTGACACAGAGAGCC 737
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Db   131 CTACATCTGCAACGTGAATCACAGCCCAGCAACCAGTGGACACAGACGTGACACAGAAGTTGAGCC 190

Qy   738 CAAATCTTGTGACAAAACTCACACAGCTCACAGACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG 797
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Db   191 CAAATCTTGTGACAAAACTCACACAGCTCACAGACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG 250

Qy   798 ACCGTCAGTCTTCCTCTTCCCCCAAAAACCAAGGACACCCTCATGATCTCCCGGACCCC 857
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Db   251 ACCGTCAGTCTTCCTCTTCCCCCAAAAACCAAGGACACCCTCATGATCTCCCGGACCCC 310

Qy   858 TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG 917
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Db   311 TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG 370

Qy   918 GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA 977
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Db   371 GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA 430

Qy   978 CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA 1037
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Db   431 CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA 490

Qy   1038 GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC 1097
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Db   491 GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC 550

Qy   1098 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA 1157
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Db   551 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA 610

Qy   1158 GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT 1217
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Db   611 GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT 670

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Db    62  CTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGCACCCAGACGACCTACAT   121
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Qy   684  CTGCAACGTGAATCACAAGCCCAGCAACAACCAAGGTGGACAAGAAAGCAGAGCCCAAATC   743
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Db   122  CTGCAACGTGAATCACAAGCCCAGCAACAACCAAGGTGGACAAGAAAGTTGAGCCCAAATC   181
Qy   744  TTGTGACAAACTCACACATGCCCACGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTC    803
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Db   182  TTGTGACAAACTCACACATGCCCACGTGCCCAGCACCTGAACTCCTGGGGGGGACCGTC    241
Qy   804  AGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCGGACCCCTGAGGT     863
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Db   242  AGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCGGACCCCTGAGGT     301
Qy   864  CACATGCGTGGTGGTGACGTGAGCGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT   923
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Db   302  CACATGCGTGGTGGTGACGTGAGCGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT   361
Qy   924  GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC   983
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Db   362  GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC   421
Qy   984  GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA  1043
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Db   422  GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA   481
Qy  1044  CAAGTGCAAGGTCTCAACAAAGCCCTCCAACAAAGCCCCATCTCCAAAGC            1103
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Db   482  CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACAAAGCCCCATCTCCAAAGC           541
Qy  1104  CAAAGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGATGAGCTGAC    1163
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Db   542  CAAAGGGCAGCCCCGAGAACCACAGTGTACACCCTGCCCCCATCCCGGATGAGCTGAC     601
Qy  1164  CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT  1223
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Db   602  CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT   661
Qy  1224  GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA  1283
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Db   662  GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA   721
Qy  1284  CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA  1343
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Db   722  CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA   781
Qy  1344  GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA  1403
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Db   782  GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACACTACACGCAGAA   841
Qy  1404  GAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
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Db   842  AAAGCCTCTCCTGTCTCCGGGTAAATGA   869
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RESULT 5
BQ708857
LOCUS   BQ708857   988 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8352194 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277561
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ACCESSION   BQ708857
VERSION   BQ708857.1 GI:21847756
KEYWORDS   EST.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 988)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.

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Qy  1218  CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT  1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671  CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT   730
Qy  1278  GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG  1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731  GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG   790
Qy  1338  GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC  1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791  GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC   850
Qy  1398  GCAG-AAGAGCCTCTCCCTGTCTCCGGGTAAA  1428
          |||| ||||||||||||||||||||||| ||
Db   851  ACAGAAAGAGCCTCTCCCTGTCTCCGGGTAA   882
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RESULT 4
BG755166
LOCUS   BG755166   926 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602711488F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',
            mRNA sequence.
ACCESSION   BG755166
VERSION   BG755166.1 GI:14065819
KEYWORDS   EST.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 926)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1695 row: o column: 21
            High quality sequence stop: 888.
FEATURES   Location/Qualifiers
     source   1..926
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4852076"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT   225 a   309 c   244 g   148 t
ORIGIN

Query Match   58.9%; Score 842.4; DB 12; Length 926;
Best Local Similarity   98.2%; Pred. No. 6.5e-204;
Matches 852; Conservative   0; Mismatches 16; Indels 0; Gaps   0;

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Qy   564  CTCAGGGCGCCTGACCAGCCGGCTGCACACCTTCCCGGCTGTGTCCTACAGTCCTCAGGACT  623
          |||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db     2  CTCAGGGCCCCTGACCAGCCGGCTGCACACCTTCCCCGCTGTGTCCTACAGTCCTCAGGACT   61
Qy   624  CTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCCTCCAGCAGCTTGGGCACCCAGACGACCTACAT  683
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Db    605 GGTCAGCGCTCCACCGTCCTGCGACCAGGACTGCCTGGCTGGTGAATGGCAAGGAGTACAAGTGCAA 664
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1053 GGTTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA 1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 GGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA 724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1113 GCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCA 1172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 GCCCCGAGAAACACAGGTGTACACCCTGCCCCCATCCCGGATGAGCTGACCACAGAA-CA 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1173 GGTCAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA 1232
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Db    784 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1233 GAGCAATGGGCAG-CCGGAGAACAACTACAAGACCACGCCTCCCGTG---CTGGACTCCG 1288
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    844 GAGCCATGGGCAGCCGGAGAACAACTACCAGAACACCAGGCTCCCCGTGCTGGACTCCG 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1289 ACGGC-TCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 1343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 ACGGCTTCCTTCTTCCTCTACAGAAAGCTCCCGGGGACAAGAGCAGGTGGCA 959
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RESULT 6
BM007892
LOCUS   BM007892   901 bp   mRNA   linear   EST 30-OCT-2001
DEFINITION 603617577F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450611 5',
            mRNA sequence.
ACCESSION   BM007892
VERSION   BM007892.1 GI:16522233
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 901)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1939 row: j column: 20
            High quality sequence stop: 834.
FEATURES   Location/Qualifiers
     source   1..901
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5450611"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT   209 a   315 c   234 g   143 t
ORIGIN

Query Match   58.1%; Score 831.2; DB 13; Length 901;
Best Local Similarity   97.7%; Pred. No. 4.6e-201;
Matches 864; Conservative   0; Mismatches 18; Indels 2; Gaps 2;

```
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464  row: c  column: 02
High quality sequence stop: 716.
FEATURES             Location/Qualifiers
     source          1..988
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6277561"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT      230 a    338 c    258 g    162 t
ORIGIN

Query Match             58.1%;  Score 832;  DB 14;  Length 988;
Best Local Similarity   94.7%;  Pred. No. 3e-201;
Matches  905;  Conservative   0;  Mismatches  45;  Indels  6;  Gaps  4;
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Qy    393 CTGGTTCGATGTCTGGGGCCCGGAGTCTCCTCAGCTAGCACCGTGTCACCGTTCTCCTCACCGAC    452
          ||  || |||||  ||||    ||| ||   ||| || |||  ||| ||||||||||||
Db      5 CTACTTTGACTACTGGGGCCCAGGGAACCGTGGTCACCGTCTCCTCCGGCTCCTCCGGCTCCCACCTAGGG    64
Qy    453 CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT    512
          |||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT    124
Qy    513 GGGCTGCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC    572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC    184
Qy    573 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT    632
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT    244
Qy    633 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT    692
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT    304
Qy    693 GAATCACAACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAA    752
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 GAATCACAACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA    364
Qy    753 AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCT    812
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Db    365 AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCT    424
Qy    813 CTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT    872
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Db    425 CTTCCCCCCAAAACCAAGGACACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT    484
Qy    873 GGTGGTGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT    932
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 GGTGGTGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT    544
Qy    933 GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT    992
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT    604
Qy    993 GGTCAGCGCTCCTCACCGTCCTGCGACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA    1052
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REFERENCE    1 (bases 1 to 1029)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2095 row: g  column: 10
             High quality sequence stop: 723.
FEATURES             Location/Qualifiers
     source          1..1029
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5924769"
                     /tissue_type="lymphoma, cell line"
                     /clone_lib="NIH_MGC_99"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
BASE COUNT      237 a      350 c      276 g      165 t      1 others
ORIGIN

Query Match             57.6%;  Score 824.4;  DB 14;  Length 1029;
Best Local Similarity   99.0%;  Pred. No. 2.6e-199;
Matches  861;  Conservative   0;  Mismatches   6;  Indels   3;  Gaps   3;
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Qy    483 CAAGAGACACCTCTGGGGGCACAGCGGCCCTCGGCTCTCCTGGTCAAGGACTACTTCCCGA 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 CCAGAGACACCTCTGGGGGCACAGCGGCCCTCGGCTCTCCTGGTCAAGGACTACTTCCCGA  63

Qy    543 ACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCAGCGGCGTGCACACCTTCCCGGC 602
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 ACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCAGCGGCGTGCACACCTTCCCGGC 123

Qy    603 TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG 662
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG 183

Qy    663 CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAACTCACAAATCTTGTGACAAA 722
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAACTCACAAATCTTGTGACAAA 243

Qy    723 CAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC 782
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Db    244 CAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC 303

Qy    783 TGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 842
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 TGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 363

Qy    843 GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA 902
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA 423

Qy    903 GGTCAAGTTCAACTGGTACGTGACGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGG 962
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 GGTCAAGTTCAACTGGTACGTGACGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGG 483

Qy    963 GGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTGCTGCACCAGGA 1022
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    408 GGGCCGGGAGTCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCC 467
              ||||||||| |||||||||||||||||||||||||| |||||||||||||||||||||
Db     19 GGGCCAGGAGAACCCTGGTCTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC  78

Qy    468 CCTGGCACCCTCCTCCAAGAGCACACCTCTGGGGGCACAGCGGCCCTCGGCTGCCTGGTCAA 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 CCTGGCACCCTCCTCCAAGAGCACACCTCTGGGGGCACAGCGGCCCTCGGCTGCCTGGTCAA 138

Qy    528 GGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT 587
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 GGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT 198

Qy    588 GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC 647
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC 258

Qy    648 CGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG 707
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 CGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG 318

Qy    708 CAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCC 767
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 CAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCC 378

Qy    768 ACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACC 827
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 ACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACC 438

Qy    828 CAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAG 887
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 CAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAG 498

Qy    888 CCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC 558

Qy    948 CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCAC 1007
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 CAAGAACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCAC 618

Qy   1008 CGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC 1067
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC 678

Qy   1068 CCTCCCAGCCCCCATCGAGAAAACCATCTCAAAGGCAAAGGGCAGCCCCGAGAACCACA 1127
              ||||||||||||| |||||||||||||||||||||| ||||||||||||||||||||
Db    679 CCTCCCAGCCCCCATCTCCAAAGCC-AAGGGCAGCCCCGAGAACCACA 737

Qy   1128 GGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG 1187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738 GGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG 797

Qy   1188 CCTGGTCAAAGGCTTCTATCCCAGCGACATCG-CCGGTGGAGTGGGAGAGCAATGGGCAGC 1246
              ||||||||||||| |||||||||||||||| ||||||||||||||||||||||||||
Db    798 CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCCGGTGGAGTGGGAGAGCGCGGGCAGC 857

Qy   1247 CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC 1290
              ||||||| ||||||||||||||||||||||||||||||||
Db    858 CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC 901
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RESULT 7
BQ063185
LOCUS       BQ063185               1029 bp    mRNA    linear    EST 02-APR-2002
DEFINITION  AGENCOURT_6876667 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924769
            5', mRNA sequence.
ACCESSION   BQ063185
VERSION     BQ063185.1  GI:19890681
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 97.6%;   Pred. No. 6.3e-199;
Matches 866;   Conservative 0;   Mismatches 18;   Indels 3;   Gaps 3;

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Qy    541  GAACCGGTGACGGTGTCGTGGAACTTCCAACAAAGCCCTGCACCTTCCG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GAACCGGTGACGGTGTCGTGGAACTTCCAACAAAGCCCTGCACCTTCCG   60

Qy    601  GCTGTCCTACAGTCCTCCAGGACTCTCCTCAGCAGGTGGTGACCGTGCCCTGCCCTCCAGC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCTGTCCTACAGTCCTCCAGGACTCTCCTCAGCAGGTGGTGACCGTGCCCTGCCCTCCAGC  120

Qy    661  AGTTGGGCACCCAGACCTACATCTCGAACGTGAATCACAAGCCCAACACCACCAAGGTG  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AGTTGGGCACCCAGACCTACATCTCGAACGTGAATCACAAGCCCAACACCACCAAGGTG  180

Qy    721  GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATCACATCACACGTGCCCAGCA  780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GACAAGAAAGTTGAGCCCAAATCTTGCACAAAACTCACACATCACATCACACGTGCCCAGCA  240

Qy    781  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCCCCCCAAAACCCAAGGACACCCTC  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCCCCCCAAAACCCAAGGACACCCTC  300

Qy    841  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGGACCCT  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGGACCCT  360

Qy    901  GAGGTCAAGTTCAACTGGTACGTGACGGCGGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GAGGTCAAGTTCAACTGGTACGTGACGGCGGTGGAGGTGCATAATGCCAAGACAAAGCCG  420

Qy    961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  480

Qy   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  540

Qy   1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACCAGGTGTACACCCTG  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  600

Qy   1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  660

Qy   1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  720

Qy   1261  AAGA-CCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC  1319
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  NAGACCCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC  780

Qy   1320  CGT-GACAAGAGCAGTGGCAGC-AGGGGAACGTCTTTCTCATGCTCCGTGATGCATGAG  1377
           ||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    781  CGTGGGCAAAAGCAAGTGGCAGCAAGGGAACGTCTTTCTCATGCTCCGTGATGCATGAA  840

Qy   1378  GCTCTGCACAACCACTACACCCGAGAGAGCCTCTCCCTGTCTCCGGG  1424
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GCTCTGCACAACCACTACACCCGAGAGAAGTTCTCCCTGGTCTCCG  887
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RESULT 9
BQ708022
LOCUS   BQ708022   AGENCOURT_8353641 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279643
DEFINITION 5', mRNA sequence.   918 bp   mRNA   linear   EST 16-JUL-2002
ACCESSION   BQ708022
VERSION   BQ708022.1   GI:21846921
KEYWORDS   EST.
SOURCE   human.

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Db    484  GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA  543
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1023  CTGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT  1082
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    544  CTGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT  603

Qy   1083  CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  1142
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604  CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  663

Qy   1143  CCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTT  1202
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    664  CCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTT  723

Qy   1203  CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAA  1262
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Db    724  CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAA  783

Qy   1263  GACCACGCCT-CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACA-GCAAGCTCACC  1320
           |||||||||| |||||||||||||||||||||||||||||||||||| ||||||||||||
Db    784  GAACACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGGCAAGCTCACC  843

Qy   1321  GTGGACAAGAGCA-GGTGGCAGCAGGGGGAA  1349
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Db    844  GTGGACCAGCAGCGGGGTGGCAGCAGGGGGA  873
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RESULT 8
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LOCUS   BQ711255   AGENCOURT_8443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
DEFINITION 5', mRNA sequence.   887 bp   mRNA   linear   EST 16-JUL-2002
ACCESSION   BQ711255
VERSION   BQ711255.1   GI:21850154
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 887)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474 row: m column: 20
            High quality sequence stop: 681.
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                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGACGAGG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   218 a   295 c   230 g   143 t   1 others
ORIGIN
Query Match   57.5%;   Score 822.8;   DB 14;   Length 887;

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ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 918)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Mark Watson
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2469 row: i    column: 20
           High quality sequence stop: 667.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT     208 a     316 c     245 g     147 t      2 others
ORIGIN
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Query Match             57.5%;  Score 822.2;  DB 14;  Length 918;
Best Local Similarity   95.4%;  Pred. No. 9.2e-199;
Matches  867;  Conservative   0;  Mismatches  40;  Indels   2;  Gaps   2;

Qy    398 TCGATGTCTGGGGCCCGGGAGTCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCAT 457
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTGACGGCTGGGGCCCAGGGAACGCTGGTCACCGTCTCCTCAGCCTCCAGCCTCCAGGGCCCAT 60

Qy    458 CGGTCTTCCCCCTGGCACCCTCCTCCAGAGCACACCTCTGGGGCACAGCGGCCCTGGGGCT 517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGGTCTTCCCCCTGGCACCCTCCTCCAGAGCACACCTCTGGGGCACAGCGGCCCTGGGGCT 120

Qy    518 GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGA 577
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGA 180

Qy    578 CCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA 637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA 240

Qy    638 GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC 697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC 300

Qy    698 ACAAGCCCAGCAACACCAAGGTGGACAAGAGCAGACCCAAATCTTGTGACAAAACTC 757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACAAGCCCAGCAACACCAAGGTGGACAAGAAGTTGAGCCCAAATCTTGTGACAAAACTC 360

Qy    758 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 420

Qy    818 CCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATCGTGGTGG 877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCAAAACCCAAGGACACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGTGG 480

Qy    878 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 937
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Db    481 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    938 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA 997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA 600

Qy    998 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 660

Qy   1058 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACTATCTCCAAAGCCAAAGGGCAGCCCC 720

Qy   1118 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1177
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Db    721 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 780

Qy   1178 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT-GGAGTGGGAGAGC 1236
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    781 GCCTGGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCNCCGNGGAGTGGGAGAGC 840

Qy   1237 AATGGGCAG-CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC 1295
          | |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATGGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC 900

Qy   1296 CTTCTTCCT 1304
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Db    901 GTCCTTTCT 909
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RESULT 10
BM914540
LOCUS       BM914540                 995 bp    mRNA    linear    EST 12-MAR-2002
DEFINITION  AGENCOURT_6615506 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480223
            5', mRNA sequence.
ACCESSION   BM914540
VERSION     BM914540.1  GI:19364919
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 995)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2002 row: 1   column: 16
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
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BASE COUNT      241 a      330 c      259 g      165 t
ORIGIN
                     NIH_MGC Library."
Query Match     57.2%;      Score 818.6;   DB 14;   Length 995;
Best Local Similarity  96.0%;     Pred. No. 7.9e-198;
Matches   861;   Conservative    0;   Mismatches   34;   Indels   2;   Gaps   2;

Qy    388  AACAAACTGGTTCGATGTCTGGGGCCCCGGAGTTCCTGGTCACCGTCTTCCTCAGCTAGCACC  447
                |||||| || ||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db      1  AACTTCTACTTTGACGATTGGGGCCAGGGAACGCTGGTCACCGTCTTCCTCAGCCTCCACC   60

Qy    448  AAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCCTGGGGGCCACAGCG   507
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Db     61  AAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCCTGGGGGCACAGCG   120

Qy    508  GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACGGTGACGGTGTCGTGGAACTCA   567
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Db    121  GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACGGTGCGGTGTCGTGGAACTCA   180

Qy    568  GGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC   627
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Db    181  GGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC   240

Qy    628  TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC   687
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Db    241  TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC   300

Qy    688  AACGTGAATCACAAGGCCCAGCAACACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGT   747
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Qy    748  GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTC   807
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Db    361  GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTC   420

Qy    808  TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA   867
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Db    421  TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA   480

Qy    868  TGCGTGGTGGTGGACGTGAGCCAGGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC   927
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Db    481  TGCGTGGTGGTGGACGTGAGCCAGGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC   540

Qy    928  GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC   987
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Db    541  GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC   600

Qy    988  CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG  1047
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Db    601  CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG   660

Qy   1048  TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA  1107
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Db    661  TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA   720

Qy   1108  GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG  1167
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Db    721  GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG   780

Qy   1168  AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG  1227
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Db    781  AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG   840

Qy   1228  TGGG-AGAGCAATGGGCAGCCGGAGAACAACTACAAGA-CCACCCCTCCCGTGCTGG  1282
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RESULT 11
BQ711291
LOCUS   BQ711291   881 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096

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ACCESSION   BQ711291
VERSION     BQ711291.1  GI:21850190
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 881)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2468 row: c  column: 01
            High quality sequence stop: 721.
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      220 a      285 c      237 g      139 t
ORIGIN
Query Match     56.5%;      Score 808.8;   DB 14;   Length 881;
Best Local Similarity  99.8%;     Pred. No. 2.4e-195;
Matches   810;   Conservative    0;   Mismatches   0;   Indels   2;   Gaps   0;

Qy    612  GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC   671
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Db      1  GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC   60

Qy    672  CCAGACCTACATCTGCAACGTGAATCACAAGGTGGACAAGAAAACCATCACAAGGTGGACAAGAAAGC   731
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CCAGACCTACATCTGCAACGTGAATCACAAGGTGGACAAGAAAGTGGACAAGAAAGT   120

Qy    732  AGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT   791
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  TGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT   180

Qy    792  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG   851
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG   240

Qy    852  GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGTGAGCCAGGAAGACCCTGAGGTCAAGTT   911
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGAAGACCCTGAGGTCAAGTT   300

Qy    912  CAACTGGTACGTGGACGGCGGTGGAGGTGCATATGCCAAGACAAAGCCGCGGGAGGAGCA   971
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA   360

Qy    972  GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA  1031
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA   420
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BASE COUNT      248 a      349 c      271 g      162 t        1 others
ORIGIN

Query Match          55.9%;       Score 800.2;  DB 14;  Length 1031;
Best Local Similarity 94.4%;       Pred. No. 3.9e-193;
Matches    840; Conservative    0; Mismatches  49;  Indels    1;  Gaps    1;

Qy    491 CCTCTGGGGCACAGCGCCCTGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGA  550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 CCTCTGGGGCACAGCGCCCTGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGA   70

Qy    551 CGGTGTGCGTGGAACTCAGCGGCGCCCTGACCAGCGGCGTGCACACCTTCCGGCTGTCCTAC  610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CGGTGTGCGTGGAACTCAGCGGCGCCCTGACCAGCGGCGTGCACACCTTCCGGCTGTCCTAC  130

Qy    611 AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCAGCAGCGTTGGGCA  670
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCAGCAGCGTTGGGCA  190

Qy    671 CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAG  730
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAG  250

Qy    731 CAGAGCCCAAAATCTTGTGACAAAATCCACAAATGCCCAGCACCTGAACTCC  790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TTGAGCCCAAAATCTTGTGACAAAATCCACAAATGCCCAGCACCTGAACTCC  310

Qy    791 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC  850
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC  370

Qy    851 GGACCCCTGAGGTCACATGGGTGGTGGTGGACGTGAGCCACGAGGACCCTGAGGTCAAGT  910
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 GGACCCCTGAGGTCACATGGGTGGTGGTGGACGTGAGCCACGAGGACCCTGAGGTCAAGT  430

Qy    911 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC  970
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC  490

Qy    971 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1030
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA  550

Qy   1031 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAA 1090
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAA  610

Qy   1091 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1150
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC  670

Qy   1151 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1210
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA  730

Qy   1211 GCGACATCGCCGT-GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 1269
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Db    731 GCGACATCGCCGGT-GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG  790

Qy   1270 CCTCCCGTGCTGGACTCCGACGGGTCCTTCTTCCTCTACAGCAAGCTCACCGTGACAAG 1329
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    791 CCTCCCGTGCTGGACTCCGACGGGTCCTTCTTCCTCTACAGCAAGCTCACCGTGACAAG  850

Qy   1330 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC 1379
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 AAGCAGGGGGCAACCCGGGGGAACGTCTTTCTCAATGCTCCGTGATGC  900


Qy   1032 TGGCAAGGAGTACAAGTGCAAGGTCTTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAC 1091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGCAAGGAGTACAAGTGCAAGGTCTTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAC  480

Qy   1092 CATCTCCAAAGCCCAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 1151
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Db    481 CATCTCCAAAGCCCAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG  540

Qy   1152 GGATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 1211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG  600

Qy   1212 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 1271
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC  660

Qy   1272 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 1331
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG  720

Qy   1332 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 1391
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA  780

Qy   1392 CTACACGCAGAAGAGCCTCTCCCCGTGTCCGG 1423
          ||||||||||||||||||||||||||||||||
Db    781 CTACACGCAGAAGAGCCTCTCCCCGTGTCCGG  812


RESULT 12
BQ064886
LOCUS       BQ064886           1031 bp    mRNA      linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343
            5', mRNA sequence.
ACCESSION   BQ064886
VERSION     BQ064886.1  GI:19893932
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1031)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2107 row: e  column: 24
            High quality sequence stop: 573.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_99"
                     /tissue_type="lymphoma, cell line"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."


RESULT 13
BQ711727
LOCUS       BQ711727
DEFINITION  AGENCOURT_8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
            5', mRNA sequence.
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Db    430 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC 489
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Qy   1073 CAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT 1132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 CAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT 549

Qy   1133 ACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGG 609

Qy   1193 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA 669

Qy   1253 ACAACTACAGACCA-CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 1311
          |||||||| | |   |||||||||||||||||||||||||||||||||||||||||||
Db    670 ACAACTACNAGAACACCGGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 729

Qy   1312 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG 1371
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGGGATG 789

Qy   1372 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||  |||| | ||||||| | |||||||||||||||| ||||||||||||  |||
Db    790 CATGAGGGTCTGGAC-ACCACCAACCGCAGAAGAGCCCTCTTCCTGTCTCCGGGAAATGA 848
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RESULT 14
BQ705928
LOCUS   BQ705928   940 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7976186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214795
     5', mRNA sequence.
ACCESSION BQ705928
VERSION   BQ705928.1 GI:21844827
KEYWORDS EST.
SOURCE   human.
 ORGANISM Homo sapiens
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 940)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Dr. Mark Watson
     cDNA Library Preparation: Rubin Laboratory
     cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
     DNA Sequencing by: Agencourt Bioscience Corporation
     Clone distribution: MGC clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     http://image.llnl.gov
     Plate: LLCM2382 row: k column: 20
     High quality sequence stop: 619.
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         /clone_lib="NIH_MGC 113"
         /lab_host="DH10B (phage-resistant)"
         /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
         EcoRI; cDNA made by oligo-dT priming. Directionally cloned
         into EcoRI/XhoI sites using the following 5' adaptor:
         GGCACGAG(G). Library constructed by Ling Hong in the
         laboratory of Gerald M. Rubin (University of California,
         Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
         Superscript II RT (Life Technologies). Note: this is a
         NIH_MGC Library."
BASE COUNT 235 a 318 c 240 g 147 t
ORIGIN

ACCESSION BQ711727
VERSION   BQ711727.1 GI:21850626
KEYWORDS EST.
SOURCE   human.
 ORGANISM Homo sapiens
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 936)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Dr. Mark Watson
     cDNA Library Preparation: Rubin Laboratory
     cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
     DNA Sequencing by: Agencourt Bioscience Corporation
     Clone distribution: MGC clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     http://image.llnl.gov
     Plate: LLCM2518 row: k column: 18
     High quality sequence stop: 547.
FEATURES   Location/Qualifiers
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         /db_xref="taxon:9606"
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         /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
         EcoRI; cDNA made by oligo-dT priming. Directionally cloned
         into EcoRI/XhoI sites using the following 5' adaptor:
         GGCACGAG(G). Library constructed by Ling Hong in the
         laboratory of Gerald M. Rubin (University of California,
         Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
         Superscript II RT (Life Technologies). Note: this is a
         NIH_MGC Library."
BASE COUNT 231 a 306 c 245 g 152 t 2 others
ORIGIN

Query Match 55.7%; Score 797.4; DB 14; Length 936;
Best Local Similarity 98.3%; Pred. No. 2e-192;
Matches 826; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC 69

Qy    653 CCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA 712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 CCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA 129

Qy    713 CCAAGGTGGACAAGAAAGCAGAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT 772
          |||||||||||||||||| |  | |||||||||||||||||||||||||||||||||||
Db    130 CCAAGGTGGACAAGAAAGAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT 189

Qy    773 GCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 GCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 249

Qy    833 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACG 892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACG 309

Qy    893 AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 952
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 369

Qy    953 CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC 1012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC 429

Qy   1013 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC 1072
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REFERENCE   1 (bases 1 to 977)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2464 row: b column: 03
             High quality sequence stop: 749.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6277538"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT   227 a   331 c   154 t   264 g   1 others
ORIGIN

Query Match   55.0%; Score 787.4; DB 14; Length 977;
Best Local Similarity 92.5%; Pred. No. 7.1e-190;
Matches 886; Conservative   0; Mismatches 57; Indels 15; Gaps 5;

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Db   11 CCCTGCTCCAAGAGCACCTCCCGAGAGCACCAGCGCCCCTGGGCTGCCTGGTCAAGGACTAC 70

Qy   535 TTCCCCGAACCGTGACGGTGTGTGGAACTCAGGGCGCCCTGACCAGGCGGCGGCCTGCACACC 594
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Db   71 TTCCCCGAACCGTGACGGTGTCGTGGAACTCAGGGCGCCCTGACCAGGCGGCGGCCTGCACACC 130

Qy   595 TTCCCGGCTGTCCTACAGTCCTCCAGGACTCTACTCCCTCAGCAGGCGGTGGTGACCGTGCCC 654
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Db   131 TTCCCGGCTGTCCTACAGTCCTCCAGGACTCTACTCCCTCAGCAGGCGGTGGTGACCGTGCCC 190

Qy   655 TCCAGCAGCTTGGGCACCCAGACCTACCATCTGCAAGCGAATCACAAGCCCAGCAACACC 714
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Db   191 TCCAGCAACTTCGGCACCCAGACCTACCATCTGCAACGTAGATCACAACGCCCAGCAACACC 250

Qy   715 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 774
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Db   251 AAGGTGGACAAGAAAGACAGAGTTGAGCGCAAATGTGTGTCGA--------GTGCCCACCGTGC 301

Qy   775 CCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTCCTTCCCCCCAAAACCCAAGGAC 834
          ||||||-- |||||||||||||||||||||||||||||||||||||||||||||||||
Db   302 CCAGCACC---ACCTGTGGCAGGACCCGTCAGTCTTCCTTCCCCCCAAAACCCAAGGAC 358

Qy   835 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 894
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Db   359 ACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAA 418

Qy   895 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 954
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Db   419 GACCCCGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 478

Qy   955 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 1014
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Query Match   55.6%; Score 796; DB 14; Length 940;
Best Local Similarity 99.3%; Pred. No. 4.5e-192;
Matches 810; Conservative   0; Mismatches   5; Indels 1; Gaps 1;

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Db   1 CAGGACTCTACTCCCTCAGCAGCGGTGACCGTGCCCTGGGCTGCCTGGTCAGCAGCCCAGA 60

Qy   677 CCTACATCTGCAACGTGAATCACAAGTGCCCAGCAACAACCAAGGTGGACAAGAAAGCAGAGC 736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTACATCTGCAACGTGAATCACAAGTGCCCAGCAACAACCAAGGTGGACAAGAAAGTTGAGC 120

Qy   737 CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG 796
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGG 180

Qy   797 GACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACACCTCATGATCTCCCGGACCC 856
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACACCTCATGATCTCCCGGACCC 240

Qy   857 CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT 916
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT 300

Qy   917 GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACA 976
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACA 360

Qy   977 ACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA 1036
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA 420

Qy   1037 AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACCATCT 1096
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACCATCT 480

Qy   1097 CCAAAGCCAAAGGGCAGCCCCGAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATG 1156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATG 540

Qy   1157 AGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA 1216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA 600

Qy   1217 TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG 1276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG 660

Qy   1277 TGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGT 1336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGT 720

Qy   1337 GGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA 1396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA 780

Qy   1397 CGC-AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          ||| |||||||||||||||||||||||||||||
Db   781 CGCAAAAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 816

RESULT 15
BQ710532
LOCUS   BQ710532   977 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8352211 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277538
            5', mRNA sequence.
ACCESSION   BQ710532
VERSION   BQ710532.1 GI:21849431
KEYWORDS   .EST.
SOURCE   human.
            Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

```
Qy  1015 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1074
          ||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   539 CACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA  598

Qy  1075 GCCCCCATCGAGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1134
          |||||||||||||||||||||||||| |||||| ||||| ||||||||||||||||||||
Db   599 GCCCCCATCGAGAAAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTAC  658

Qy  1135 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGCCTGCCTGGTC 1194
          |||||||||| ||||| ||||| ||  |||||||||||||||||||||||||||||||
Db   659 ACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC  718

Qy  1195 AAAGGCTTCTATCCCAGCGACATC-GCCGTGGAGTGGGAGAGCAATGGGCAGCCCGAGAA 1253
          |||||||||||||||||||||||  |||||| ||||||||||||||||||||||||||||
Db   719 AAAGGCTTCTACCCCAGCGACATCTCCCGTGGAGTGGGAGAGCAATGGGCAGCCCGAGAA  778

Qy  1254 CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAA 1313
          ||||| ||||||  |||||||||||||| |||||||||  |||| ||| ||||||||||
Db   779 CAACTANCAGACCACACCTCCCGTGGACTCCGACGGCTCTTTCTCCCTCTACAGC-A  837

Qy  1314 GCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA 1373
          ||||||||||||||||||||| ||||||||  |||||||||||| ||||||||||||||
Db   838 GCTCACCGTGGACAAGAGCAGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA  897

Qy  1374 TGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||  ||||| |||||   ||||||||||||| |||||||||||||||
Db   898 TGAGGCTCTGGGCCCACCCCTACACACA-AAGAGCCTCTCCCCGGTCTCGGGTAAATGA  954
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Search completed: April 6, 2003, 06:20:50
Job time : 2733.68 secs

OM protein - protein search, using sw model

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              GenCore version 5.1.4_p5_4578
         Copyright (c) 1993 - 2003 Compugen Ltd.
```

Run on: March 29, 2003, 09:06:24 ; Search time 10.5919 Seconds
(without alignments)
2141.995 Million cell updates/sec

Title: US-09-758-173-10
Perfect score: 1232
Sequence: 1 MRVPAQLLGLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1027	83.4	235	2	S05270	Ig lambda chain pr
2	1014	82.3	233	2	S25752	Ig lambda chain -
3	1010.5	82.0	236	2	S25746	Ig lambda chain -
4	1006	81.7	216	2	S29258	Ig lambda chain V
5	1006	81.7	234	2	S25757	Ig lambda chain -
6	1003.5	81.5	217	2	JE0246	Ig lambda chain NI
7	1001	81.2	235	2	S25750	Ig lambda chain -
8	995	80.8	232	2	S25742	Ig lambda chain -
9	989.5	80.3	213	2	S21066	Ig lambda chain V
10	987	80.1	233	2	S25744	Ig lambda chain -
11	986	80.0	216	2	A42193	Ig lambda chain (B
12	967.5	78.5	235	2	S25754	Ig lambda chain -
13	946	76.8	216	2	S03401	Ig lambda chain (K
14	944	76.6	235	2	S14675	Ig lambda chain -
15	942	76.5	208	2	B49444	Ig lambda chain (N
16	934	75.8	235	2	S25759	Ig lambda chain -
17	923	74.9	235	2	S25758	Ig lambda chain -
18	894	72.6	232	2	S25756	Ig lambda chain -
19	884	71.8	216	2	JE0246	Ig lambda chain NI
20	879	71.3	233	2	S25748	Ig lambda chain -
21	877	71.2	231	2	S25738	Ig lambda chain -
22	875	71.0	233	2	S25741	Ig lambda chain -
23	872.5	70.8	233	2	S25747	Ig lambda chain -
24	866	70.3	231	2	S25751	Ig lambda chain -
25	861	69.9	216	2	S69130	Ig lambda chain (D
26	850	69.0	231	2	S25753	Ig lambda chain -
27	846.5	68.7	235	2	S25749	Ig lambda chain -
28	839	68.1	213	2	JE0247	Ig lambda chain NI
29	839	68.1	226	2	S25745	Ig lambda chain -
30	815	66.2	190	2	S25740	Ig lambda chain -
31	811	65.8	243	2	S25755	Ig lambda chain -
32	737.5	59.9	212	2	S70431	Ig lambda chain v-
33	649.5	52.7	181	2	PTO220	Ig lambda chain pr
34	644.5	52.3	232	2	S17399	Ig lambda chain -
35	643	52.2	230	2	S49949	Ig light chain pre
36	630.5	51.2	213	2	A21177	Ig lambda chain V
37	625.5	50.8	214	2	PC4156	Ig lambda chain (K
38	606	49.2	118	2	S12441	Ig lambda chain (K
39	603	48.9	118	2	S12442	Ig lambda chain (K
40	581	47.2	118	2	S12443	Ig lambda chain (K
41	576	46.8	118	2	S12440	Ig lambda chain (M
42	573	46.5	118	2	A39949	Ig lambda chain J-
43	550	44.6	234	2	A39956	Ig lambda chain pr
44	548	44.5	105	1	L2HU	Ig lambda chain C
45	547.5	44.4	149	2	S23626	Ig lambda chain V

ALIGNMENTS

RESULT 1
S05270
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S05270; S04601
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05270
A;Molecule type: mRNA
A;Residues: 1-235 <KIS1>
A;Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04601
A;Molecule type: mRNA
A;Residues: 1-130 <KIS2>
A;Cross-references: EMBL:X14583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-235/Product: Ig lambda chain #status predicted <MAT>
F;150-218/Domain: immunoglobulin homology <IMM>

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Query Match           83.4%;   Score 1027;  DB 2;   Length 235;
Best Local Similarity  87.0%;   Pred. No. 8.5e-60;
Matches 200;  Conservative 12;  Mismatches 18;  Indels 0;  Gaps 0;

Qy    7  LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK   66
            |||||||||||||  |||||||||||||||||||||| |||| |||  ||||||||
Db    6  LLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCGSGSSNIGNNYVSWVQQLPGTAPK  65

Qy   67  LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR  126
            ||||| ||||||| ||||||||||| ::||||||||:||||||||  ::|||| ||||| ||
Db   66  LLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTK  125

Qy  127  LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT  186
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126  LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT  185

Qy  187  TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db  186  TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  235
```

RESULT 2
S25752
Ig lambda chain - human
C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25752
R;Combriato, G.; Klobeck, H.G.
  Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match   82.3%; Score 1014; DB 2; Length 233;
Best Local Similarity 84.8%; Pred. No. 5.8e-59;
Matches 195; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Qy   7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
          ||||||||| || |||||||||||||||||||||:|||||| :||||||||||||
Db   4 LLLTLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSGSSNIGSNTVNWYQQLPGTAPK 63

Qy   67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
          ||||||||||||| ||||||||||||||| :||||||||||||||||||||
Db   64 LLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGVVFGGGTK 123

Qy 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 183

Qy 187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 184 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
S25746
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25746
R;Combriato, G.; Klobeck, H.G.
  Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-236 <COM>
A;Cross-references: EMBL:X57811; NID:g33721; PIDN:CAA40948.1; PID:g33722
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin <IMM>
F;151-219/Domain: immunoglobulin homology <IMM>

Query Match   82.0%; Score 1010.5; DB 2; Length 236;
Best Local Similarity 84.4%; Pred. No. 1e-58;
Matches 195; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

Qy   7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
          :||||||||| || |||||||||||||||||||| ::|||||| :||||||||||||
Db   6 LLLTLLAHCTGSWAQSVLTQPPSASGTPGQKITISCSGSGSSNIGAGHHVHWYQQLPGTAP 65

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
          ||||||||||||||||||||||||||||| :||||||||||| ::|||||||
Db   66 KLLIYADNNRPSGVPDRISGGKSGTSASLAITGLRAEDEADYYCQSFDSSLSGWVFGGAT 125

Qy 126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 ▓TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPPVTAGVET 185

Qy 186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          ||||||||||| |

Db 186 TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4
S29258
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C;Accession: S29258
R;Chouchane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
  Eur. J. Biochem. 207, 1115-1121, 1992
A;Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment er
A;Reference number: S29257; MUID:92362614; PMID:1499555
A;Accession: S29258
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-216 <CHO>
A;Note: only part of the coding sequence is given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

Query Match   81.7%; Score 1006; DB 2; Length 216;
Best Local Similarity 89.9%; Pred. No. 1.8e-58;
Matches 195; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

Qy   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGG-YDLHWYQQLPGTAPKLLIYDINKRPSGI 79
          |||||||||||||||||||||| ::|||||| :||||||||||||||: :|||||||
Db   1 QSVLTQPPSVSGAPGQRVTISCSGSSNIGARYDVNWYQQLPGTAPKLLIYGNTIRPSGV 60

Qy   80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSV 139
          :|||||||||||:|||||:|| |:||||||| ||::::|||::|||||||||||||||||
Db   61 PDRFSGGKSGTSASLAITGLQAEDEGDYYCQTYDISLTV-VFGGGTKLTVLGQPKAAPSV 119

Qy 140 TLFPPSSELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 120 TLFPPSSELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 179

Qy 200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||| |||||||||||||||||||||
Db 180 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 216

RESULT 5
S25757
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25757
R;Combriato, G.; Klobeck, H.G.
  Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lamt
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-234 <COM>
A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;149-217/Domain: immunoglobulin homology <IMM>

Query Match   81.7%; Score 1006; DB 2; Length 234;
Best Local Similarity 83.0%; Pred. No. 1.9e-58;
Matches 191; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

Qy   7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAPK 66
          ||||||||| || :|||||||||||||||||||| ::||||| :|||||||||||||
Db   5 LLLTLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSGTNIGSNTVNWYQQLPGTAPK 64

Qy   67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
          |||| |: ||

Db   65 VLIYNNERPSGVPDRFSGSKSGTSASLAISGLQSDEADYYCAAWDDSLNGRLLGGGTK 124
         |||||||||||||||||||||||||||||||||||||||||||
Qy   127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
Qy   187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 6
JE0246
Ig lambda chain NIG204 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Takashi, I.; Shinoda,
submitted to JIPID, November 1998
A;Description: Structural relationship of lambda type light chains with AL amyloidosis.
A;Reference number: JE0246
A;Accession: JE0246
A;Molecule type: protein
A;Residues: 1-217 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;132-200/Domain: immunoglobulin homology <IMM>

Query Match   81.5%; Score 1003.5; DB 2; Length 217;
Best Local Similarity   89.4%; Pred. No. 2.6e-58;
Matches 194; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

Qy   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAPKLLIYDINKRPSGI 79
         :|||||||||||||||:||:|:||:|::|| ||::||||||||:|||||:::|:|||||:
Db   1 ZSVLTQPPSVSGAPGQGVTLSCSGSSSNIGAGYPVHWYQQLPGAAPKLLISDNYNRPSGV 60
Qy   80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSV 139
         ||||||||||:|||||:|||||:||||||||||||||:| |||||:||||||||||||||
Db   61 PARFSGSKSGTSASLAISGLQAEDEADYYCQSYDSSLTAWVFGGGTKLTVLRQPKAAPSV 120
Qy   140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 199
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 180
Qy   200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||
Db   181 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 217

RESULT 7
S25750
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25750
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25750
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: EMBL:X57815; NID:g33729; PIDN:CAA40952.1; PID:g33730
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match   81.2%; Score 1001; DB 2; Length 235;
Best Local Similarity   83.5%; Pred. No. 4.1e-58;
Matches 192; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

Qy   7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
         || |: :||||||||||||| ||||||||||||||||||

Db   6 LLLTLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGASSNIGTNDVYWYQQLTGTAPK 65
Qy   67 LLIYDINKRPSGIDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
         |||:::::||||:||||||||||:||||||:||:|||||||||:::::||:|||||||
Db   66 LLIYRNNQRPSGVPDRFSGSKSGSSASLAISGLQSDEADYYCAAWDDSLSGPVFGGGTK 125
Qy   127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185
Qy   187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 8
S25742
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25742
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25742
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COM>
A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

Query Match   80.8%; Score 995; DB 2; Length 232;
Best Local Similarity   84.3%; Pred. No. 9.9e-58;
Matches 194; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

Qy   7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
         ||||||| ::. ::|||||||||||||||||| :::::|:||::||||||||||||||
Db   3 LLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCGSGSSNIGNNYVSWYQQLPGRAPK 62
Qy   67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
         |||:::::||||:|||||||||||:||||:::|||:|||||||||:::::|:.|||||||
Db   63 LLIFENNKRPSAIPDRFSGSKSGTSATLGIAGLQTGDEADYYCGTWDSSLTDVVFGGGTK 122
Qy   127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 182
Qy   187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   183 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 232

RESULT 9
S21066
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S21066
R;Dlouha, A.; Lecrolsey, A.; Henschen, A.; Ruttyn, Y.; Rouger, P.; Keil, B.
Protein Seq. Data Anal. 4, 319-324, 1991
A;Title: Partial amino acid sequence of the light chain of human anti-Rh(D) monoclonal ar
A;Reference number: S21066; MUID:92253545; PMID:1812484
A;Accession: S21066
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-213 <DLO>
A;Note: the sequence from Fig 4 is inconsistent with that from Fig. 1 in having 74-Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;128-196/Domain: immunoglobulin homology <IMM>

Query Match   ... ; Score ...; DB 2; Length 235;
Best Local Similarity   ... ; Pred. No. ...;
Matches ...; Conservative ...; Mismatches ...; Indels 0; Gaps 0;

Qy   7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
         || |: :||||||| |||||||||||| |:::||||

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Query Match             80.3%;  Score 989.5;  DB 2;  Length 213;
Best Local Similarity   88.5%;  Pred. No. 2.1e-57;
Matches  192;  Conservative  10;  Mismatches  10;  Indels   5;  Gaps   2;

Qy    21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGG-YDLHWYQQLPGTAPKLLIYDINKRPSGI 79
            ||||||||||||||||||||||||||||||| :|:||||||||||||||::
Db     1 QSVLTQPPSVSGAPGQRVTISCSGSSSNIGARYDVNWYQQLPGTAPKLLIYGNTIRPSGV 60

Qy    80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSV 139
            |||||||:|||      :|||||||||||||||||||||||||||  ||||||||||
Db    61 PDRFSGSKSGTSASLAITGLQAEDEGDYYCQTWD----YVVFGGGTKLTVLGQPKAAPSV 116

Qy   140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   117 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 176

Qy   200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
            |||||||||||||||||||||||||||||||||||||
Db   177 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 213

RESULT 10
S25744
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25744
R;Combriato, G.; Klobeck, H.G.
A;Title: V(lambda) and J1(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
Eur. J. Immunol. 21, 1513-1522, 1991
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25744
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57809; NID:g33714; PIDN:CAA40946.1; PID:g33715
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match             80.1%;  Score 987.;  DB 2;  Length 233;
Best Local Similarity   83.0%;  Pred. No. 3.3e-57;
Matches  191;  Conservative  16;  Mismatches  21;  Indels   2;  Gaps   1;

Qy     7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
            ||| : ||||||||||||||||||||||||:|:||||||||
Db     6 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTIISCSGSRSNVGSNNVNWYQQLPGTK 65

Qy    67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
            :||| :|| |||||||||||||||||||||||||||| :|||:|||||
Db    66 LLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDS--TVVFGGGTK 123

Qy   127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 LTVPGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 183

Qy   187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 11
A42193
Ig lambda chain (BJP-DIA) - human
N;Alternate names: amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda chain
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jan-2000
C;Accession: A42193; S18297
R;Klafki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N.
Biochemistry 31, 3265-3272, 1992
A;Title: Complete amino acid sequence determinations demonstrate identity of the urinary
A;Reference number: A42193; MUID:92207944; PMID:1554711
```

```
A;Accession: A42193
A;Molecule type: protein
A;Residues: 1-216 <KLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match             80.0%;  Score 986;  DB 2;  Length 216;
Best Local Similarity   86.1%;  Pred. No. 3.5e-57;
Matches  186;  Conservative  16;  Mismatches  14;  Indels   0;  Gaps   0;

Qy    21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
            ||||||||||||||||||||||||||||||| :|:||||||||||||||::
Db     1 QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNNVTWYQQLPGTAPKLLIYTNNQRPSGVP 60

Qy    81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSVT 140
            |||||||:|||      :|||||||||||||||||||||||||||  ||||||||||||
Db    61 GRFSGSKSGTSASLAVSGLQSEDEADYYCATWDDSVNGWVFGGGTKLTVLGQPKAAPSVT 120

Qy   141 LFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASS 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASS 180

Qy   201 YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
            ||||||||||||||||||||||||||||||||||||
Db   181 YLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 216

RESULT 12
S25754
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25754
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25754
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: EMBL:X57819; NID:g33737; PIDN:CAA40956.1; PID:g33738
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match             78.5%;  Score 967.5;  DB 2;  Length 235;
Best Local Similarity   81.0%;  Pred. No. 6e-56;
Matches  187;  Conservative  19;  Mismatches  24;  Indels   1;  Gaps   1;

Qy     7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
            ||| : ||||||||||||||||||||||||:|:||||||||
Db     5 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVIISCSGSSSNIGGNTVNWYQQLPGRAPK 64

Qy    67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGGT 125
            :|||: :||:||||||||||||||||||| :|||||| :|||:|||||||    |||||
Db    65 LLIHSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGRYVFGTGT 124

Qy   126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVET 185
            :|||||||||| |:|||||||||||||||||||||||||||||||||||||  ||||||
Db   125 KVTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVET 184

Qy   186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
            :|||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 TKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 13
S03401
Ig lambda chain (Kol) - human
C;Species: Homo sapiens (man)
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```
Db      64  APKLMIYEVTKRPSGGVPNRFSGSKSGNTASLTVSGLQAEDEADYCSSYAGS-NSLIFGG  122

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: S03401
R;Kratzin, H.D.; Palm, W.; Stangel, M.; Schmidt, W.E.; Friedrich, J.; Hilschmann, N.
  Biol. Chem. Hoppe-Seyler 370, 263-272, 1989
A;Title: The primary structure of the crystallizable monoclonal immunoglobulin IgG1 Kol.
A;Reference number: S03401; MUID:89228564; PMID:2711105
A;Accession: S03401
A;Molecule type: protein
A;Residues: 1-216 <KRA>
A;Note: article in German with English abstract
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match           76.8%;  Score 946;  DB 2;  Length 216;
Best Local Similarity 83.3%;  Pred. No. 1.4e-54;
Matches 180;  Conservative  15;  Mismatches 21;  Indels  0;  Gaps  0;

Qy      21  ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGDLHWYQQLPGTAPKLLIYDINKRPSGIS   80
             : ||||||||||||||      :|||||||||||||  ::|||    :||||:|||||  :||:|
Db       1  QSVLTQPPSASGTPGQRVTISCSGSTSNIGSSTVNWYQQLPGMAPKLLIYRDAMRPSGVP   60

Qy      81  DRFSGSKSGTAASLAITGLQTEDEADYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSVT  140
             ||||||||:|    ||||| || || ||:|| : |:||:|||: ||:||||| |:|
Db      61  DRFSGSKSGASASLAIGGLQSEDETDYYCAAWDVSLNAYVFGTGTKVTVLGQPKANPTVT  120

Qy     141  LFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASS  200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  LFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASS  180

Qy     201  YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
             ||||||||||||||||||||||||||||||||||||
Db     181  YLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  216

RESULT 14
S14675
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
A;Accession: S14675, S12445
R;Vasicek, T.J.
  submitted to the EMBL Data Library, February 1990
A;Reference number: S14675
A;Accession: S14675
A;Molecule type: DNA
A;Residues: 1-235 <VAS1>
A;Cross-references: EMBL:X51754
R;Vasicek, T.J.; Leder, P.
  J. Exp. Med. 172, 609-620, 1990
A;Title: Structure and expression of the human immunoglobulin lambda genes.
A;Reference number: S12440; MUID:90324881; PMID:2115572
A;Accession: S12445
A;Molecule type: DNA
A;Residues: 1-129 <VAS2>
A;Cross-references: EMBL:X51754
C;Genetics:
A;Introns: 16/1; 130/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match           76.6%;  Score 944;  DB 2;  Length 235;
Best Local Similarity 78.5%;  Pred. No. 2e-54;
Matches 183;  Conservative  20;  Mismatches 28;  Indels  2;  Gaps  2;

Qy       5  AQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGT   63
             |::     ||| :|::|: :||||||||||||||||||||||::: :|| :||||||
Db       4  ALLILTLLTQGTGSWAQSALTQPPSASGSLGQSVTFSCSGTSSDIGNYNYVSWYRQHPGK   63

Qy      64  APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG  123
             |||||:  :|||||| : ||||||   ||||| || ||||   ||||  || || :|||
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```
Db     124  GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV  183
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123  GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV  182

Qy     184  ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183  ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  235

RESULT 15
B49444
Ig lambda chain (New) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 21-Jan-2000
C;Accession: B49444
R;Saul, F.A.; Poljak, R.J.
  Proteins 14, 363-371, 1992
A;Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A reso
A;Reference number: A49444; MUID:93066153; PMID:1438175
A;Accession: B49444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-208 <SAU>
A;Note: sequence modified after extraction from NCBI backbone
A;Note: this sequence report includes corrections based on crystal structure refinement
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;123-191/Domain: immunoglobulin homology <IMM>

Query Match           76.5%;  Score 942;  DB 2;  Length 208;
Best Local Similarity 85.7%;  Pred. No. 2.4e-54;
Matches 186;  Conservative  12;  Mismatches  9;  Indels  10;  Gaps  3;

Qy      21  ESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAPKLLIYDINKRPSGI   79
             : |||||||||||||||||||||||||||||  :::|||||||||||||||||:
Db       1  QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGHNVKWYQQLPGTAPKLLIFHNNA-----   55

Qy      80  SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSV  139
             |  ||||||||||||||||||||||||||||||     ::|||||||:|||||||||||||
Db      56  --RFSVSKSGTSSATLAITGLQAEDEADYYCQSYDRSL--RVFGGGTKLTVLRQPKAAPSV  111

Qy     140  TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS  199
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112  TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTTPSKQSNNKYAAS  171

Qy     200  SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  236
             ||||||||||||||||||||||||||||||||||||
Db     172  SYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS  208

Search completed: March 29, 2003, 09:16:20
Job time : 11.5919 secs
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                    GenCore version 5.1.4_p5_4578
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      March 29, 2003, 09:06:23 ; Search time 5.62693 Seconds
                                         (without alignments)
                                         1739.566 Million cell updates/sec

Title:       US-09-758-173-10
Perfect score: 1232
Sequence:    1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 236

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:    112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:     112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    SwissProt_40:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES

Result              Query        %
No.     Score  Length DB ID          Match  Description
---------------------------------------------------------------------
  1     548     105  1  LAC_HUMAN      44.5   P01842 homo sapien
  2     527     213  1  ILL1_HUMAN     42.8   P15814 homo sapien
  3     463     130  1  LV1G_HUMAN     37.6   P06316 homo sapien
  4     454     111  1  LV1D_HUMAN     36.9   P01702 homo sapien
  5     432     111  1  LV1C_HUMAN     35.1   P01701 homo sapien
  6     426     109  1  LV1F_HUMAN     34.6   P04208 homo sapien
  7     424.5   112  1  LV2K_HUMAN     34.5   P04209 homo sapien
  8     415     105  1  LAC_PIG        33.7   P01846 sus scrofa
  9     413.5   112  1  LV1H_HUMAN     33.6   P06887 homo sapien
 10     412     105  1  LAC1_MOUSE     33.4   P01845 mus musculu
 11     407.5   112  1  LV1B_HUMAN     33.1   P01700 homo sapien
 12     402     109  1  LV1I_HUMAN     32.6   P06888 homo sapien
 13     399     105  1  LAC_RABIT      32.4   P01847 oryctolagus
 14     396     111  1  LV1A_HUMAN     32.1   P01699 homo sapien
 15     396     111  1  LV2B_HUMAN     32.1   P01705 homo sapien
 16     395     111  1  LV2H_HUMAN     32.1   P01711 homo sapien
 17     393     103  1  LV1E_HUMAN     31.9   P01703 homo sapien
 18     392     111  1  LV2F_HUMAN     31.8   P01709 homo sapien
 19     391     111  1  LV2I_HUMAN     31.7   P01712 homo sapien
 20     385.5   104  1  LAC1_RAT       31.3   P20766 rattus norv
 21     381     111  1  LV2D_HUMAN     30.9   P01707 homo sapien
 22     380.5   104  1  LAC2_RAT       30.9   P20767 rattus norv
 23     377     105  1  LAC5_MUSSP     30.6   P20765 mus spretus
 24     374.5   104  1  LAC3_MOUSE     30.4   P01845 mus musculu
 25     372     111  1  LV2A_HUMAN     30.2   P01704 homo sapien
 26     371     111  1  LV2C_HUMAN     30.1   P01706 homo sapien
 27     370     109  1  LV2E_HUMAN     30.1   P01708 homo sapien
 28     369.5   104  1  LAC2_MOUSE     30.0   P01844 mus musculu
 29     368     111  1  LV2G_HUMAN     29.9   P01710 homo sapien
 30     352.5   110  1  LV2J_HUMAN     28.6   P01713 homo sapien
 31     347     105  1  LAC5_MOUSE     28.2   P20764 mus musculu
 32     344.5   112  1  LV6A_HUMAN     28.0   P01721 homo sapien
 33     342     111  1  LV6C_HUMAN     27.8   P06317 homo sapien
 34     341     111  1  LV6D_HUMAN     27.7   P06318 homo sapien
 35     340.5   129  1  KV1W_HUMAN     27.6   P04431 homo sapien
 36     339     108  1  LV3A_HUMAN     27.5   P01714 homo sapien
 37     339     111  1  LV3B_HUMAN     27.5   P80748 homo sapien
 38     334.5   131  1  LV6E_HUMAN     27.2   P06319 homo sapien
 39     329.5   117  1  KV1J_HUMAN     26.7   P01602 homo sapien
 40     326.5   103  1  LAC_CHICK      26.5   P20763 gallus gall
 41     326     106  1  LV4E_HUMAN     26.5   P06889 homo sapien
 42     322     108  1  LV5A_HUMAN     26.1   P01719 homo sapien
 43     319     106  1  LV4B_HUMAN     25.9   P01716 homo sapien
 44     318     106  1  LV4A_HUMAN     25.8   P01715 homo sapien
 45     314     111  1  LV2L_HUMAN     25.5   P80422 homo sapien

                              ALIGNMENTS

RESULT 1
LAC_HUMAN
ID   LAC_HUMAN       STANDARD;       PRT;     105 AA.
AC   P01842; P80423;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig lambda chain C regions.
GN   IGLC1 AND IGLC2 AND IGLC3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (BENCE-JONES PROTEIN SH).
RX   MEDLINE=70166723; PubMed=4909564;
RA   Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT   complete amino acid sequence and the location of the disulfide
RT   bridges.";
RL   J. Biol. Chem. 245:2171-2176(1970).
RN   [2]
RP   SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX   MEDLINE=69088380; PubMed=4883841;
RA   Milstein C., Clegg J.B., Jarvis J.M.;
RT   "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT   Bence-Jones protein.";
RL   Biochem. J. 110:631-652(1968).
RN   [3]
RP   SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RX   MEDLINE=71150336; PubMed=5549568;
RA   Ponstingl H., Hess M., Hilschmann N.;
RT   "Structural rule of antibodies. Primary structure of a monoclonal
RT   immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT   protein Kern). V. The complete amino acid sequence and its genetic
RT   interpretation.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
RN   [4]
RP   SEQUENCE (BENCE-JONES PROTEIN KERN).
RX   MEDLINE=73186114; PubMed=6404090;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. IV. Assignment of a subsubgroup.";
RL   J. Biochem. 93:421-429(1983).
RN   [5]
RP   PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX   MEDLINE=74109253; PubMed=4814727;
RA   Chen B.L., Poljak R.J.;
RT   "Amino acid sequence of the (lambda) light chain of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 13:1295-1302(1974).
RN   [6]
RP   SEQUENCE (DOT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
```

RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX   MEDLINE=75046825; PubMed=4215080;
RA   Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA   Saul F.;
RT   "The three-dimensional structure of the fab' fragment of a human
RT   myeloma immunoglobulin at 2.0-A resolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
RN   [8]
RP   PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY OF MCG.
RX   MEDLINE=90133913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
RN   [11]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82080680; PubMed=6273747;
RA   Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
RT   "Clustered arrangement of immunoglobulin lambda constant region genes
RT   in man.";
RL   Nature 294:536-540(1981).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
CC   FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE
CC   KERN+ MARKER, THE NEWM PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN
CC   HAS THE KERN+ MARKER, AND THE MCG+ MARKER.
CC   -!- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
CC   3 MOST 5' WERE SEQUENCE. THESE CORRESPOND TO THE MCG SEQUENCE
CC   (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
CC   SEQUENCE (LAMBDA-3).

DR   EMBL; J00253; AAA59107.1; -.
DR   EMBL; L38562; AAB36581.1; ALT_INIT.
DR   EMBL; X51754; CAB38569.1; ALT_INIT.
DR   EMBL; X51755; CAA36049.1; -.
DR   EMBL; X51755; CAA36051.1; -.
DR   PIR; A02125; L2HU.
DR   PDB; 2MCG; 15-JUN-92.
DR   PDB; 7FAB; 31-JAN-94.
DR   Genew; HGNC:5855; IGLC1.
DR   Genew; HGNC:5856; IGLC2.
DR   Genew; HGNC:5857; IGLC3.
DR   MIM; 147220; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_C1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.

KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT   NON_TER   1   1
FT   DISULFID   27   86
FT   DISULFID   104   104
FT   DISULFID   INTERCHAIN (WITH HEAVY CHAIN).
FT   VARIANT   5   5   A -> N (IN MCG+ MARKER).
FT   /FTId=VAR_003898.
FT   VARIANT   7   7   S -> T (IN MCG+ MARKER).
FT   /FTId=VAR_003899.
FT   VARIANT   45   45   S -> G (IN KERN+ MARKER).
FT   /FTId=VAR_003900.
FT   VARIANT   56   56   T -> K (IN MCG+ MARKER).
FT   /FTId=VAR_003901.
FT   VARIANT   82   82   R -> K (IN OZ+ MARKER).
FT   /FTId=VAR_003902.
FT   STRAND   4   4
FT   STRAND   7   11
FT   HELIX   15   19
FT   TURN   20   21
FT   STRAND   23   33
FT   STRAND   38   43
FT   TURN   44   45
FT   STRAND   46   48
FT   TURN   50   51
FT   STRAND   52   54
FT   STRAND   58   59
FT   TURN   61   62
FT   STRAND   65   73
FT   HELIX   75   79
FT   TURN   80   80
FT   STRAND   84   90
FT   TURN   91   92
FT   STRAND   93   99
SQ   SEQUENCE   105 AA;   11236 MW; DCD9C7C201C13CC2 CRC64;

Query Match   44.5%; Best Local Similarity 100.0%; Pred. No. 5.3e-37;
                       Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

                       Score 548; DB 1; Length 105;

Qy   132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 60

Qy   192 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
              |||||||||||||||||||||||||||||||||||||||||||||
Db   61 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 105

RESULT 2
ILL1_HUMAN
ID   ILL1_HUMAN   STANDARD;   PRT;   213 AA.
AC   P15814;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
DE   related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
DE   (CD179b antigen).
GN   IGLL1 OR IGL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89315835; PubMed=2501791;
RA   Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
RA   McKearn J.P.;
RT   "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
RT   expressed in pre-B cells and may encode the human immunoglobulin
RT   omega light-chain protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989).
RN   [2]
RP   SEQUENCE FROM N.A.

```
RC   TISSUE=Lymphoid;
RX   MEDLINE=91108327; PubMed=1703205;
RA   Evans R.J., Hollis G.F.;
RT   "Genomic structure of the human Ig lambda 1 gene suggests that it may
RT   be expressed as an Ig lambda 14.1-like protein or as a canonical B
RT   cell Ig lambda light chain: implications for Ig lambda gene
RT   evolution.";
RL   J. Exp. Med. 173:305-311(1991).
CC   -!- SUBUNIT: Associates non-covalently with VPREB1.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
CC       B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 1:64-67(2000);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/696419174_g.htm".
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; M27749; AAA36100.1; -.
DR   EMBL; M34513; AAA36096.1; -.
DR   EMBL; M34511; AAA36096.1; JOINED.
DR   EMBL; M34512; AAA36096.1; JOINED.
DR   PIR; A33911; A33911.
DR   HSSP; P01842; 7FAB.
DR   Genew; HGNC:5870; IGLL1.
DR   MIM; 146770; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; B-cell; Signal.
FT   SIGNAL        1     37       POTENTIAL.
FT   CHAIN        38    213       IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 1.
FT   DOMAIN       97    108       J REGION (BY SIMILARITY TO LAMBDA
FT                                LIGHT-CHAIN).
FT   DOMAIN      109    213       C REGION (BY SIMILARITY TO LAMBDA
FT                                LIGHT-CHAIN).
SQ   SEQUENCE    213 AA;  22963 MW;  9133A7742B943C79 CRC64;

Query Match             42.8%;  Score 527;  DB 1;  Length 213;
Best Local Similarity   52.3%;  Pred. No. 5.8e-35;
Matches   125;  Conservative   15;  Mismatches   47;  Indels   52;  Gaps    7;

Qy    2 RVPAQLLGLLL---LWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWY 57
         |:|| ||||||    |||||||:||||||||||||||||||||||| |:  |||||
Db   23 RWPLLLLGGLAVVTHGLLLRPTAASQSRALGP---GAPGGS--SRSSLRSRWGRFLL--- 72

Qy   58 QQLPGTAPKLLIYDINKRPSGISDRFSGGKSGTAASLAITGLQTEDEADYYCQSYDSSLN 117
         :|| ||||||||||||||||||||||||||| :||||:|||:||||||||||||||||
Db   73 QRGSWTGPRCW------PRGF----------------------------QSKHNSV--- 94

Qy  118 AQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS 177
         ||||||||||||||||||:||||||||||||||||||||||||:|||| :||:||||
Db   95 THVFGSGTQLTVLSQPKATPSVTLFPPSSEELQANKATLVCLMNDFYPGILTVTWKADGT 154

Qy  178 PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |:|| ||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db  155 PITQGVEMTTPSKQSNNKYAASSYLSLTPEQWRSRRSYSCQVMHEGSTVEKTVAPAECS 213

RESULT 3
LVIG_HUMAN
ID   LVIG_HUMAN     STANDARD;     PRT;    130 AA.
AC   P06316;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
```

```
DE   Ig lambda chain V-I region BL2 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85062823; PubMed=6095199;
RA   Tsujimoto Y., Croce C.M.;
RT   "Molecular cloning of a human immunoglobulin lambda chain variable
RT   sequence.";
RL   Nucleic Acids Res. 12:8407-8414(1984).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X01147; CAA25598.1; -.
DR   PIR; A01966; L1HUBL.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    130       IG LAMBDA CHAIN V-I REGION BL2.
FT   DOMAIN       20    115       V SEGMENT.
FT   DOMAIN      116    130       J SEGMENT.
FT   DISULFID     41    108       BY SIMILARITY.
FT   NON_TER     130    130
SQ   SEQUENCE    130 AA;  13564 MW;  FA44B17D3A55EBF CRC64;

Query Match             37.6%;  Score 463;  DB 1;  Length 130;
Best Local Similarity   72.8%;  Pred. No. 3.7e-30;
Matches    91;  Conservative   15;  Mismatches   19;  Indels    0;  Gaps    0;

Qy    7 LLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
         || ||| ||:||||||||||||||:|||||||||||: :|||| :|||| :|||||:
Db    6 LLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCGSGSSNIGNDVVSWYQQVPGTAPK 65

Qy   67 LLIYDINKRPSGISDRFSGGKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFCGGTR 126
         ||||| |||||||  ||||||||: :||:||:||||: ||||||||:  ::|||||||||:
Db   66 LLIYDNNKRPSGIPDRFSGGKSKGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTK 125

Qy  127 LTVLG 131
         |||||
Db  126 LTVLG 130

RESULT 4
LVID_HUMAN
ID   LVID_HUMAN     STANDARD;     PRT;    111 AA.
AC   P01702;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region NIG-64.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83186114; PubMed=6404900;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. IV. Assignment of a subsubgroup.";
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RL   J. Biochem. 93:421-429(1983).
DR   PIR; A01965; L1HUNG.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     89       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11454 MW;  A21C6121C18A61E0 CRC64;

Query Match             36.9%;  Score 454;  DB 1;  Length 111;
Best Local Similarity   78.4%;  Pred. No. 1.6e-29;
Matches   87;  Conservative  12;  Mismatches  12;  Indels   0;  Gaps   0;

Qy     21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
          :||||||||||:||||||| ::||||||||:|||||||||||||||||:|||||||||
Db      1 QSVLTQPPSVSAAPGQEVTISCSGSSSNIGDNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy     81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLG 131
          ||||||||||||:|:||||||||||||||::||||| :|||||||||||
Db     61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSVGMFGGGTRVTVLG 111

RESULT 5
LV1C_HUMAN
ID   LV1C_HUMAN   STANDARD;   PRT;   111 AA.
AC   P01701;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region NEW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69060892; PubMed=4177823;
RA   Langer B., Steinmetz-Kayne M., Hilschmann N.;
RT   "The complete amino acid sequence of Bence Jones protein New (lambda-
RT   type). Subgroups in the variable part of immunoglobulin L-chains of
RT   the lambda-type.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01964; L1HUNW.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     89       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11453 MW;  AAECBCA3C49F2AD3 CRC64;

Query Match             35.1%;  Score 432;  DB 1;  Length 111;
Best Local Similarity   73.9%;  Pred. No. 8.6e-28;
Matches   82;  Conservative  14;  Mismatches  15;  Indels   0;  Gaps   0;

Qy     21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
          :||||||||||:||||||| ::||||||||:||||||||||||||||||:|||||||||
Db      1 QSVLTQPPSVSAAPGQKVTISCSGGSTNIGNNYVSWHQHLPGTAPKLLIYEDNKRPSGIP 60

Qy     81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLG 131
          ||||||||||||:|||||||||:::|||||| :||||||||:||||||||
Db     61 DRISASKSGTSATLGITGLRTGDEADYYCATWDSSLNAVFGGGGTKVTVLG 111

RESULT 6
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LV1F_HUMAN
ID   LV1F_HUMAN   STANDARD;   PRT;   109 AA.
AC   P04208;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region WAH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83221661; PubMed=6607018;
RA   Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT   "Complete covalent structure of a human immunoglobulin D: sequence of
RT   the lambda light chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR   PIR; A01967; L1HUWA.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     97       V SEGMENT.
FT   DOMAIN       98    109       J SEGMENT.
FT   DISULFID     22     89       BY SIMILARITY.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11725 MW;  B17785F6A8DF9BAC CRC64;

Query Match             34.6%;  Score 426;  DB 1;  Length 109;
Best Local Similarity   74.5%;  Pred. No. 2.5e-27;
Matches   82;  Conservative  13;  Mismatches  13;  Indels   2;  Gaps   1;

Qy     21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
          :||||||||||:|||||||:||||||||| :||||||||||||||||||:|||||||||::
Db      1 QSVLTQPPSASGTPGQRVTISCFGSSSNIGRYYVWYQQLPGTTPKLLIYKDNQRPSGVP 60

Qy     81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVL 130
          |||||||||||:||||||::|||||||||| :::||| :||||||||||
Db     61 DRFSGSKSGTSASLAISGLRSDEADYYCAAWDDSL--WVFGGGTTLTVL 108

RESULT 7
LV2K_HUMAN
ID   LV2K_HUMAN   STANDARD;   PRT;   112 AA.
AC   P04209;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region NIG-84.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85204383; PubMed=3922791;
RA   Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT   "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT   myeloma-associated systemic amyloidosis.";
RL   FEBS Lett. 185:139-141(1985).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
CC       INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
DR   PIR; A01971; L2HUNG.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT   DISULFID     22     90       BY SIMILARITY.
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FT   NON_TER       112
SQ   SEQUENCE     112 AA;  11581 MW;  988FEF363AE1E4F3 CRC64;

Query Match             34.5%;
Best Local Similarity   70.5%;
Matches    79;  Conservative   16;  Mismatches   16;  Indels    1;  Gaps    1;

Qy    21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
         ::|:|||||||| |||||| ||||||||||||||:|||||||||||||||:||||||||||
Db     1 QSALTQPASVSGSPGQSITISCTGTTSDVGGYDFVSWYQQHPGKAPKLLIYDVNSRPSGI 60

Qy    80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSLNAQVFGGGTRLTVLG 131
         |:||||||||| |||||||| |||||| :: : |||||||:|:|:|||
Db    61 SNRFSGSKSGNTASLTISGLQAEDEADYYCSSFTTNSRAVFGGGTKLSVLG 112


RESULT 8
LAC_PIG
ID   LAC_PIG      STANDARD;      PRT;   105 AA.
AC   P01846;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain C region.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=78000254; PubMed=409425;
RA   Novotny J., Franek F., Margolies M.N., Haber E.;
RT   "Amino acid sequence of normal (microheterogeneous) porcine
RT   immunoglobulin lambda chains.";
RL   Biochemistry 16:3765-3772(1977).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MIXTURE OF NORMAL
CC       IMMUNOGLOBULINS.
DR   PIR; A02129; L1PG.
DR   HSSP; P01842; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER        1
FT   DISULFID      27     86
FT   DISULFID     104    104       INTERCHAIN (WITH HEAVY CHAIN).
SQ   SEQUENCE     105 AA;  11003 MW;  3817AAEBD747C396 CRC64;

Query Match             33.7%;
Best Local Similarity   74.3%;
Matches    78;  Conservative    9;  Mismatches   18;  Indels    0;  Gaps    0;

Qy   132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
          ||||||||:||||||||||||||:|||| ||||||||| |||||||||||||||| |||
Db     1 QPKAAPTVNLFPPSSEELGTNKATLVCLISDFYPGAVTVTWKAGGTVTQGVETTKPSKQ 60

Qy   192 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          ||||||||||::|| :||||::|: |||||||:||:|:|
Db    61 SNNKYAASSYLALSASDWKSSSGFTCQVTHEGTIVEKTVTPSECA 105


RESULT 9
LV1H_HUMAN
ID   LV1H_HUMAN   STANDARD;      PRT;   112 AA.
AC   P06887;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region MEM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85257662; PubMed=2410269;
RA   Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
RT   "The amino acid sequence of a lambda light chain presenting abnormal
RT   physicochemical and antigenic features.";
RL   Eur. J. Biochem. 150:349-357(1985).
CC   -!- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
CC       WERE POSITIONED BY HOMOLOGY.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC       MARKERS.
DR   PIR; A25479; L1HUMM.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Monoclonal antibody.
FT   MOD_RES        1              PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID      22     90       BY SIMILARITY.
FT   NON_TER      112    112
SQ   SEQUENCE     112 AA;  11789 MW;  748124F079CFFBE4 CRC64;

Query Match             33.6%;              Score 413.5;  DB 1;  Length 112;
Best Local Similarity   69.4%;              Pred. No. 2.5e-26;
Matches    77;  Conservative   19;  Mismatches   14;  Indels    1;  Gaps    1;

Qy    21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
         :|||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db     1 QSVLTQPPSASGTPGGRVTISCSGSSSNVGSNZPAYWYQQLPGTAPKLLIYNNQRPSGV 60

Qy    80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSLNAQVFGGGTRLTVL 130
         |||||||||||||||||||||||||||||||| || |:||||||:||:||
Db    61 PDRFSASRGTSASLAISGLQSEDEADYYCAAWDDSLDGYVFGTGTKVTVL 111


RESULT 10
LAC1_MOUSE
ID   LAC1_MOUSE   STANDARD;      PRT;   105 AA.
AC   P01843;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda-1 chain C region.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83014953; PubMed=6812053;
RA   Selsing E., Miller J., Wilson R., Storb U.;
RT   "Evolution of mouse immunoglobulin lambda genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
RN   [2]
RP   SEQUENCE FROM N.A. (MOPC 315).
RX   MEDLINE=81148806; PubMed=6259534;
RA   Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA   Gefter M.L., Baltimore D.;
RT   "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL   Nature 290:65-67(1981).
RN   [3]
RP   SEQUENCE FROM N.A. (S43).
RX   MEDLINE=82220143; PubMed=6283385;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Somatic variants of murine immunoglobulin lambda light chains.";
RL   Nature 298:380-382(1982).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX   MEDLINE=71107854; PubMed=5276767;
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RA   Appella E.;
RT   "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
CC   -!- MISCELLANEOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1
CC       NORMAL LAMBDA-2 CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING
CC       A LARGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
CC       APPEARS COMPLETELY NORMAL.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00582; AAA51636.1; -.
DR   EMBL; J00587; AAB59672.1; -.
DR   PIR; A02126; LIMS.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DISULFID     27     86
FT   DISULFID    104    104       INTERCHAIN (WITH HEAVY CHAIN).
FT   CONFLICT     19     20       ET -> TE (IN REF. 4).
FT   CONFLICT     56     56       Q -> E (IN REF. 4).
FT   CONFLICT     75     75       MISSING (IN REF. 4).
FT   CONFLICT     81     82       HS -> SH (IN REF. 4).
FT   CONFLICT     85     85       S -> SS (IN REF. 4).
FT   CONFLICT     96     96       E -> Q (IN REF. 4).
SQ   SEQUENCE   105 AA;  11575 MW;  A89F2B09BCFCA018 CRC64;

Query Match             33.4%;  Score 412;  DB 1;  Length 105;
Best Local Similarity   71.4%;  Pred. No. 3.1e-26;  Indels 0;  Gaps 0;
  Matches   75;  Conservative   12;  Mismatches   18;  Indels   18;  Gaps    0;

Qy      132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
                ||::||||||||||||::|||||||:|||||:::| |:| |||||  :|:||||||||||
Db        1 QPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGAVTVDWKVDGTPVTQGMETTQPSKQ 60

Qy      192 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                |||||.||||||||:||.::|||||:|||:|:|:||||:::::|
Db       61 SNNKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKSLSRADCS 105

RESULT 11
LV1B_HUMAN
ID   LV1B_HUMAN     STANDARD;      PRT;   112 AA.
AC   P01700;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region HA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71103824; PubMed=5532227;
RA   Shinoda T., Titani K., Putnam F.W.;
RT   "Amino acid sequence of human lambda chains. II. Chymotryptic
RT   peptides and sequence of protein Ha.";
RL   J. Biol. Chem. 245:4475-4487(1970).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01963; L1HUHA.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11896 MW;  8D73378F3F5CD039 CRC64;

Query Match             33.1%;  Score 407.5;  DB 1;  Length 112;
Best Local Similarity   71.2%;  Pred. No. 7.6e-26;
  Matches   79;  Conservative   17;  Mismatches   14;  Indels    1;  Gaps    1;

Qy       21 ESVLTQPPSVSGAPGQKVTISCTGSTSN-IGGYDLHWYQQLPGTAPKLLIYDINKRPSGI 79
               :||||||||||||||||||||||||||| |||||||||||||||||||||||||||::|
Db        1 QSVLTQPPSVSGTPGQRVTISCSGSSNGTGNNYVYWYQQLPGTAPKLLIYRDDKRPSGV 60

Qy       80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVL 130
               ||||||||||||||||:|||||||||||||.|:|.:|||||||:|||:|
Db       61 PDRFSGSKSGTSASLAISGLRSEDEAHYHCAAWDYRLSAVVFGGGTQLTVL 111

RESULT 12
LV1I_HUMAN
ID   LV1I_HUMAN     STANDARD;      PRT;   109 AA.
AC   P06888;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region EPS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86000126; PubMed=3929803;
RA   Toft K.G., Sletten K., Husby G.;
RT   "The amino-acid sequence of the variable region of a carbohydrate-
RT   containing amyloid fibril protein EPS (immunoglobulin light chain,
RT   type lambda) ";
RL   Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC   -!- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
CC       PEPTIDES WERE POSITIONED BY HOMOLOGY.
DR   PIR; A24656; L1HUEP.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Amyloid; Glycoprotein.
FT   CARBOHYD    104    104       N-LINKED (GLCNAC...).
FT   DISULFID     22     89       BY SIMILARITY.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11414 MW;  556A313E24D5AC73 CRC64;

Query Match             32.6%;  Score 402;  DB 1;  Length 109;
Best Local Similarity   70.3%;  Pred. No. 2e-25;
  Matches   78;  Conservative   16;  Mismatches   15;  Indels    2;  Gaps    1;

Qy       21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
               :||||||||||:|||:|||||.:|:.||||||||||||||||||||||||||||:||
Db        1 QSVLTQPPSLSAAPGQRVSLSCSGSSSNIGKNYVDWYQQLPGTAPKLLIFNNNKRPSGIP 60

Qy       81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLG 131
               ||||||||||||||||||||||||:|||.:|:|.:|||||||||||:|.:|
Db       61 DRFSGSKSGTSATLGITGLQTGDEAIYYCGTWDN--RRSVFGGGTNVTVVG 109

RESULT 13
LAC_RABIT
ID   LAC_RABIT      STANDARD;      PRT;   105 AA.
AC   P01847;
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DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain C region.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82091105; PubMed=6797414;
RA   Garcia I., Jaton J.-C.;
RT   "The primary structure of the constant region of Basilea-rabbit
RT   immunoglobulin lambda-chains.";
RL   Biochem. J. 197:177-183(1981).
CC   -!- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC
CC       SPECIFICITY.
DR   PIR; A02130; L7RB.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER         1      1
FT   DISULFID       27     86
FT   DISULFID      104    104       INTERCHAIN (WITH HEAVY CHAIN).
SQ   SEQUENCE   105 AA;  11484 MW;  B42751327 2E8663D CRC64;

Query Match             32.4%;  Score 399;  DB 1;  Length 105;
Best Local Similarity   72.4%;  Pred. No. 3.3e-25;  Indels  0;  Gaps  0;
Matches  76;  Conservative   9;  Mismatches  20;  Indels   0;  Gaps   0;

Qy  132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
            ||||||||||||||| |||||:: ||:|||| :: |:|| |||
Db    1 QPAVTPSVILFPPSSEELKDNKATLVCLISDFYPRTVKVNWKADGNSVTQGVDTTQPSKQ 60

Qy  192 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
            ||||||:| |||||||| ||::|| :||||||:: |
Db   61 SNNKYAASSFLHLTANQWKSYQSVTCQVTHEGHTVEKSLAPAECS 105

RESULT 14
ID   LV1A_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01699;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region VOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023790; PubMed=809332;
RA   Engelhard M., Hilschmann N.;
RT   "Pattern of antibody structure. The amino acid sequence of a
RT   monoclonal immunoglobulin L-chain of lambde-type, subgroup I
RT   (Bence-Jones-protein Vor.) A contribution to the elucidation of the
RT   origin of antibody specificity.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:1413-1444(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01962; L1HUVO.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Bence-Jones protein.


FT   MOD_RES         1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID       22     89       BY SIMILARITY.
FT   NON_TER       111    111
SQ   SEQUENCE   111 AA;  11514 MW;  21D9F64250DFC8E0 CRC64;

Query Match             32.1%;  Score 396;  DB 1;  Length 111;
Best Local Similarity   65.8%;  Pred. No. 6.1e-25;  Gaps  0;
Matches  73;  Conservative  20;  Mismatches  18;  Indels   0;  Gaps  0;

Qy   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
           :||||||||||| |||| |||: ||:||| :|| |||||||||||||||: :|:||:
Db    1 QSVLTQPPSASGTPGQRVTISCSGGNFDIGRNSVNWYQVHPGTAPRLLIYSSDQRSSGVP 60

Qy   81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLG 131
           ||||||||||:|: |||||||||||||||| || |: ||||||| |||||
Db   61 DRFSGSKSGTSASLAISGLQSENEADYFCATWDDSLDGPVFGGGTKVTVLG 111

RESULT 15
ID   LV2B_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01705;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-II region NEI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72233223; PubMed=5043326;
RA   Garver F.A., Hilschmann N.;
RT   "The primary structure of a monoclonal human lambda-type
RT   immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL   Eur. J. Biochem. 26:10-32(1972).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01970; L2HUNI.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Bence-Jones protein; Glycoprotein.
FT   MOD_RES         1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID       22     90       BY SIMILARITY.
FT   CARBOHYD       96     96       N-LINKED (GLCNAC. . .).
FT   NON_TER       111    111
SQ   SEQUENCE   111 AA;  11591 MW;  AD6D156584D087EB CRC64;

Query Match             32.1%;  Score 396;  DB 1;  Length 111;
Best Local Similarity   68.5%;  Pred. No. 6.1e-25;  Indels  2;  Gaps  2;
Matches  76;  Conservative  17;  Mismatches  16;  Indels   2;  Gaps  2;

Qy   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
           :||||||||:|| |||| ||||||::|:|||||  ||||||||||||| |: :||:||
Db    1 QSALTQPASVSGSPGQSITISCTGTTSDVGSYNFVSWYQQNPGKAPKLMIYEGNKRPSGV 60

Qy   80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVL 130
           |:|||||||||::| |||||||:||||||:|| :||| :: |||||| |||
Db   61 SNRFSGSKSGKTASLTISGLQVEDEADYYCCSYAGN-STRVFGGGTRVTVL 110

Search completed: March 29, 2003, 09:11:15
Job time : 5.62693 secs
```

```
          GenCore version 5.1.4_p5_4578
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        March 29, 2003, 09:06:23 ; Search time 21.4044 Seconds
                                           (without alignments)
                                           2271.829 Million cell updates/sec

Title:         US-09-758-173-10
Perfect score: 1232
Sequence:      1 MRVPAQLLGLLLLWLPGARC..........CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:        671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_21:*
          1: sp_archea:*
          2: sp_bacteria:*
          3: sp_fungi:*
          4: sp_human:*
          5: sp_invertebrate:*
          6: sp_mammal:*
          7: sp_mhc:*
          8: sp_organelle:*
          9: sp_phage:*
         10: sp_plant:*
         11: sp_rodent:*
         12: sp_virus:*
         13: sp_vertebrate:*
         14: sp_unclassified:*
         15: sp_rvirus:*
         16: sp_bacteriap:*
         17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1045	84.8	237	4	Q8WUK4	Q8wuk4 homo sapien
2	1045	84.8	237	4	Q8WTU6	Q8wtu6 homo sapien
3	991.5	80.5	236	4	Q96E61	Q96e61 homo sapien
4	888	72.1	233	4	Q8TBC9	Q8tbc9 homo sapien
5	805.5	65.4	233	4	Q96I69	Q96i69 homo sapien
6	767.5	62.3	240	4	Q8WUK3	Q8wuk3 homo sapien
7	722	58.6	235	11	Q99M11	Q99m11 mus musculu
8	551	44.7	106	4	Q8TCJ5	Q8tcj5 homo sapien
9	488.5	39.7	234	11	Q8VCP0	Q8vcp0 mus musculu
10	472	38.3	130	11	Q9D8W4	Q9d8w4 mus musculu
11	472	38.3	239	4	Q8TCD0	Q8tcd0 homo sapien
12	466	37.8	235	11	Q91W12	Q91w12 mus musculu
13	464.5	37.7	234	11	Q8R062	Q8r062 mus musculu
14	461.5	37.5	238	11	Q8VCI6	Q8vci6 mus musculu
15	453.5	36.8	238	11	Q99M37	Q99m37 mus musculu
16	450.5	36.6	233	11	Q91WS9	Q91ws9 mus musculu
17	447.5	36.3	234	11	Q91WF8	Q91wf8 mus musculu
18	439	35.6	110	4	Q8TE63	Q8te63 homo sapien
19	439	35.6	239	11	Q8VC55	Q8vc55 mus musculu
20	433.5	35.2	234	11	Q8R028	Q8r028 mus musculu
21	410.5	33.3	214	11	Q8R1A5	Q8r1a5 mus musculu
22	385	31.2	108	4	Q96B0	Q96b0 homo sapien
23	378	30.7	116	4	Q96JD0	Q96jd0 homo sapien
24	375.5	30.5	105	11	Q99JC1	Q99jc1 mus musculu
25	373	30.3	112	4	Q96JD2	Q96jd2 homo sapien
26	349.5	28.4	112	4	Q96JD1	Q96jd1 homo sapien
27	332	26.9	107	4	Q9NSD6	Q9nsd6 homo sapien
28	292.5	23.7	684	13	Q90544	Q90544 ginglymosto
29	287.5	23.3	107	4	Q9UL82	Q9ul82 homo sapien
30	283	23.0	268	13	Q90524	Q90524 ginglymosto
31	282.5	22.9	127	11	Q92589	Q92589 mus musculu
32	268.5	21.8	267	13	Q90529	Q90529 ginglymosto
33	265.5	21.6	134	11	Q8VDD0	Q8vdd0 mus musculu
34	262	21.3	109	4	Q9UL78	Q9ul78 homo sapien
35	260	21.1	471	4	Q8TC77	Q8tc77 homo sapien
36	258	20.9	257	13	Q90536	Q90536 ginglymosto
37	255	20.7	101	11	Q9JL78	Q9jl78 mus musculu
38	250.5	20.3	259	11	Q90530	Q90530 ginglymosto
39	250.5	20.3	469	11	Q8R3V9	Q8r3v9 mus musculu
40	249.5	20.3	252	13	Q90568	Q90568 ginglymosto
41	246	20.0	109	4	Q9UL86	Q9ul86 homo sapien
42	245	19.9	106	5	Q9U410	Q9u410 schistosoma
43	245	19.9	107	4	Q96SA9	Q96sa9 homo sapien
44	243	19.7	109	4	Q9UL85	Q9ul85 homo sapien
45	241.5	19.6	484	11	Q8VEA0	Q8vea0 mus musculu

ALIGNMENTS

```
RESULT 1
Q8WUK4
ID   Q8WUK4          PRELIMINARY;      PRT;    237 AA.
AC   Q8WUK4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 24.9 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020233; AAH20233.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  24897 MW;  73C7D70B8039D186 CRC64;

Query Match             84.8%;  DB 4;  Length 237;
Best Local Similarity   88.4%;  Pred. No. 6.1e-82;
Matches  205;  Conservative   10;  Mismatches   15;  Indels    2;  Gaps    2;

Qy     7 LLGLLLWLPGARCRSVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
           : .||:  |||||||||||||||:||||||||||:||| :||||||||||||||
Db     6 LLLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65

Qy    66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNA-QVFGGG 124
```

Db |||||: . |||||: . |||||||||||||||||||||||||: . |||||||||||||||||||||: . ||||||
          66 KLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGFVVFGGG 125

Qy   125 TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
             |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185

Qy   185 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237

RESULT 2
Q8WTU6
ID   Q8WTU6   PRELIMINARY;   PRT;   237 AA.
AC   Q8WTU6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 24.9 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022098; AAH22098.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;   24884 MW; E6CF371E753968E8 CRC64;

Query Match   84.8%; Score 1045; DB 4; Length 237;
Best Local Similarity   88.4%; Pred. No. 6.1e-82;
Matches 205; Conservative 10; Mismatches 15; Indels   2; Gaps   2;

Qy   7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
             |: .:|||||||||: . ||||||||||||||||||||||||||| |||||||||||||
Db   6 LLLTLLAHCTGSWAQSVLAQPPSVSGAPGQVTVISCTGSSNIGAGYDVHWYQQLPGTAP 65

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGG 124
             |: . |||||||||: .|||||||||||:||||||||||:||||||||||: |||||
Db   66 KLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDYSLSASGVFGGG 125

Qy   125 TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185

Qy   185 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237

RESULT 3
Q96E61
ID   Q96E61   PRELIMINARY;   PRT;   236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown protein for MGC:17259).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;   24712 MW; 7EC9FB3622FED957 CRC64;

Query Match   80.5%; Score 991.5; DB 4; Length 236;
Best Local Similarity   83.1%; Pred. No. 2.4e-77;
Matches 192; Conservative 12; Mismatches 26; Indels   1; Gaps   1;

Qy   7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
             |: .:|||||||||: . ||||||||||||||||||||||||| |||||||||||||
Db   6 LLLTLLAHCTGSWAQSVLAQPPSVSGAPGQTVTISCTGSSNIGAGYAVHWYQQFPGAAP 65

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
             |: . |||||||||: . |||||||||||:||||||||||:|||||||||| |: .||||
Db   66 KVLIYGNVNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGAGT 125

Qy   126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
             |||||||||: . |||||||||||||||||||||||||||||||||||||||||||||||
Db   126 KVTVLGQPXANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVET 185

Qy   186 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 TKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4
Q8TBC9
ID   Q8TBC9   PRELIMINARY;   PRT;   233 AA.
AC   Q8TBC9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 24.9 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022823; AAH22823.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;   24867 MW; 367411BFD6F4DF92 CRC64;

Query Match   72.1%; Score 888; DB 4; Length 233;
Best Local Similarity   74.0%; Pred. No. 1.8e-68;
Matches 174; Conservative 16; Mismatches 33; Indels 12; Gaps   2;

Qy   12 LLWLP--------GARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLP 61
             ||: .|: | : .|||||||||||: . ||||||||||||: .||||||||||
Db   1 MAWIPLLLPLLTLCTGSEASYELTQPPSVSVSPGQTARITCSGDA--LPKQYAYWYQQKP 58

Qy   62 GTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVF 121
             |: . |||: . |||||||||||||||||||||||: . |||||||||||||||||
Db   59 GQAPVLVIYKDNERPSGIPERFSGSSGTVTLTISGVQAEDEADYYCQSADSSGTYWVF 118

Qy   122 GGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA 181
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 GGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA 178

Qy   182 GVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db    179 GVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 5
Q96I69
ID   Q96I69       PRELIMINARY;       PRT;    233 AA.
AC   Q96I69;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:12849).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-CELL;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC007782; AAH07782.1; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE  233 AA;  24802 MW;  C694F8397B27650B CRC64;

Query Match             65.4%;  Score 805.5;  DB 4;  Length 233;
Best Local Similarity   70.0%;  Pred. No. 2.2e-61;
Matches  161;  Conservative   21;  Mismatches   45;  Indels    3;  Gaps    2;

Qy      7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
          ||| ||| ||  |||||||||||||||||| ||||| : ||:|:||||||||||| ::||
Db      7 LLG-LLSHCTGSGTSVVLTQPASVSVAPGQTARITCGG--SNLGSKSVNWYQLRPGQAPI 63

Qy     67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
          |:|: :|:|| : :|||||||||||||: |||||||||||| ||| ||||  ||| |||
Db     64 LVVYENKERPAGIPERLSALTSEETATLTISSVVAGDEADYFCQVWDTTSQQYVFGTGTQ 123

Qy    127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
          :|||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||
Db    124 VTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETT 183

Qy    187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 KPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 6
Q8WUK3
ID   Q8WUK3       PRELIMINARY;       PRT;    240 AA.
AC   Q8WUK3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.0 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020236; AAH20236.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
KW   Hypothetical protein; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE  240 AA;  25977 MW;  921E47DDCA7259F0 CRC64;

Query Match             62.3%;  Score 767.5;  DB 4;  Length 240;
Best Local Similarity   69.2%;  Pred. No. 4.2e-58;
Matches  153;  Conservative   21;  Mismatches   38;  Indels    9;  Gaps    4;

Qy     23 VLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIY----DINKRPSG 78
          |||||||||||||||||||||||||||||||||||||||||||| :|:    :|||||||
Db     22 VLTQPPSASAFLGASIKLTCTLSREH-SSYTIEWYQQRPGRSPQYIMKVKSDGSHNKGDG 80

Qy     79 ISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ---VFGGGTRLTVLGQPKA 135
          ||||:||| ||||: |||:| :|||||||||||||: ::|   | ||||| ||||||||
Db     81 IPDRFMGSSSGADRYLTLSNLQSDDEAEYHC-GESHTIDGQVGWVFGGGTKLTVLSQPKA 139

Qy    136 APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK 195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK 199

Qy    196 YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||
Db    200 YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 240

RESULT 7
Q99M11
ID   Q99M11       PRELIMINARY;       PRT;    235 AA.
AC   Q99M11;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 25.4 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002129; AAH02129.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE  235 AA;  25403 MW;  39807BFE6782A3FB CRC64;

Query Match             58.6%;  Score 722;  DB 11;  Length 235;
Best Local Similarity   61.1%;  Pred. No. 3.3e-54;
Matches  143;  Conservative   29;  Mismatches   58;  Indels    4;  Gaps    2;

Qy      5 AQLLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTA 64
          | |||:|::|||||| |||||||||||: |:|||:||:| ||||||||||||||||||
Db      4 APLLLVFLHHLTGSCAQLVLTQPSSVSTSLGSTAKLPCKASTGNIGDSYVNWYQQYMGRS 63

Qy     65 PKLLIYDINKRPSGISDRFSGS--KSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFG 122
          | ||| :|:||||| |||||||  |||:||:||: :||| ||||||||||| : |||
Db     64 PTNMIYGDDLRPSGVSDRFSGSIDSSSNSAFLTIQNVQADDEADYYCQSYSSGI--RVFG 121
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KW   Hypothetical protein.
SQ   SEQUENCE  234 AA;  25702 MW;  10255lC58AC2FA9F CRC64;

Query Match            39.7%;   Score 488.5;  DB 11;   Length 234;
Best Local Similarity  44.8%;   Pred. No. 3.6e-34;
Matches 107; Conservative 42; Mismatches 81; Indels 9; Gaps 7;

Qy     1 MRVPAQLLGLLLWLPGARCESVLTQ-PPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQ 59
           |||||||||||||||  ||||| : ||| ||||| | |||||  | | ||| | ||||||
Db     1 MSVPFQVLGLLLLCLTGARCDIQLTQSPASLSASVGETVTITCRAS-ENIYSY-LAWYQQ 58

Qy    60 LPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYCCQSYDSSLNAQ 119
           |||:||| | :||| :|||   |:||||||  | :| | |  ||:|| || |: :| ||
Db    59 KQGKSPQLLVYNAKTLADGVPSRFSGSRSGTQFSLKINSLQPEDFGSYYCQHHSGI--PF 116

Qy   120 VFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV 179
           ||||||||||  | ||||||||||||||  |||||| ||||||||||||||||| || |
Db   117 TFGSGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 175

Qy   180 KAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 235
           ||||  | | | :|||||||||||:||:|| : :|| |:|  | | :   ||||| |||
Db   176 QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234

RESULT 8
Q8TCJ5
ID   Q8TCJ5        PRELIMINARY;    PRT;    106 AA.
AC   Q8TCJ5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 11.3 kDa protein (Fragment).
GN   DKFZP667J0810.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH NODE;
RA   Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL713800; CAD28551.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE  106 AA;  11265 MW;  145272BB65F4565 CRC64;

Query Match            44.7%;   Score 551;  DB 4;   Length 106;
Best Local Similarity  99.1%;   Pred. No. 5.4e-40;
Matches 105; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   131 GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK 190
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK 60

Qy   191 QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
           |||||||||||||||||||||||||| ||||||||||||||||||||
Db    61 QSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGHTVEKTVAPTECS 106

RESULT 9
Q8VCP0
ID   Q8VCP0        PRELIMINARY;    PRT;    234 AA.
AC   Q8VCP0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 25.7 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019474; AAH19474.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IGc1; 1.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.

Qy   123 GGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 182
           |||||||| ||| ||||||||||||||  ||| |||||| ||| ||||||||| |||| |
Db   122 GGTKLTVLSQPKTSPSVTLFPPSSEELETNKATLVCTISDFYPGVTTVDWKADGTPVTQG 181

Qy   183 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
           |||| ||||||||||| | ||| ||| ||  | :|||||| | |||| || |
Db   182 VETTQPSKQNNNKYMASSYLTLTAKAWETHSSYSCQVTHEGHTVEKSLSRADCS 235
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RESULT 10
Q9D8W4
ID   Q9D8W4        PRELIMINARY;    PRT;    130 AA.
AC   Q9D8W4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810027O01Rik protein.
GN   1810027O01RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto Y.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007622; BAB25142.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:1916426; 1810027O01Rik.
DR   InterPro; IPR003599; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE  130 AA;  14253 MW;  4381797SE766E54 CRC64;

Query Match            38.3%;   Score 472;  DB 11;   Length 130;
Best Local Similarity  69.6%;   Pred. No. 4.3e-33;
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Matches       87;  Conservative   15;  Mismatches   23;  Indels    0;  Gaps    0;

Qy    112 YDSSLNAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA 171
              :::||||||||||||||:|||||||||||||||||||||||||||||||||||:|||
Db      6 HESISQCWVFGGGTKLTVLGQPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVD 65

Qy    172 WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA 231
              ||| ::|||||||||||||||||||||||||||||||||||||||||||:|||||
Db     66 WKVDGTPVTQGMETTQPSKQSNNKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKSLS 125

Qy    232 PTECS 236
              :|||
Db    126 RADCS 130

RESULT 11
Q8TCD0
ID   Q8TCD0;
AC   Q8TCD0;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.2 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022362; AAH22362.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   239 AA;  26234 MW;  FACEDC3A3B03871D CRC64;

Query Match             38.3%;  Score 472;  DB 4;  Length 239;
Best Local Similarity   42.0%;  Pred. No. 9.7e-33;
Matches      102;  Conservative   52;  Mismatches   77;  Indels   12;  Gaps    7;

Qy      1 MRVPAQLLGLLLWLPGARCESVLTQPP-SVSGAPGQKVTISCTGTSNI--GGYDLHW 56
            ||||||||||:|:||: :|||||||: |||||||||  |||:|
Db      1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNW 60

Qy     57 YQQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSL 116
            |||| ||:|||||:|  :||  :: |:||:  ::: ||:
Db     61 FQQRPGQSPPRLIYKVSNRDSGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCM--QGTH 118

Qy    117 NAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS 176
            ||| ||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119 WPSTFGGGTKLEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN 177

Qy    177 SPVKAG--VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAP 232
            ||:|::  :|| ||  :: :|: |:::|
Db    178 A-LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR 236

Qy    233 TEC 235
            :||
Db    237 GEC 239

RESULT 12
Q91W12
ID   Q91W12;
AC   Q91W12;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:6582).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST TUMOR;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006643; AAH06643.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE   235 AA;  26021 MW;  5F73BDEBD5B8FEF CRC64;

Query Match             37.8%;  Score 466;  DB 11;  Length 235;
Best Local Similarity   44.1%;  Pred. No. 3.1e-32;
Matches       98;  Conservative   47;  Mismatches   67;  Indels   10;  Gaps    6;

Qy     18 ARCESVLTQPPSV-SGAPGQKVTISCTGTSNIGGYDLHWYQQLPGTAPKLLIYDINKRP 76
            :: ||||||:  :|||||| ||||:|||:| |: |||||
Db     20 SRGQIVLTQSPAIMSASPGERVTMTCSASSS---VSHMHWYQQKSGTSPKRWIYDTFKLT 76

Qy     77 SGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAA 136
            |||:|||||:  ||| ||| || ||: |:|| ::: |:|
Db     77 SGVPDRFSGSGSGTSYSLTISNMEAEDVATYYCQQW--SRNPFTFGVGTKLE-LKRADAA 133

Qy    137 PSVTLFPPSSELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV-ETTTPSKQSNNK 195
            ||::|||||||||||||||||||||||||||| || ||: :::: |||:
Db    134 PTVSIFPPSSEQLTSGGASVVCFLNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDST 193

Qy    196 YAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 235
            |:::| ::: ::|||:  :||||||||||:|   |:|
Db    194 YSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235

RESULT 13
Q8R062
ID   Q8R062;
AC   Q8R062;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 25.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027418; AAH27418.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25857 MW;  4EB08C81426AEAB1 CRC64;

Query Match             37.7%;  Score 464.5;  DB 11;  Length 234;
Best Local Similarity   44.4%;  Pred. No. 4.2e-32;
Matches      106;  Conservative   40;  Mismatches   84;  Indels    9;  Gaps    7;

Qy      1 MRVPAQLLGLLLWLPGARCESVLTQ-PPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQ 59
            |: | ||:||||  :  | :| |::|| ||| ::::|
Db      1 MMSSAQFLGLLLCFQGTRCDIQMTQTTSSLASLGDRVTISCSAS-QGISNY-LNWYQQ 58

Qy     60 LPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ 119
            ||| ||||| : |:|||||| || || ||::|:: |:||
Db     59 KPDGTVKLLIYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPDIATYYCQQY--SQPPF 116

Qy    120 VFGGGTRLTVLGQPKAAPSVTLFPPSSELQANKATLVCLISDFYPGAVTVAWKADSSPV 179
            ||||||:|: |: || :|||||||| |:|:|| ||
Db    117 TFGSGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 175

Qy    180 KAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 235
            |:| :||: ::|: :: :|||||||| |:|
Db    176 QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
```

RESULT 14
Q8VCI6
```
ID   Q8VCI6      PRELIMINARY;      PRT;     238 AA.
AC   Q8VCI6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created).
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.2 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019760; AAH19760.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 238 AA;  26224 MW;  35EC08E3DE5414AD CRC64;

Query Match     37.5%;  Score 461.5;  DB 11;  Length 238;
  Best Local Similarity   40.9%;  Pred. No. 7.7e-32;
  Matches   99;  Conservative  53;  Mismatches 79;  Indels  11;  Gaps   7;

Qy     1 MRVPAQLGLLLLWLPGARCESVLTQPP-SVSGAPGQKVTISCTGSTSNI--GGYDLHW 56
Db     1 MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLHW 59

Qy    57 YQQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSL 116
Db    60 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS--QSTH 117

Qy   117 NAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS 176
Db   118 VPPTFGGGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDG 176

Qy   177 SPVKAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPT 233
Db   177 SERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRN 236

Qy   234 EC 235
Db   237 EC 238
```

RESULT 15
Q99M37
```
ID   Q99M37      PRELIMINARY;      PRT;     238 AA.
AC   Q99M37;
DT   01-JUN-2001 (TrEMBLrel. 17, Created).
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 26.3 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002635; AAH02035.1; -.
```

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DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 238 AA;  26344 MW;  FB2B06A0B801330A CRC64;

Query Match     36.8%;  Score 453.5;  DB 11;  Length 238;
  Best Local Similarity   40.5%;  Pred. No. 3.8e-31;
  Matches   98;  Conservative  52;  Mismatches 81;  Indels  11;  Gaps   7;

Qy     1 MRVPAQLLGLLLLWLPGARCESVLTQPP-SVSGAPGQKVTISCTGSTSNI--GGYDLHW 56
Db     1 MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEW 59

Qy    57 YQQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSL 116
Db    60 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC--FQGSH 117

Qy   117 NAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS 176
Db   118 VPYTFGSGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDG 176

Qy   177 SPVKAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPT 233
Db   177 SERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRN 236

Qy   234 EC 235
Db   237 EC 238
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Search completed: March 29, 2003, 09:14:40
Job time : 21.4044 secs

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                GenCore version 5.1.4_p5_4578
        Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:       March 29, 2003, 09:06:23 ; Search time 24.273 Seconds
                                          (without alignments)
                                          1295.559 Million cell updates/sec

Title:        US-09-758-173-10
Perfect score: 1232
Sequence:     1 MRVPAQLLGLLLLWLPGARC........CQVTHEGSTVEKTVAPTECS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:     908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:      908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    A_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1232	100.0	236	19	AAW63764	Macaque primatized
2	1232	100.0	236	23	AAU11645	Protein sequence o
3	1229	99.8	236	18	AAW01821	Primatised anti-hu
4	1052.5	85.4	236	22	AAB36209	Human immune syste
5	1006	81.7	235	20	AAW88465	Monoclonal antibod
6	1001	81.2	236	22	ABG23083	Novel human diagno
7	979.5	79.5	217	14	AAR42163	Anti-HIV-1 recombi
8	973	79.0	234	18	AAW01817	Primatised anti-hu
9	973	79.0	234	19	AAW63760	Macaque primatized
10	973	79.0	234	23	AAU11538	Protein sequence o
11	971.5	78.9	217	19	AAW40533	Antibody HB4C5 lig
12	968.5	78.6	248	22	ABG26352	Novel human diagno
13	965	78.3	235	22	AAB36212	Human immune syste
14	965	78.3	235	22	AAB36214	Human immune syste
15	958.5	77.8	236	22	ABG19293	Novel human diagno
16	957	77.7	235	22	AAG64472	Human type antihum
17	957	77.7	614	23	ABB06275	Plasmid scFv(CC046
18	955	77.5	235	14	AAR31024	Antibody D light c
19	950.5	77.2	219	21	AAB30594	Variable and first
20	945	76.7	235	22	AAG64474	Human type antihum
21	945	76.7	235	22	AAG64476	Human type antihum
22	944	76.6	249	22	ABG12886	Novel human diagno
23	941	76.4	244	22	ABG19296	Novel human diagno
24	935	75.9	235	22	AAG64470	Human type antihum
25	934.5	75.8	250	22	ABG19301	Novel human diagno
26	934	75.8	235	22	ABG19290	Novel human diagno
27	927	75.2	251	22	ABG19291	Novel human diagno
28	911.5	74.0	236	22	ABG22850	Novel human diagno
29	898	72.9	235	22	AAM78781	Human protein SEQ
30	891.5	72.4	236	22	ABG19298	Novel human diagno
31	890	72.2	235	21	AAB15547	Human immune syste
32	888	72.1	218	22	AAU08381	Anti-OPGbp antibod
33	885	71.8	235	22	AAW75214	Human secreted pro
34	884	71.8	233	9	AAP81260	VDJC regions of hu
35	882	71.6	235	19	AAW75231	Human secreted pro
36	877	71.2	238	22	ABG19299	Novel human diagno
37	876	71.1	233	23	AAU82012	Human secreted pro
38	875	71.0	238	22	ABG19297	Novel human diagno
39	871.5	70.7	232	22	AAU14412	Human novel protei
40	867.5	70.4	232	22	AAM23527	Human EST encoded
41	866	70.3	231	22	AAU14176	Human novel protei
42	866	70.3	231	22	ABP41361	Human ovarian anti
43	863.5	70.1	269	23	ABG19295	Novel human diagno
44	857.5	69.6	233	18	AAW14924	Ant-CD4 monkey-hum
45	854.5	69.4	244	21	AAB43979	Human cancer assoc

ALIGNMENTS

```
RESULT 1
AAW63764
ID   AAW63764 standard; Protein; 236 AA.
XX
AC   AAW63764;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 16C10 light chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35488.
XX
```

```
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5a; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 16C10 light
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence  236 AA;

Query Match             100.0%;  Score 1232;  DB 19;  Length 236;
Best Local Similarity   100.0%;  Pred. No. 1.2e-66;
Matches  236;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60

Qy    61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy   181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 2
AAU11645
ID   AAU11645 standard; Protein; 236 AA.
XX
AC   AAU11645;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Protein sequence of primatised form of the light chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
```

```
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   N-PSDB; AAS17246.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 5a; 99pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present protein
CC   sequence represents the light chain of 16C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence  236 AA;

Query Match             100.0%;  Score 1232;  DB 23;  Length 236;
Best Local Similarity   100.0%;  Pred. No. 1.2e-66;
Matches  236;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60

Qy    61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy   181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 3
AAW01821
ID   AAW01821 standard; Protein; 236 AA.
XX
AC   AAW01821;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 light chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
```

KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996; 96WO-US10053.
XX
PR   07-JUN-1995; 95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT62512.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease.
XX
PS   Claim 14; Fig 10A; 81pp; English.
XX
CC   2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC   heavy variable genes (see also AAT62512 and AAT62513) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 236 AA;

Query Match   99.8%; Score 1229; DB 18; Length 236;
Best Local Similarity 99.6%; Pred. No. 1.8e-66;
Matches 235; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60

Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy   181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4
AAB36209
ID   AAB36209 standard; protein; 236 AA.
XX
AC   AAB36209;
XX
DT   15-FEB-2001 (first entry)
XX
DE   Human immune system associated protein HISAP-7.

XX
KW   Human; immune system associated protein; HISAP-7; immune disorder;
KW   infection; autoimmune disease; cancer.
XX
OS   Homo sapiens.
XX
PN   US613941-A.
XX
PD   24-OCT-2000.
XX
PF   27-MAR-1998; 98US-0049672.
XX
PR   27-MAR-1998; 98US-0049672.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI   Hillman JL, Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   N-PSDB; AAC66525.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing
PT   immune or cell proliferative disorders or infections -
XX
PS   Claim 1; Column 59-62; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ   Sequence 236 AA;

Query Match   85.4%; Score 1052.5; DB 22; Length 236;
Best Local Similarity 88.3%; Pred. No. 6.6e-56;
Matches 204; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

Qy   7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
          ||| :|: ||||:|||||:||||||||||||| :|| || |||||
Db   6 LLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65

Qy   66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
          |||| |:|||||||: |||||||||:||||||||:||||||||||||||||: :||||||
Db   66 KLLIYGSRNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGVVFGGGT 125

Qy   126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
          :||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db   126 KLTVLGQPKAAPSVTLFPPSSEELQANRATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185

Qy   186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 5
AAW88465
ID   AAW88465 standard; Protein; 235 AA.
XX
AC   AAW88465;
XX
DT   10-MAY-1999 (first entry)
XX
DE   Monoclonal antibody 4B5 light chain variable region.
XX
KW   Antigen binding fragment 4B5; monoclonal antibody; cancer;
KW   neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
KW   sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;

```
KW   GD2 antigen; human.
XX
OS   Homo sapiens.
XX
PN   WO9902545-A2.
XX
PD   21-JAN-1999.
XX
PF   08-JUL-1998;   98WO-IB01046.
XX
PR   08-JUL-1997;   97US-0051945.
XX
PA   (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI   Dan MD;
XX
DR   WPI; 1999-120769/10.
DR   N-PSDB; AAX06953.
XX
PT   New antibody 4B5 polynucleotides and polypeptides - used to develop
PT   products for the diagnosis and treatment of cancers and for
PT   prophylactic therapy to reduce risk of recurrence
XX
PS   Claim 1; Page 81; 83pp; English.
XX
CC   This polypeptide comprises the light chain variable region of the
CC   recombinant human monoclonal antibody (MAb) 4B5.  4B5 recognises
CC   antibodies specific for GD2 antigen antibodies.  Antibodies
CC   specific for GD2 recognise various cancers including glioblastoma,
CC   neuroblastoma, malignant and/or metastatic melanoma, breast
CC   adenocarcinoma, lung adenocarcinoma, small cell lung carcinoma,
CC   colon adenocarcinoma and prostate adenocarcinoma.  The invention
CC   encompasses 4B5 derivatives with immunologic specificity for
CC   antibodies specific for GD2.  These derivatives, or antigen binding
CC   fragments, comprise regions of the 4B5 VDJ junction and regions
CC   spanning the 4B5 CDRs.  Other derivatives include Fab, F(ab')2,
CC   Fab', scFv and isolated heavy and light chains (see also AAW88464).
CC   Polynucleotide fragments (see AAX06951-54) encoding 4B5 antibody V
CC   regions are also provided, and therapeutic plasmids and vectors,
CC   including vaccinia virus vectors, comprising these polynucleotides.
CC   4B5 has been shown to mimic GD2, and is particularly useful in
CC   generating a host immune response to cancer.  Products of the
CC   invention can be used in the detection and treatment of e.g.
CC   astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
CC   primitive neural ectodermal tumour (PNET), pancreatic ductal
CC   adenocarcinoma, small and large cell lung adenocarcinoma,
CC   squamous cell carcinoma, bronchoalveoarcarcinoma, epithelial
CC   adenocarcinoma, and liver metastases; hepatoma, cholangiocarcinoma,
CC   breast tumours such as ductal and lobular adenocarcinoma, squamous
CC   and adenocarcinomas of the uterine cervix, uterine and ovarian
CC   epithelial carcinoma, prostatic adenocarcinoma, transitional
CC   squamous cell carcinoma of the bladder, B and T cell lymphoma
CC   (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC   malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
XX
SQ   Sequence  235 AA;

Query Match        81.7%;  Score 1006;  DB 20;  Length 235;
Best Local Similarity   83.9%;  Pred. No. 4e-53;
Matches 193;  Conservative 14;  Mismatches 23;  Indels 0;  Gaps 0;

Qy   7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
         |||||||||||||||||||||| ||||||||||||:||||||||||||||||||||||||
Db   6 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSSNSNIGSKTVNWYQQLPGTAPK 65

Qy  67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
         |||:|||:|||||:|||||||||||:||||| ||||||||||||:|| |||||::|||||:
Db  66 FLIYSNNQRPSGSVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTK 125

Qy 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
         ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db 126 LTVLGQPKAAPSVTLFPPSSEELQANKPTLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

Qy 187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235
```

```
RESULT 6
ABG23083
ID   ABG23083 standard; Protein; 236 AA.
XX
AC   ABG23083;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #23074.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS87270.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 53442; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II), is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence  236 AA;

Query Match        81.2%;  Score 1001;  DB 22;  Length 236;
Best Local Similarity   83.5%;  Pred. No. 8e-53;
Matches 192;  Conservative 18;  Mismatches 20;  Indels 0;  Gaps 0;

Qy   7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
         ||| || |||||||||||||||:||||:||||||||||||:::||||||||||||||||||
```

```
Db      7 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGASSNIGTNDVYWYQQLTGTAPK 66
          |||     ||| |||||||||||||||| ||||||:||||||::||||  :|:|| ||| ||
Qy     67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
          |||      :||||:||||||||||||  :|||:||:|:|||||| ::|||   |||||
Db     67 LLIYRNNQRPSGVPDRFSGSKSGSGSSASLAISGLQSDEADYYCAAWDDSLSGPVFGGGTK 126

Qy    127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186

Qy    187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
```

RESULT 7
AAR42163
ID   AAR42163 standard; Protein; 217 AA.
XX
AC   AAR42163;
XX
DT   27-APR-1994   (first entry)
XX
DE   Anti-HIV-1 recombinant antibody 447-52D light chain.
XX
KW   Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW   HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW   acquired immune deficiency syndrome; chimeric antibody;
KW   surface glycoprotein gp120; V3 loop.
XX
OS   Homo sapiens.
XX
PN   WO9319785-A.
XX
PD   14-OCT-1993.
XX
PF   23-MAR-1993;   93WO-US02629.
XX
PR   01-APR-1992;   92US-0861701.
XX
PA   (MERI) MERCK & CO INC.
PA   (JOHN/) JOHNSON L S.
PA   (PFAR/) PFARR D S.
XX
PI   Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;
XX
DR   WPI; 1993-336600/42.
DR   N-PSDB; AAQ49835.
XX
PT   New recombinant human antibody - with HIV neutralising activity
PT   against at least two isolates, useful for preventing or treating
PT   infection in diagnosis, etc.
XX
PS   Example 9; Fig 2B; 154pp; English.
XX
CC   EBV-transformed cell lines and mouse-human heterohybridomas
CC   producing human MAbs specific for the gp120 V3 loop of HIV-1 MN
CC   isolate were obtained. MAb 447-52D was found to recognise the
CC   tetrapeptide motif GPGR, i.e. the Principal Neutralising
CC   Determinant common to the V3 loop of different HIV isolates.
CC   A recombinant Ab was produced in which the L chain V region was
CC   derived from 447-52D and to which a signal sequence and a L chain
CC   intronic sequence are appended, fused to a fragment contg. a short
CC   intronic segment of the human lambda 2 C region and the human
CC   lambda 2 constant encoding domain.
XX
SQ   Sequence   217 AA;

Query Match   79.5%;   Score 979.5;   DB 14;   Length 217;
Best Local Similarity   87.6%;   Pred. No. 1.4e-51;
Matches 190; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

```
Qy     21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
```

```
Db        :||||||||||||||||||||:|||:||||  :||||  |||||||||||
        1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVLWYQQFPGTAPKLLIYGNNKRPSGIP 60

Qy     81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGGTRLTVLGQPKAAPSV 139
          ||||||:::|::|||||||||||||||:|:||||||||    :||||||||||:||||||
Db     61 DRFSGSKSGTSATLGITGLQTGDEADYFCATWDGSLSADWFGGGTKLTVLSQPKAAPSV 120

Qy    140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 180

Qy    200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
          |||||||||||||||||||||||||||||||||||||
Db    181 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 217
```

RESULT 8
AAW01817
ID   AAW01817 standard; Protein; 234 AA.
XX
AC   AAW01817;
XX
DT   25-MAY-1997   (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 light chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US10053.
XX
PR   07-JUN-1995;   95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT62509.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 6; Fig 8A; 81pp; English.
XX
CC   2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
CC   variable genes (see also AAT62509 and AAT62510) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   234 AA;

Query Match   79.0%;   Score 973;   DB 18;   Length 234;
Best Local Similarity   80.1%;   Pred. No. 3.7e-51;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

Qy   MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
      |||||||||||||||||||| |||| :||||
Db   MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58

Qy 61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
      ||| :|| : ||| | |||||| :|| : | | |: : :
Db 59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118

Qy 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
       |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178

Qy 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 9
AAW63760
ID   AAW63760 standard; Protein; 234 AA.
XX
AC   AAW63760;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 7C10 light chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35484.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3a; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7C10 light
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   MAb's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions

CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 234 AA;

Query Match   79.0%;   Score 973;   DB 19;   Length 234;
Best Local Similarity   80.1%;   Pred. No. 3.7e-51;
Matches 189; Conservative 13; Mismatches 32; Indels   2; Gaps 1;

Qy   1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
        |||||||||||||||||||| |||| :||||
Db   1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58

Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
        ||| :|| : ||| | |||||| :|| : | | |: : :
Db   59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118

Qy 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
        |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178

Qy 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 10
AAU11538
ID   AAU11538 standard; Protein; 234 AA.
XX
AC   AAU11538;
XX
DT   12-MAR-2002 (first entry)
XX
DE   Protein sequence of primatised form of the light chain of 7C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   N-PSDB; AAS17242.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   (CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 3a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is

CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present protein
CC   sequence represents the light chain of 7C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 234 AA;

Query Match   79.0%;   Score 973;   DB 23;   Pred. No. 3.7e-51;
Best Local Similarity   80.1%;
Matches 189; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

Qy   1 MRVPAQLLGLLLLWLPGARCSVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
         |||||||||||||||||||||| ||||||:|||||||| :|:| |||||||||
Db   1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58

Qy   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
         | |:|||||||:|:::||||| |::|||||| |:||||||||||||:|| |::: :
Db   59 PARAPILVIYDDSDRPSGIPRFSGSKSGNTATLTINGVEAGDEADYYCQWDRASDHPV 118

Qy 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178

Qy 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 11
AAW40533
ID   AAW40533 standard; Protein; 217 AA.
XX
AC   AAW40533;
XX
DT   27-AUG-1998 (first entry)
XX
DE   Antibody HB4C5 light chain sequence.
XX
KW   Antibody light chain; carboxypeptidase; bovine pancreas; cancer;
KW   porcine pancreas; radioimminoimaging.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Region   1..112
FT   /note= "light chain fragment that is claimed for in
FT   claim 11"
FT   Domain   23..35
FT   /note= "complementarity determining region (CDR) -1;
FT   sequence claimed in claim 17"
FT   Domain   51..57
FT   /note= "complementarity determining region (CDR) -2;
FT   sequence claimed in claim 17"
FT   Domain   90..101
FT   /note= "complementarity determining region (CDR) -3;
FT   sequence claimed in claim 17"
XX
PN   JP10075791-A.
XX
PD   24-MAR-1998.
XX

PF   30-AUG-1996;   96JP-0246825.
XX
PR   30-AUG-1996;   96JP-0246825.
XX
PA   (MOMI) MORINAGA & CO LTD.
XX
DR   WPI; 1998-244364/22.
DR   N-PSDB; AAV11293.
XX
PT   New antibody light chain or its fragment - useful for preparation of
PT   therapeutic(s) or cancer radio-immuno-imaging agent(s)
XX
PS   Claim 10; Fig 11; 20pp; Japanese.
XX
CC   This represents a antibody HB4C5 light chain. This antibody light chain
CC   or its fragment is specific for carboxypeptidase from bovine or porcine
CC   pancreas and is reactive with human cancer tissue. The antibody light
CC   chain and its fragment can be used for preparation of a cancer
CC   radioimmunoimaging reagent and therapeutic compositions.
XX
SQ   Sequence 217 AA;

Query Match   78.9%;   Score 971.5; DB 19;   Length 217;
Best Local Similarity   86.6%;   Pred. No. 4.3e-51;
Matches 188; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
         :||||||||||||||||||||||||||:|||:||||||||| |||||||||||||||||
Db   1 QSVLTQPPSVSAAPGQKVTISCSGNSSNIGNNYVSWYQHLPGTAPKLLIYDNNKRPSSIP 60

Qy   81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGGTRLTVLGQPKAAPSV 139
         ||||||||||:|: ||||||| || |||||| :: :| |||||:|||||||||||
Db   61 DRFGGSKSGTSATLGITGLQTGDEADYYCATWTSILRVNWLFGGGTKLTVLGQPKAAPSV 120

Qy 140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 180

Qy 200 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||||||||
Db 181 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 217

RESULT 12
ABG26352
ID   ABG26352 standard; Protein; 248 AA.
XX
AC   ABG26352;
XX
DT   18-FEB-2002 (first entry)
XX
DE   Novel human diagnostic protein #26343.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C,   Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS90539.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 56711; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 248 AA;

Query Match   78.6%; Score 968.5; DB 22; Length 248;
Best Local Similarity   79.2%; Pred. No. 7.4e-51;
Matches 190; Conservative 18; Mismatches 25; Indels   7; Gaps   2;

Qy   4 PAQLLGLLLWL------PGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWY 57
         ||| |||||: |: :||||||| ::||
Db   9 PAWPAGALLLTLLTHCAVPGSWAQSVLTQAPSASGTPGQRVTISCSGSSSNIGNNPVNWY 68

Qy   58 QQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLN 117
         ||||||||||||||||||||||||:|||||||:|||:|| ::|: ||||||| :|||
Db   69 QQLPGTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEAQYYCAAWDDSLN 128

Qy 118 -AQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS 176
          |::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 129 GSYVFGTGTKVTVLGQPKANPVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADG 188

Qy 177 SPVKAGVETTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCCQVTHEGSTVEKTVAPTECS 236
         ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db 189 SPVKAGVETNKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 248

RESULT 13
AAB36212
ID AAB36212 standard; protein; 235 AA.
XX
AC AAB36212;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-10.
XX
KW Human; immune system associated protein; HISAP-10; immune disorder;
KW infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-0049672.

XX
PR 27-MAR-1998; 98US-0049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX
DR WPI; 2001-030926/04.
DR N-PSDB; AAC66528.
XX
PT New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing
PT immune or cell proliferative disorders or infections -
XX
PS Claim 1; Column 65-68; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ Sequence 235 AA;

Query Match   78.3%; Score 965; DB 22; Length 235;
Best Local Similarity   80.3%; Pred. No. 1.1e-50;
Matches 187; Conservative 19; Mismatches 25; Indels   2; Gaps   2;

Qy   5 AQLLGLLLWLPLGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGT 63
         ||: :||||:: |||||||||||||||||||||||||||||||||||| :|||||||
Db   4 ALLFLTLLTQGTGSWAQSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQSPGT 63

Qy   64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
         |||||:: |||||||||||||||||||||:|||:||||||||||||| : |||||
Db   64 APKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYVGN-NIVVFGG 122

Qy 124 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183
         || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 123 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 182

Qy 184 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCCQVTHEGSTVEKTVAPTECS 236
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 183 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 14
AAB36214
ID AAB36214 standard; protein; 235 AA.
XX
AC AAB36214;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-12.
XX
KW Human; immune system associated protein; HISAP-12; immune disorder;
KW infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-0049672.
XX
PR 27-MAR-1998; 98US-0049672.
XX
PA (INCY-) INCYTE PHARM INC.

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XX
PI   Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI   Hillman JL, Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   N-PSDB; AAC66530.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing
PT   immune or cell proliferative disorders or infections -
XX
PS   Claim 1; Column 69-72; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ   Sequence   235 AA;

Query Match             78.3%;  Score 965;  DB 22;  Length 235;
Best Local Similarity   80.0%;  Pred. No. 1.1e-50;
Matches 184;  Conservative  20;  Mismatches  26;  Indels  0;  Gaps  0;

Qy          7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
              || |  | :||||:||||||:||:|:||| :||||| :|||:| :|||  ||||||||||
Db          6 LLLALLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGTTSNIASNSVHWYQLVPGAAPK 65

Qy         67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
              |||| :  : ||||| ||||||||||| |||| || |||||||| ::  |   ||| ||:
Db         66 LLIYANDQRASGVPDRFSGSKSGTSASLAISGLRPEDETDYYCATWDDSVSGWMFGGGTK 125

Qy        127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

Qy        187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
              ||||||||||||||||||||||||||:||||||||||||||||||||||:
Db        186 TPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 15
ABG19293
ID   ABG19293 standard; Protein; 236 AA.
XX
AC   ABG19293;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #19284.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
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DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS83480.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID NO 49652; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   236 AA;

Query Match             77.8%;  Score 958.5;  DB 22;  Length 236;
Best Local Similarity   79.8%;  Pred. No. 2.8e-50;
Matches 186;  Conservative  18;  Mismatches  28;  Indels  1;  Gaps  1;

Qy          5 AQLLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDL-HWYQQLPGT 63
              | || |  | :||||:||||||:||:|:|||:||||| : |||:| :|| :|| |||||
Db          4 ALLLTLLTQDTGSWAQSALTQPASVSGSPGQSITISCTGTNNDVGSYNLVSWYQQHPGK 63

Qy         64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
              ||| |||| :  : ||||| :|||||||||| |||| || |||||||| ::  |   |||
Db         64 APKIMIYEVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYCCSYTSSRPDVVFGG 123

Qy        124 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183
              ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183

Qy        184 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
              ||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db        184 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPAECS 236

Search completed: March 29, 2003, 09:10:21
Job time : 25.273 secs
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 32.3734 Seconds
                                          (without alignments)
                                          6735.375 Million cell updates/sec

Title: US-09-758-173-9
Perfect score: 0
Sequence: 1 ATGAGGGTCCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 711

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched :   441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents NA:*
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        2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
        3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
        4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
        5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
        6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	711	100.0	711	3	US-08-487-550-9	Sequence 9, Appli
2	582.6	81.9	935	3	US-09-049-672A-20	Sequence 20, Appl
3	540.2	76.0	705	3	US-08-487-550-1	Sequence 1, Appli
4	74.6	74.6	895	3	US-09-049-672A-25	Sequence 25, Appl
5	510.6	71.8	891	3	US-09-049-672A-23	Sequence 23, Appl
6	502.6	70.7	902	3	US-08-378-939-11	Sequence 11, Appl
7	484.2	68.1	885	4	US-09-152-060-47	Sequence 47, Appl
8	482.6	67.9	879	4	US-09-152-060-29	Sequence 29, Appl
9	468.4	65.9	702	3	US-08-523-894-5	Sequence 5, Appli
10	416.4	58.6	919	3	US-09-049-672A-24	Sequence 24, Appl
c	11	412	57.9	928	4	US-09-152-060-46	Sequence 46, Appl
12	367.4	51.7	716	4	US-08-793-450-5	Sequence 5, Appli
c	13	323.6	45.5	584	4	US-09-404-879A-268	Sequence 268, App
c	14	306.2	43.1	771	4	US-08-991-789A-241	Sequence 241, App
c	15	306.2	43.1	771	4	US-09-062-451-241	Sequence 241, App
c	16	306.2	43.1	771	4	US-09-598-326-241	Sequence 241, App
17	264.4	37.2	408	4	US-09-025-769B-169	Sequence 169, App
18	255.4	35.9	393	1	US-08-305-683A-3	Sequence 3, Appli
19	254.8	35.8	933	4	US-09-079-029-8	Sequence 8, Appli
20	253.2	35.6	642	2	US-08-634-783A-4	Sequence 4, Appli
21	253.2	35.6	642	2	US-09-070-817-4	Sequence 4, Appli
22	246.8	34.7	346	2	US-08-761-277A-50	Sequence 50, App
23	244.2	34.3	330	4	US-09-240-274-132	Sequence 132, App
24	242.4	34.1	318	2	US-08-646-981-4	Sequence 4, Appli
25	242.4	34.1	333	2	US-08-477-553A-43	Sequence 43, Appl
26	242.2	34.1	774	2	US-08-665-202-4	Sequence 4, Appli
27	242.2	34.1	908	4	US-09-273-839A-9	Sequence 9, Appli
28	241.2	33.9	327	4	US-09-240-274-223	Sequence 223, App
29	237.6	33.4	333	1	US-08-264-093-5	Sequence 5, Appli
30	236.6	33.3	396	2	US-08-345-321-3	Sequence 3, Appli
31	234.8	33.0	327	4	US-09-240-274-128	Sequence 128, App
32	233.2	32.8	327	4	US-09-240-274-126	Sequence 126, App
33	231.6	32.6	327	4	US-09-240-274-129	Sequence 129, App
34	231.6	32.6	327	4	US-09-240-274-130	Sequence 130, App
35	226.6	31.9	330	1	US-08-199-911-1	Sequence 1, Appli
36	226.6	31.9	336	4	US-09-240-274-133	Sequence 133, App
37	226.4	31.8	318	1	US-08-436-463-9	Sequence 9, Appli
38	226.4	31.8	318	1	US-08-024-253-9	Sequence 9, Appli
39	223	31.4	330	4	US-09-240-274-134	Sequence 134, App
40	220.4	31.0	327	4	US-09-240-274-123	Sequence 123, App
41	217.4	31.0	327	4	US-09-240-274-125	Sequence 125, App
42	217.4	30.6	342	4	US-09-240-274-131	Sequence 131, App
43	216.2	30.4	327	4	US-09-240-274-124	Sequence 124, App
44	208.8	29.4	333	2	US-08-652-816A-27	Sequence 27, Appl
45	204.4	28.7	327	4	US-09-240-274-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-487-550-9
; Sequence 9, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..711
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..711
US-08-487-550-9

Query Match   100.0%; Score 711; DB 3; Length 711;

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Best Local Similarity  100.0%;  Pred. No. 2.4e-187;  Indels    0;  Gaps    0;
Matches  711;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 ATGAGGGTCCCGCCTCAGCTCCTGGGGCTCCTGCTGCTCTGCCTGCTCCCAGGTGCACGATGT  60
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Db    1 ATGAGGGTCCCGCCTCAGCTCCTGGGGCTCCTGCTGCTCTGCCTGCTCCCAGGTGCACGATGT  60

Qy   61 GAGTCTGTCCTGACACAGCCCCCTCAGTGTCTGGGGCCCCAGGGCGAGAGGTCACCATC  120
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Db   61 GAGTCTGTCCTGACACAGCCCCCTCAGTGTCTGGGGCCCCAGGGCAGAGAGGTCACCATC  120

Qy  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC  180

Qy  181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT  240
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Db  181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT  240

Qy  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGCCTCCTGGCCATCACTGGGCTCCAG  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGCCTCCTGGCCATCACTGGGCTCCAG  300

Qy  301 ACTGAGGATGAGGCTGATTATTACTGCAGTCCTGATGACAGCAGCTGAATGCTCAGGTA  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 ACTGAGGATGAGGCTGATTATTACTGCAGTCCTGATGACAGCAGCTGAATGCTCAGGTA  360

Qy  361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACG  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACG  420

Qy  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  480

Qy  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  540

Qy  541 GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGCAGC  600
        | |||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 G.CGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGCAGC  600

Qy  601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG  660

Qy  661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA  711
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA  711
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RESULT 2
US-09-049-672A-20
; Sequence 20, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Yue, Henry
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Baughn, Mariah R.
;   TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA

;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/049,672A
;   FILING DATE: HEREWITH
;   CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Cerrone, Michael C
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX:
; INFORMATION FOR SEQ ID NO: 20:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 935 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: ADRETUT05
;   CLONE: 2492122
US-09-049-672A-20

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Query Match            81.9%;  Score 582.6;  DB 3;  Length 935;
Best Local Similarity  89.8%;  Pred. No. 7.8e-152;
Matches  637;  Conservative    0;  Mismatches   69;  Indels    3;  Gaps    1;

Qy    4 AGGGTCCCGCCTCAGCTCCTGGGGCTCCTGCTGCTCTGCCTGCTCCCAGGTGCACGATGTCAG   63
        ||||| |||||||| |||||||||||||||| || |||||||||||||||||||||||||
Db   74 ATGGCCTGGTCTCCTCTCCTCCCCTCACTCTCCTCTGCTCGACAGAGGGTCCTGGGCCCAG  133

Qy   64 TCTGTCCTGACACAGCCCGCCTCAGTGTCTGGGGCCCCAGGGCGAGAAGTCACCATCTCG  123
        |||||||||||||| |||| ||||||||||||||||||||||||| || || |||| ||
Db  134 TCTGTGCTGACGCAGCCGCCGCCGTCCCAGTGTCTGGGCCCCAGGGCCAGGAGGGTCACCATCTCC  193

Qy  124 TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTC  180
        ||||||||||||||||||||  || |    ||| || || || ||||||||||||||||
Db  194 TGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTT  253

Qy  181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT  240
        ||||||||| ||||||||  || || |||||  ||||| || || ||| |||| || |
Db  254 CCAGGAACAGCCCCCCAAACTCCTCATCTATAGTAGTAATCGGCCCTCAGGGGTCCCT  313

Qy  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGCCTCCTGGCCATCACTGGGCTCCAG  300
        |||||||||||||||||  || || |||| |||||||||||||||||||||||||||||
Db  314 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG  373

Qy  301 ACTGAGGATGAGGCTGATTATTACTGCAGTCCTGATGACAGCAGCTGAATGCTCAGGTA  360
        ||||||||||||||||| |||||||||||  || ||||| ||||||||||||||||||
Db  374 GCTGAGGATGAGGCTGATTATTACTGCAGTCCTATGACAGCAGCCTGAGTGGTGTGGTA  433

Qy  361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT  420
        ||||||||||||||| ||||||||||| |||||||||||||||| |||||||||||||
Db  434 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT  493

Qy  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  494 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  553

Qy  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  540
        |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  554 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  613

Qy  541 GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGCAGC  600
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Db   614 GCGGGAGTGGAGACCACCACCACCCCTCCAAACAAACAAACAACAAGCAACAACAACAGTACCGCGGCCAGCAGC 673
          |||||||||||||||||||||||| |||||||||||||||||||||

Db   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
          | | || || | | | || |||||||||| |||||||||||||
Db   121 ACCTGTGGGGG-------AGACAACAGTAGAAATGAATGAATATGTCCACTGTACCAGCAGAAG 174

Qy   601 TACCTGAGCCTGAGCGCTGGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 CCAGGAACGGCGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT 240

Db   674 TACCTGAGCCTGAGCGCTGGAGCAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 733
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   175 CCAGCGCGGGCCCCCTATACTGGTCATCTATGATGATGACCGCCCTCAGGGATCCCT 234

Qy   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 709
          ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCGCCTCCTGGCCATCACTGGGCTCCAG 300

Db   734 CATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 782
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   235 GAGCGATTCTCTGCTCCAAATCAGGAACACCGCCACCCTGACCATCAACGGGGTCGAG 294

                                                                    Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360
                                                                              ||| || | || ||| ||||||||||
                                                                    Db   295 GCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGGCTAGTGATCATCCGGTC 354

RESULT 3   Qy   361 TTCGGAGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
US-08-487-550-1 ||| || || || |||||||| |||||||||||||
; Sequence 1, Application US/08487550   Db   355 TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCCAAGGTGCCCCCTCGGTCACT 414
; Patent No. 6113898
; GENERAL INFORMATION: Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGGCCACACTGGTGTGTCTCATA 480
; APPLICANT: Anderson, Darrell R. ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC   Db   415 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGGCCACACTGGTGTGTCTCATA 474
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS   Qy 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
; TITLE OF INVENTION: IMMUNOSUPPRESANTS" ||| |||||||||||||||||||||||||||||||||||||||
; NUMBER OF SEQUENCES: 12   Db   475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 534
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS   Qy   541 GCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGCGGCCAGCAGC 600
;   STREET: 699 Prince Street ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;   CITY: Alexandria   Db   535 GCGGGAGTGGAGACCACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGCGGCCAGCAGC 594
;   STATE: VA
;   COUNTRY: USA   Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGCTGCCAGGTCACG 660
;   ZIP: 22314 |||||||||||||||||||||||||||||||||||||||||||||||||||
; COMPUTER READABLE FORM: Db   595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGCTGCCAGGTCACG 654
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible   Qy   661 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCATGA 711
;   OPERATING SYSTEM: PC-DOS/MS-DOS ||||||||||||||||||||||||||||||||||||||||||||||||||
;   SOFTWARE: Patentin Release #1.0, Version #1.30   Db   655 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCATGA 705
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE: 07-JUN-1995   RESULT 4
;   CLASSIFICATION: 435   US-09-049-672A-25
; ATTORNEY/AGENT INFORMATION: ; Sequence 25, Application US/09049672A
;   NAME: Teskin, Robin L.   ; Patent No. 6135941
;   REGISTRATION NUMBER: 35,030   ; GENERAL INFORMATION:
;   REFERENCE/DOCKET NUMBER: 012712-131   ; APPLICANT: Hillman, Jennifer L.
; TELECOMMUNICATION INFORMATION: ; APPLICANT: Lal, Preeti
;   TELEPHONE: 703-836-6620   ; APPLICANT: Tang, Y. Tom
;   TELEFAX: 703-836-2021   ; APPLICANT: Yue, Henry
INFORMATION FOR SEQ ID NO: 1:   ; APPLICANT: Au-Young, Janice
; SEQUENCE CHARACTERISTICS: ; APPLICANT: Corley, Neil C.
;   LENGTH: 705 base pairs   ; APPLICANT: Guegler, Karl J.
;   TYPE: nucleic acid   ; APPLICANT: Baughn, Mariah R.
;   STRANDEDNESS: not relevant   ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   TOPOLOGY: linear   ; NUMBER OF SEQUENCES: 28
; MOLECULE TYPE: peptide   ; CORRESPONDENCE ADDRESS:
; FEATURE: ;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   NAME/KEY: CDS   ;   STREET: 3174 Porter Drive
;   LOCATION: 1..705   ;   CITY: Palo Alto
; FEATURE: ;   STATE: CA
;   NAME/KEY: mat_peptide   ;   COUNTRY: USA
;   LOCATION: 1..705   ;   ZIP: 94304
US-08-487-550-1   ; COMPUTER READABLE FORM:
                                                                ;   MEDIUM TYPE: Diskette
Query Match   76.0%;   Score 540.2; DB 3; Length 705;   ;   COMPUTER: IBM Compatible
Best Local Similarity 86.1%; Pred. No. 3.6e-140;   ;   OPERATING SYSTEM: DOS
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;   ;   SOFTWARE: FastSEQ for Windows Version 2.0
                                                                ; CURRENT APPLICATION DATA:
Qy   1 ATGAGGGTCCCGCTCCAGCTCCTGGGGCTCCTGCTGCTCCTGCGTGCCCAGGTGCACGATGT 60   ;   APPLICATION NUMBER: US/09/049,672A
         ||||||| |||| |||||||||||||||||||||||||||||||||||||||||||||||| ;   FILING DATE: HEREWITH
Db   1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCCTGCGTGCCCAGGTGCACGATGT 60   ;   CLASSIFICATION: 536
                                                                ; PRIOR APPLICATION DATA:
Qy   61 GAGTCTGTCCTGACAACAGCCCGCCCTCCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120
         |||||||| | || ||||||| |||||||||||||| || ||||||||||||||
Db   61 GCCTATGAACTGACTCAGCCACCCTCCGGTGCCGGGTCCGGGTCAGTGTCCAGTGTCCCCAGGACAGAGACGCGGCCAGGATC 120

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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: Cerrone, Michael C
  REGISTRATION NUMBER: 39,132
  REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-855-0555
  TELEFAX: 650-845-4166
  TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
  LENGTH: 895 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
IMMEDIATE SOURCE:
  LIBRARY: LUNGTUT13
  CLONE: 3116314
US-09-049-672A-25

Query Match          74.6%;  Score 530.2; DB 3; Length 895;
Best Local Similarity 87.5%;  Pred. No. 2.3e-137;
Matches 580; Conservative  0; Mismatches 83; Indels  0; Gaps  0;

Qy   47 CAGGTGCACGATGTGAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCCAGGGC 106
           ||||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||
Db   80 CAGGGTCCTGGGCCCAGTCTGTGCTCAGCCCCCCTCAGCGTCTGGGACCCCCCGGGC    139

Qy  107 AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATT 166
           |||||||||||||||||||||||||||||||  |||||||||||| |||||||| |||
Db  140 AGAGGGTCACCATCTCTTGTTCTGGAACACCTCCAACATCGCAAGTAATTCTGTGCATT  199

Qy  167 GGTACCAGCAGCTCCCAGGAAACGCCCCCAAACTTCCTCATCTATGACATTAACAAGCGAC 226
           |||  |  ||  ||||||||||||||||||||||||||||||||||||||  |  ||||
Db  200 GGTACCAATTAGTTCCAGGAGCGCGGCCCCCAAACTTCCTCATCTATGATCAGCGTG    259

Qy  227 CCTCAGGAAATTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGCCTCCCTGGCCA 286
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  260 CCTCCGGGGTCCCTGGGCCCGGGGAGCACCTCCAAGCTGGCGGCCTCCCTGGCCA      319

Qy  287 TCACTGGCCTCCAGACTGAGGATGAGAGCTGATTATTACTGCAGTCCTATGACAGCAGCC 346
           ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db  320 TCAGTGGCCTCCGGCCCGGAGATGAAACTGATTATTACTGTGCAACATGGGATGACAGTG 379

Qy  347 TGAATGCTCAGGTATTCGGAGGAGGGAACCCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTG 406
           ||||||||||||| |||||||||||  |||||||||||||  |||||||||||||||||||
Db  380 TCAGTGGTGTTGGATGTTCGGCGGAGGGACCGGCGGCCTGAGCTGGCTCCTAGGTCAGCCCAAGGCTG 439

Qy  407 CCCCCTGGTCACTCTGTTCCCGCCCTCCCTGAGGAGCTTCAAGCAACAAGGCCACAC 466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  440 CCCCCTGGTCACTCTGTTCCCACCCTCCCTGAGGAGCTTCAAGCCAACAAGGCCACAC 499

Qy  467 TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCGGCCGTGACACGTGGGCCTGAAGGCAGATA 526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  500 TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGCCTGGAAGGCAGATA 559

Qy  527 GCAGCCCCGTCAAGGCGGGAGTGGAGACACCACCACCCTCCAAACAAAGCAACAACAAGT 586
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  560 GCAGCCCCGTCAAGGCGGGAGTGGAGACACCACCACCCTCCAAACAAAGCAACAACAAGT 619

Qy  587 ACGGGCGGCCAGCAGCTACCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACA 646
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  620 ACGGGCGGCCAGCAGCTACCTGAGCCTGAGCAGTGGAAGTCCCACAAAAGCTACA 679

Qy  647 GCTGCCAGGTCACGCATGAAGGAGCACCGTGGAGAGACAGTGGCGGCCCTACAGAATGTT 706
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  680 GCTGCCAGGTCACGCATGAAGGAGCACCGTGGAGAGACAGTGGCGGCCCTACAGAATGTT 739

Qy  707 CAT 709
        |||
Db  742 CAT 742
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RESULT 5
US-09-049-672A-23
; Sequence 23, Application US/09049672A
; Patent No. 6135941
GENERAL INFORMATION:
  APPLICANT: Hillman, Jennifer L.
  APPLICANT: Lal, Preeti
  APPLICANT: Tang, Y. Tom
  APPLICANT: Yue, Henry
  APPLICANT: Au-Young, Janice
  APPLICANT: Corley, Neil C.
  APPLICANT: Guegler, Karl J.
  APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Incyte Pharmaceuticals, Inc.
  STREET: 3174 Porter Drive
  CITY: Palo Alto
  STATE: CA
  COUNTRY: USA
  ZIP: 94304
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/049,672A
  FILING DATE: HEREWITH
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: Cerrone, Michael C
  REGISTRATION NUMBER: 39,132
  REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-855-0555
  TELEFAX: 650-845-4166
  TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
  LENGTH: 891 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
IMMEDIATE SOURCE:
  LIBRARY: THYRNOT10
  CLONE: 2872705
US-09-049-672A-23

Query Match          71.8%;  Score 510.6; DB 3; Length 891;
Best Local Similarity 84.5%;  Pred. No. 5.9e-132;
Matches 599; Conservative  0; Mismatches 104; Indels  6; Gaps  2;

Qy    4 AGGTCCCCGGCTCAGCTCCTGGGGGCTCCTGCTCCTCTGGCTCCCAGTGCACGATGTGAG 63
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   34 ATGGCCTGGGCTCGCTATTCCTCCACCCTCCTCACTCAGGGGCACAGGGGTCCTGGGCCCAG 93

Qy   64 TCTGTCCTGACACAGCCGCCCTCCCAGTGTCTGGGGCCCCCAGGGCAGGAGAAGGTCACCATCTCG 123
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   94 TCTGCCCTGACTCAGCCTCGCTGTGTCCTCCGGGGTCTCGGGCTCCTGGCAGCAGTCGATCACCAATCTCC 153

Qy  124 TGCACTGGGAGCACCTCCAACATTGGAGGTTAT---GATCTACATTGGTACCAGCAGCTC 180
          ||||||||||||||||||||||||| ||| |||   |||| || ||||| ||||||||||
Db  154 TGCACTGGAACCAGCAGCTGTGGTGTTAACTATGTCTCCTGGTACCAACAGTCC 213

Qy  181 CCAGGAACGGCCCCCCAAACTCCTCATCATCTATGACATTAACAAGGACCCCTCAGGAATTTCT 240
          ||||| |||||||| | |||||||||||| |||| |||||||||| |||||||||| ||||||
Db  214 CCAGGACGCACGGCCCCCAAACTCATCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCT 273
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;   STRANDEDNESS: both
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 32..739
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 89..739
;   FEATURE:
;     NAME/KEY: sig_peptide
;     LOCATION: 32..86
; US-08-378-939-11

Query Match     70.7%;  Score 502.6;  DB 2;  Length 902;
Best Local Similarity   83.8%;  Pred. No. 9.6e-130;
Matches  594;  Conservative   0;  Mismatches 109;  Indels   6;  Gaps   2;

Qy      4 AGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCCTGCTGCTCCTGGCTGTGCACGATGTGAG 63
            ||||||  ||||||||||||||||| |||| ||||  |  |||||||  ||   ||| ||
Db     32 ATGGCCTGGGGCTCTGCTGCTGCTGGTGCTCCTCACCCTCCTCACTCAGGACACAGGTCCTGGGCCCAG 91

Qy     64 TCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGGCTCGGGGCCAGGAAGGTCACCATCTCG 123
            ||||| |||||||||||||||||| ||||| |||
Db     92 TCTGCCCTGACTCAGCCTGCCTGCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCC 151

Qy    124 TGCACTGGGAGCACCTCCAACATTGGAGTTATGA---TCTACATTGGTACCAGCAGCTC 180
            ||||||||||||||||||
Db    152 TGCACTGGAACCAACAATGATGTTGGAGTTATAACCTTGTCTCCTGGTACCAGCAGCAC 211

Qy    181 CCAGGAACGGCCCCAAACTCCTCATCATGATTATGAGGTCAGTCAGCCCTCCCCTGGCCTCCTCA 240
            ||||||||  |||||||| ||| | |||  ||| |||||||||||||  ||||||||||||||||
Db    212 CCAGGCAAAGCCCCCAAAATCATGATTTATGAGTGTCAGCCCCATCACTGGGCTCCAG 271

Qy    241 GACCGATTCTCTGGCTCCAAGTCTGGTACGGCGGCCTCCCTGCCCATCACTGGGCTCCAG 300
            |||| || || || ||||||||||||||| | || |||  | || |||||||||||||||
Db    272 AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAG 331

Qy    301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360
            |||||||  |||||||||||||||||| || ||| ||||| ||| ||  ||||||||| 
Db    332 GCTGAGGACGAGGCTGATTATTACTGCTCATATGCAGGTAG---TTACACTGTGGTT 388

Qy    361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
            |||||||||||||| |||||||| ||||||||||||| |||||||||||||||||||||||
Db    389 TTCGGCGGAGGGACCAAACTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGTCACT 448

Qy    421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
            ||||||||||||||||||||||||||||||||||||||| ||||| | || ||||||||||
Db    449 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 508

Qy    481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    509 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 568

Qy    541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAACAGCAACAGCACAGCGGCCAGCAGC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    569 GCGGGAGTGGAGACCACCACACCCTCCAAACAAACAGCAACAGCACAGCGGCCAGCAGC 628

Qy    601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCACAGTGAAGTCCACAGTTACAGCTGCACG 660
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    629 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGTGAAGTCACAGAGCTACACG 688

Qy    661 CATGAAGGAGCACCGTGGAAGAGAGACAGTGGCCCCTACAGAATGTTCAT 709
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 CATGAAGGAGCACCGTGGAAGAGAGACAGTGGCCCCTACAGAATGTTCAT 737

RESULT 7
US-09-152-060-47
; Sequence 47, Application US/09152060
; Patent No. 6448230
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```
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P1.US
  CURRENT APPLICATION NUMBER: US/09/152,060
  CURRENT FILING DATE: 1998-09-11
  EARLIER APPLICATION NUMBER: PCT/US98/04858
  EARLIER FILING DATE: 1998-03-12
  EARLIER APPLICATION NUMBER: 60/040,762
  EARLIER FILING DATE: 1997-03-14
  EARLIER APPLICATION NUMBER: 60/040,710
  EARLIER FILING DATE: 1997-03-14
  EARLIER APPLICATION NUMBER: 60/050,934
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/048,100
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/048,357
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/048,189
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/057,765
  EARLIER FILING DATE: 1997-09-05
  EARLIER APPLICATION NUMBER: 60/048,970
  EARLIER FILING DATE: 1997-06-06
  EARLIER APPLICATION NUMBER: 60/068,368
  EARLIER FILING DATE: 1997-12-19
  NUMBER OF SEQ ID NOS: 118
  SOFTWARE: PatentIn Ver. 2.0
US-09-152-060-47
  SEQ ID NO 47
  LENGTH: 885
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-152-060-47

Query Match             68.1%;  Score 484.2;  DB 4;  Length 885;
Best Local Similarity   80.9%;  Pred. No. 1.2e-124;
Matches  564;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;
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RESULT 8
US-09-152-060-29
; Sequence 29, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P1.US
  CURRENT APPLICATION NUMBER: US/09/152,060
  CURRENT FILING DATE: 1998-09-11
  EARLIER APPLICATION NUMBER: PCT/US98/04858
  EARLIER FILING DATE: 1998-03-12
  EARLIER APPLICATION NUMBER: 60/040,762
  EARLIER FILING DATE: 1997-03-14
  EARLIER APPLICATION NUMBER: 60/040,710
  EARLIER FILING DATE: 1997-03-14
  EARLIER APPLICATION NUMBER: 60/050,934
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/048,100
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/048,357
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/048,189
  EARLIER FILING DATE: 1997-05-30
  EARLIER APPLICATION NUMBER: 60/057,765
  EARLIER FILING DATE: 1997-09-05
  EARLIER APPLICATION NUMBER: 60/048,970
  EARLIER FILING DATE: 1997-06-06
  EARLIER APPLICATION NUMBER: 60/068,368
  EARLIER FILING DATE: 1997-12-19
  NUMBER OF SEQ ID NOS: 118
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 29
  LENGTH: 879
  TYPE: DNA
  ORGANISM: Homo sapiens
US-09-152-060-29

Query Match             67.9%;  Score 482.6;  DB 4;  Length 879;
Best Local Similarity   80.8%;  Pred. No. 3.2e-124;
Matches  563;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;
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;   ORIGINAL SOURCE:
;     ORGANISM: Homo sapiens
;   POSITION IN GENOME:
;     CHROMOSOME/SEGMENT: lambda variable and constant domains in
;     CHROMOSOME/SEGMENT: CE9.1
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..702
;   FEATURE:
;     NAME/KEY: mat_peptide
;     LOCATION: 1..702
US-08-523-894-5

  Query Match             65.9%;  Score 468.4;  DB 3;  Length 702;
  Best Local Similarity   79.9%;  Pred. No. 2.5e-120;
  Matches  566;  Conservative   0;  Mismatches 136;  Indels   6;  Gaps   1;

Qy      4 AGGGTCCCGCTCAGCTCTGGGGCTTCCTGGTCTCTGCTCCCAGTGCACGATGTGAG  63
            ||| ||| | ||||| |||| | ||| |||||||| |  ||| |||||||||||
Db      1 ATGGCCTGGGCCTGCTGCTGCTCACTTTACAGACTCTGCGGCCTCG          60

Qy     64 TCTGTCCTGACACAGCCGCCTCAGTGTCTGGGGCCCAGGGCAGAAGGTCACCATCTCG 123
            ||| || || ||| || || ||| | ||| |||||| ||| ||||||------CCGGG
Db     61 TATGAGTTGAGTCAGCCTCGCTCAGTGTCCGTGTCCCAGGACAGACG------CCGGG 114

Qy    124 TGCACTGGAGCAGTGAAGTTATGATGGTTATGATCTCCAACATTGGTACCAGCAGCTCCA 183
            ||  ||| ||| || ||| |||| || | ||||||||||||| ||||||||||||||| ||
Db    115 TTCACCTGTGGGGGAGACAACGTTGGAAGGAAAAGTGTACAGTGGTACCAGCAGAAGCCA 174

Qy    184 GGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGGCGACCCTCAGGAATTTCTGAC 243
            ||||| ||||| |||||||| || |||||| | ||||| || ||| |||||| |||||
Db    175 CCCGGCAGGCCCCTGTGCTGGTCATCTATGTCATGGGGATCCCCTGCG          234

Qy    244 CGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCGGGCCATCACTGGGCTTCCAGACT 303
            ||||||||||| ||||| || ||||| ||||||||| ||| |||||||||| | |||| |
Db    235 CGATTCTCTGGCTCCAACTCAGGGAACACCGCCACCCTGACCATCAGCGGGGTCGAGGCC 294

Qy    304 GAGGATGAGGCTGATTATTACTTGGTACCGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTATTC 363
            |||||||||| |||| || ||||| ||  ||  || || || ||| |||| || |||
Db    295 GGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGTACTGCTGATCATTGGGTCTTC 354

Qy    364 GGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTG 423
            ||||||||||||| || ||||| || ||||||||||||||||| || |||||||||||||
Db    355 GGCCGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTG 414

Qy    424 TTCCCGCCCTCCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTCATAAGT 483
            ||||| |||||||||||||||||||||||||||||||||||| ||||||| || |||||
Db    415 TTCCCGCCCTCCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTCATAAGT 474

Qy    484 GACTTCTACACCGGGAGCCGTGACAGTGGCCTGGAAGCGAGCAGATAGCAGCCCGTCAAGGCG 543
            ||||||||||| ||||||||||| ||||||| |||||| ||||| || ||| |||||||||||
Db    475 GACTTCTACACCGGGAGCCGTGACAGTGGCCTGGAAGCGAGCAGATAGCAGCCCGTCAAGGCG 534

Qy    544 GGAGTGGAGACCACCACACCCTCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTAC 603
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    535 GGAGTGGAGACCACCACACCCTCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTAC 594

Qy    604 CTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGTGCGAAGTCCCACAGAGCTCACGCAT 663
            ||||||||||| |||||||||||||||| || |||||| |||||| |||||| ||||||||
Db    595 CTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGTGAAGTCCCACAGAGCTCACGCAT 654

Qy    664 GAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTTACAGAATGTTCATGA 711
            |||||||||||||||||||||| |||||||||||| |||||||||||||
Db    655 GAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 702
```

```
RESULT 10
US-09-049-672A-24
;  Sequence 24, Application US/09049672A
;  Patent No. 6135941
;  GENERAL INFORMATION:
;    APPLICANT: Hillman, Jennifer L.
;    APPLICANT: Lal, Preeti
```

(continuation, left side of page)

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Db    262 GCATCCAGTGCAGGAGCCACCATCTCCCTGACCATTACTGGACTCCAGCCTGAGGACGAG 321

Qy    313 GCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTATTCCGGAGGAGGG 372
            |||| || ||||| ||||| || |||||| |||||||||||||| || |||| |||||
Db    322 GCTGACTATTACTGCGCGCAGCATATGACAGCAGCCTCCGCAGTTTGGATGTTCGGCGGAGGG 381

Qy    373 ACCCGGCTGACCGTCCTAGGTCAGCCCCCTCGGTCACTCTGTTCCCGCCC 432
            |||  ||||||||||| ||||||||||| | ||||| ||||||||||||||
Db    382 ACCAAGCTGACCGTCCTAGGTCAGCCCCCTCGGTCACTCTGTTCCCACCC 441

Qy    433 TCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTAC 492
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    442 TCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTAC 501

Qy    493 CCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAG 552
            |||||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||
Db    502 CCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAG 561

Qy    553 ACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTG 612
            |||||||||||| |||||||||||||||||||||||| |||||||||||||||||||||
Db    562 ACCACCACACCCTCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTG 621

Qy    613 ACGCCTGAGCAGTGGAAGTCCCACAGTGAAGTCCCACAGAGCTCACGCAT 672
            |||||||||||||||||||| |||||||||||||||||||||||||||||
Db    622 ACGCCTGAGCAGTGGAAGTCCCACAGTCCACAGAGCTCACGCAT 681

Qy    673 ACCGTGGAGAAGACAGTGGCCCCCTTACAGAATGTTCAT 709
            ||||||||||||||||||||||||| ||||||||||||||
Db    682 ACCGTGGAGAAGACGGTGGCCCCCTTACAGAATGTTCAT 718
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RESULT 9
US-08-523-894-5
;  Sequence 5, Application US/08523894
;  Patent No. 6136310
;  GENERAL INFORMATION:
;    APPLICANT: Hanna, Nabil
;    APPLICANT: Newman, Roland A.
;    APPLICANT: Reff, Mitchell E.
;  TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;  TITLE OF INVENTION: Therapy
;  NUMBER OF SEQUENCES: 59
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314-3187
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/523,894
;    FILING DATE: 06-SEP-1995
;    CLASSIFICATION: 424
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-165
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 702 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
```

```
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Incyte Pharmaceuticals, Inc.
  STREET: 3174 Porter Drive
  CITY: Palo Alto
  STATE: CA
  COUNTRY: USA
  ZIP: 94304
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: DOS
  SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/049,672A
  FILING DATE: HEREWITH
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: Cerrone, Michael C
  REGISTRATION NUMBER: 39,132
  REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-855-0555
  TELEFAX: 650-845-4166
  TELEX:
INFORMATION FOR SEQ ID NO: 24:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 919 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  IMMEDIATE SOURCE:
  LIBRARY: LNODNOT08
  CLONE: 3056213
US-09-049-672A-24
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Query Match       58.6%;  Score 416.4;  DB 3;  Length 919;
Best Local Similarity  78.7%;  Pred. No. 6.2e-106;
Matches  524;  Conservative  0;  Mismatches 136;  Indels   6;  Gaps   2;

Qy    47 CAGGTGCAGCGATGTGAGTCTGCTGTCTGACACAGCCGCGCTCCAGTGTCTGGGGCCCAGGGC 106
         |||||||  ||  |||||  ||| || |||||||| |||| || |||||||||||||
Db   106 CAGGAGTGGGATTCTCAGACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCCTGGAG 165

Qy   107 AGAAGTGCACCATCTCGTGCACTCGGGAGCAC---CTCCAACATTGGAGTTATGATCTAC 163
         ||||| | ||||| || | |||||||||||||   ||||| | ||||||  | ||| ||
Db   166 GGACAGTCACACTCACTGTGGCTTGGCTCGGCTCAGTCTCTACTAGTAACTACCCCA 225

Qy   164 ATTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGC 223
         ||||||||||||||  || ||| | | |||| ||||| |||| ||  | || |
Db   226 GCTGGTACCAGCAGCACCCCAGGCCAGGCTCCACGCACGCTCATATACGGCACAAGTGTTC 285

Qy   224 GACCCTCAGGAATTCTGACCGATTCTGCTCCAAGTCTGGTACCGCGGCCTCCCTG 283
         |||||  | ||| ||  |||  || ||  |||||||| |||||||| | |||
Db   286 GTTCTTCTGAGTCCCTAGTCCATCGTTCTCTGCTCCATCCTTGGGAACAAAGCCCGGCCTCA 345

Qy   284 CCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACACGA 343
         |||| ||  ||||||| | || | |||||||| || ||| || || || | | ||||
Db   346 CCATCACGGGGGCCCAGGCAGCAGATGAATCTGATTATTATTGTCCCTATAT---AGGC 402

Qy   344 GCCTGAATGCTCAGGTATTCGGAGGAGGGACCGGCTGACCGTCCTAGGTCAGCCCCAAGG 403
         | || | |  | | ||||||||| ||||| ||| || |||| || |||||||||||||
Db   403 GTAGTGCTCTTGGGGTGTTCGGCGGAGGGACCAAGCTGTCCGTCCTAGGTCCTAGTCAGCCCAAGG 462
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Qy   404 CTGCCCCTCGGTCACTCTGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCA 463
         ||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   463 CTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTGAGGAGCTTCAAGCCAACAAGGCCA 522

Qy   464 CACTCGTGTGTCTCATAAGTGACTTCTACCCGGGAGAGTGGGCCTGGAAGGCAG 523
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   523 CACTCGTGTGTCTCATAAGTGACTTCTACCCGGGAGAGTGGGCCTGGAAGGCAG 582

Qy   524 ATAGCAGCCCGTCAAGGCGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACA 583
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   583 ATAGCAGCCCCGTCAAGGCGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACA 642

Qy   584 AGTACGCGGCCAGCAGCTACCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCT 643
         ||||||||||||||||||||||||||||||||||||||||||  |||||
Db   643 AGTACGCGGCCAGCAGCTACCTGAGCCTGAGCAGTGGAAGTCCCACAAAAGCT 702

Qy   644 ACAGCTGCCAGGTCACGCATGAAGGGAGCACGTGGAGAGAGACAGTGGCCCCTACAGAAT 703
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   703 ACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAGAGACAGTGGCCCCTACAGAAT 762

Qy   704 GTTCAT 709
         ||||||
Db   763 GTTCAT 768
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RESULT 11
US-09-152-060-46/c
;  Sequence 46, Application US/09152060
;  Patent No. 6448230
;  GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 28 Human Secreted Proteins.
;   FILE REFERENCE: PZ003P1.US
;   CURRENT APPLICATION NUMBER: US/09/152,060
;   EARLIER APPLICATION NUMBER: PCT/US98/04858
;   EARLIER FILING DATE: 1998-03-12
;   EARLIER APPLICATION NUMBER: 60/040,762
;   EARLIER FILING DATE: 1997-03-14
;   EARLIER APPLICATION NUMBER: 60/040,710
;   EARLIER FILING DATE: 1997-03-14
;   EARLIER APPLICATION NUMBER: 60/050,934
;   EARLIER FILING DATE: 1997-05-30
;   EARLIER APPLICATION NUMBER: 60/048,100
;   EARLIER FILING DATE: 1997-05-30
;   EARLIER APPLICATION NUMBER: 60/048,357
;   EARLIER FILING DATE: 1997-05-30
;   EARLIER APPLICATION NUMBER: 60/057,765
;   EARLIER FILING DATE: 1997-09-05
;   EARLIER APPLICATION NUMBER: 60/048,970
;   EARLIER FILING DATE: 1997-06-06
;   EARLIER APPLICATION NUMBER: 60/068,368
;   EARLIER FILING DATE: 1997-12-19
;   NUMBER OF SEQ ID NOS: 118
;   SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 46
;   LENGTH: 928
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (49)
;    OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (78)
;    OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (148)
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;  OTHER INFORMATION: n equals a,t,g, or c
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (163)
;  OTHER INFORMATION: n equals a,t,g, or c
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (532)
;  OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-46

Query Match            57.9%;  Score 412;  DB 4;  Length 928;
Best Local Similarity   83.9%;  Pred. No. 1e-104;
Matches  464;  Conservative  18;  Mismatches  69;  Indels  2;  Gaps  2;

Qy  158 ATCTACATTGGTACCAGCAGCTCCCAGGAACGGCCCC-CAAACTCCTCATCTATGACATT 216
        ||:: ||||||||| ||  ||||| ||||||||||||||| |||| |||||||||||
Db  893 ATGTWTATTGGTACCAMCAGAAGTCAGGCCAGGCCCCTGTGCCTGGTCATCTATGAGGAC 834

Qy  217 AACAAGCGACCCTCAGGAATTCTGACCGATTCTCGGCTTCCAAGTCTGGTACCGCGGCC 276
        |||  ||||||||||||||||||  |: ||:|||||||| ||| |: || ||||||||
Db  833 AACAAACGACCCTCCGG-ATCCCTSAGAGATTCTYGGCTCCAGYTCAGGGACAGTGGCC 775

Qy  277 TCCCTGCCATCACGTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTAT 336
        ||||| ||| |||  ||||||||||||||||||||||||| |||| |||||||
Db  774 ACCTTGACTATCAGTGGGGCCCAGTGACGATGCGGCTGACTACTACTGTTACTCAACA 715

Qy  337 GACAGCAGCCTGAATGCTCAGGTATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAG 396
        |||| |||| |||  ||||| |||||||||||||||||||||||||||
Db  714 GACAGCAGTGTAATCATGGKGTCTTCGGAACTGGGACCAAGGTCACCGTCCTAGGTCAG 655

Qy  397 CCCAAGGCTGCCCCCTCGGTCACTCGTTCCCGCCCTCCTGAGGAGTTCAAGCCAAC 456
        |||||||||||||::|||||:|||||||||||||||| ||||||
Db  654 CCCAAGGCYRMCCCWCKGTCACTCGTTCCCGCCCTCCTGAGGAGTYCAAGCCAAC 595

Qy  457 AAGGCCACACTGGTGTGTCTCATARGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGG 516
        ||||||||||||| |||||: |:| ||||||||||||||||||||||||||||||||
Db  594 AAGGCCACACTRGTGTGTCTSATMAGTGACTTCTACCCGGGAGCYGTGACAGTGGCCTGG 535

Qy  517 AAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCTCCAAACAAAGC 576
        ||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db  534 AANGCAGATRGCAGCCCCGTCAAGGCGGGAGTGGAGACCGGGAGACCACCCACAACARAGC 475

Qy  577 AACAACAAGTACGCGCCGCCCAGCAGCTACCTGAGCCTGAGCAGTGGAAGTCCCAC 636
        |||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  474 AACAACAAGTACGCGCCGCCCAGCAGCTACCTGAGCCCTGAGCAGTGGAAGTCCCAC 415

Qy  637 AGAAGCTACAGCTGCCAGGTCACGCGATGAGGCAGCACCCGGGAGAAGACAGTGCCCCCT 696
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  414 AGAAGCTACAGCTGCCAGGTCACGCGATGAGGCAGCACCCGGGAGAAGACAGTGCCCCCT 355

Qy  697 ACAGAATGTTCAT 709
        ||||||||||||
Db  354 ACAGAATGTTCAT 342
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;  STATE: VA
;  COUNTRY: USA
;  ZIP: 22202
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/793,450
;  FILING DATE: 03-MAR-1997
;  CLASSIFICATION: 536
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: FR 94/10566
;  FILING DATE: 02-SEP-1994
;  ATTORNEY/AGENT INFORMATION:
;  NAME: OBLON, NORMAN F.
;  REGISTRATION NUMBER: 24,618
;  REFERENCE/DOCKET NUMBER: 660-118-0 PCT
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 703-413-3000
;  TELEFAX: 703-413-2220
;  INFORMATION FOR SEQ ID NO: 5:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 716 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: other nucleic acid
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: 1..716
;  FEATURE:
;  NAME/KEY: sig_peptide
;  LOCATION: 1..57
;  FEATURE:
;  NAME/KEY: mat_peptide
;  LOCATION: 58..716
;  OTHER INFORMATION:  /product= "IMMUNOGLOBIN, LIGHT
;  OTHER INFORMATION: CHAIN"
US-08-793-450-5

Query Match            51.7%;  Score 367.4;  DB 4;  Length 716;
Best Local Similarity   75.2%;  Pred. No. 2e-92;
Matches  521;  Conservative  0;  Mismatches  121;  Indels  51;  Gaps  3;

Qy  47 CAGTGCACGATGTGAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
        ||||| ||||||||||||||||||||||||||||||||||||||||
Db  44 CAGTGTCCACTCCGACATCCGAGACCTCACTCGAGACCCTGCTGTGTGGCCTTGGGAC 103

Qy  107 AGAAGGTCACCATCTCGTGCACTGGGAGGAGCACCTCCAACATTGGAGGTTATGATCTACATT 166
        |||||||||||||||||||||||||| ||||||||||       |||||||||||||
Db  104 AGACAGTCAGGATCACATGCCAAGGAGACAGCAGCCTCA-----GAACCTATTATGCAAGCT 157

Qy  167 GGTACCAGCAGCTCCCAGGAACGGCCCCCAAAACTCCTCATCTATGACATTAACAAGCGAC 226
        ||||||||||||||||||||||||||||| |||||| ||||||||||| ||||| |||
Db  158 GGTACCAGCAGAAGCCAGGACAGGCACCTGGTCATCTGGTCATCTGGTGTCATCATGTGTAAAAACAACCGC 217

Qy  227 CCTCAGGAATTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCA 286
        |||||| |||||  || |||| |||||||||| |||||||||||||||||||||
Db  218 CCTCAGGGATCCCAGACCCATTCTCTGGCTCCAGCTCAGGAAACACAGCTTCCTTGACCA 277

Qy  287 TCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC 346
        ||||| || |||| ||||||| |||||||| ||| |||||||| |||||||||
Db  278 TCACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTTCTGTAACAGCGGTGGGA------ 331

Qy  347 TGAATGCTCAGGTATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTG 406
        |||||||| |||| |||||||||||||||||||||||||||| |||||||||||||||
Db  332 --------AGGTTTCGGCGGCGGGACCAAGGTGACCGTCCTAGGTCAGCCCCAAGGCTG 382

Qy  407 CCCCCTCGGTCACTCGTGTTCCCGCCCTCC------------------------T 436
        ||||||||||||| ||||||||||||||||                        |
Db  383 CCCCCTCGGTCACTCGTGTTCCCGCCCTCCCTGAGGAGCTTCAAGCCAACAAGGCCACAC 442
```

Left column:

```
RESULT 13
US-09-404-879A-268/c
; Sequence 268, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: King, Gordon E.
;  APPLICANT: Algate, Paul A.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE:  210121.462C2
;  CURRENT APPLICATION NUMBER: US/09/404,879A
;  CURRENT FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  393
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 268
;  LENGTH: 584
;  TYPE: DNA
;  ORGANISM: Homo sapien
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)..(584)
;  OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-268
```

```
Query Match             45.5%;    Score 323.6;  DB 4;   Length 584;
Best Local Similarity   87.3%;    Pred. No. 2.3e-80;
Matches   378;   Conservative    0;   Mismatches   47;   Indels    8;   Gaps    2;

Qy   220  AAGGGACCCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTAC-----CGCCGG  274
          ||| || |  ||||||  ||||| |||| |||||||||||||||||||||||     || ||
Db   450  AAGCGGCCGTCCAGGGGTCCCGATCGCTNNTCTGGCTTCCAAGTCTTGGCAAACACGGGC  391

Qy   275  CCTCCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCT  334
          ||||||||||||| |||||||||||||||||||||||||||||  ||||||||||||||||
Db   390  CTCCCTTGACNGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCAT  331

Qy   335  ATGACAGCAGCCTGAATGCTCAGGTATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTC  394
          || | |||||||||                   ||| ||||||| |||||||||||||||||
Db   330  ATGCAGGCAAC---AACAATTGGGTGTTCCGGCGGAGGAGGGACCAAGTGACGTCCTAGGTC  274

Qy   395  AGCCCAAGGCTGCGCCCCTCGGTCACTCTGGTCTCCCGCGCCCTCCTCTGAGGAGCTTCAAGCCA  454
          ||  ||||||||||| |||| || || ||| | |||||| |||||||||||||||| |||||||||
Db   273  AGCCCAAGGCTGCCCCCTCGTCACTCTGTTCCCACCCTGTCCCCACCCTTCCTGAGGAGCTTCAAGCCA  214

Qy   455  ACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCT  514
          |||||||| |||||||||||| ||||| ||||||| || |||||| ||||| |||||||||
Db   213  ACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCT  154

Qy   515  GGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTTGGAGACACCACCACCCTCCAAACAA  574
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   153  CTAATCGTTCTTCTCTGGCTCCAAGTNTGCAACACGGCGTCCTCCCTCCCTGACCATCTCTGGGGCTCC  269
```

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Qy   437  CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG  496
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   443  TCGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCGATCAGTGACTTCTACCCGG  502

Qy   497  GAGCCGTGACAGTGGCTGGCCGAAGGCAGAGATAGCAGCCCCGTCAAGGCGGGAGACCA  556
          |||||||||| ||||| |||||||||| || ||| ||||||||||||||||||||||||||
Db   503  GAGCTGTGACATTGGCTTGGAAGGCAGCAGATGGCAGGCCCGTCAAGGCGCAGCAGGACCA  562

Qy   557  CCACACCCTCCAAACAAGCAACAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGC  616
          ||||| |||||||||||||||  |||| |||||||||||||||||||||||||||||||||
Db   563  ACAAACCCTCCAAACAGAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGC  622

Qy   617  CTGAGCAGTGAAGTCCCACAGAAGTACAGCTGCCAGGTCACGCATGAGGGGAGGACCACCG  676
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   623  CCGAGCAGTGGAAGTCCCACAGCTACAGCTGCCAGGTCACGCATGAGGGGAGGACCACTG  682

Qy   677  TGGAGAAGACAGTGGCCCCTACAGATGTTCAT  709
          |||||||||||||||| |||||||||||||||
Db   683  CAGAGAAGACCGTGGCCCCTGCCCTGCAGATGTTCAT  715
```

Right column:

```
Db   153  GGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTTGGAGACACCACCACCCTCCAANCAA  94
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   575  GCAACAACAAGTACGCGGCCGGCCAGCAGCTACCTGAGCCTGAGCGTGAGCAGTGGAAGTCCC  634
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    93  GCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGAGCGTGAGCAGTGGAAGTCCC  34

Qy   635  ACAGAAGCTACAG  647
          |||||||||||||
Db    33  ACAGAAGCTACAG  21
```

```
RESULT 14
US-08-991-789A-241/c
; Sequence 241, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
;  APPLICANT: Frudakis, Tony N.
;            Smith, John M.
;            Reed, Steven G.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;                      TREATMENT AND DIAGNOSIS OF BREAST CANCER
;  NUMBER OF SEQUENCES: 292
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Seed IP Law Group
;   STREET: 701 Fifth Avenue, Suite 6300
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104-7092
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0,  Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/991,789A
;   FILING DATE: 11-Dec-1997
;   CLASSIFICATION: <Unknown>
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Potter, Jane E. R.
;   REGISTRATION NUMBER: 33,332
;   REFERENCE/DOCKET NUMBER: 210121.419C3
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 241:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 771 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
;  SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-991-789A-241
```

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Query Match             43.1%;      Score 306.2;  DB 4;   Length 771;
Best Local Similarity   83.7%;      Pred. No. 1.6e-75;
Matches  370;   Conservative    0;   Mismatches   66;   Indels    6;   Gaps    2;

Qy   122  CGTGCACTGGGAGGCACCTCCACATTCCAACATTGGAGGTTA---TGATCTACATTGGTACCAGCAGC  178
          ||| |||||||||||||||  ||||||| || | ||||||||   ||| ||| |||||||||||||
Db   448  CCTGCANTGGAACCAGCAGTGACGTTGGTTGTTATAATAATGTCTCNTGGTACCAACAGC  389

Qy   179  TCCCAGGAACGGCGCCCCAAACTTCCTCCATCTATGACATTAACAAGCGACCCTCAGGAATTT  238
          ||||||||| |||||  ||||| || || |||| ||||| ||| | |||||||||||||||||
Db   388  ACCCAGGCAAAGCCCCAAAATTCATGATTTATGAGGTCGGTAATCGGCCTCCGCCTCAGGGGTTT  329

Qy   239  CTGACCGATTCTGCTCCAAGTCTCGTGCTACCCGGGAGCCGTCCCGGCCATCACTGGGCTCC  298
          |||| | ||||| || |||||  |||  |||||||||| ||||| ||||||||||||||||
Db   328  CTAATCGTTCTTCTCTGGCTCCAAGTNTGCAACACGGCGTNTGCAACATCTCTGGGGCTCC  269
```

```
Qy   179 TCCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACACAGCGACCCTCAGGAATTT 238
         |||||||| ||||||| |||| |||||||| ||| ||   ||||| ||||||||||
Db   388 ACCCAGGCAAAGCCCCCAAATTCATGATTTATGAGGTCGGTAATCGGCCCCCAGGGGTTT 329

Qy   239 CTGACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGCCTCCCCTGGCCATCACTGGGCTCC 298
         |||||||| ||||| ||||||||| |   ||||| |||||||||||||| |||||||
Db   328 CTAATCGCTTCTCTGGCTCCAAGTNTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCC 269

Qy   299 AGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGG 358
         || |||||||| ||||||||||||||||||    |||||  || |||||    |||
Db   268 AGGCTGAGGACGAGGCTGATTATTACTGCCAGCTCATATACAAGCAGC---AGCACTCTCG 212

Qy   359 TATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCA 418
         |||||||||||||||||||||||||   ||||| ||||||||||||||||||||||||||
Db   211 TGTTTGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA 152

Qy   419 CTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA 478
         |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 CTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA 92

Qy   479 TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA 538
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    91 TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA 32

Qy   539 AGGCGGGGAGTGGAGACCACCAC 560
         ||||||||||||||||| |||
Db    31 AGGCGGGAGTGGAGACCACTAC 10
```

Search completed: April 6, 2003, 06:26:26
Job time : 35.3734 secs

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Qy   299 AGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGG 358
         || |||||||| ||||||||||||||||||    |||||  || |||||    |||
Db   268 AGGCTGAGGACGAGGCTGATTATTACTGCCAGCTCATATACAAGCAGC---AGCACTCTCG 212

Qy   359 TATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCA 418
         |||||||||||||||||||||||||   ||||| ||||||||||||||||||||||||||
Db   211 TGTTTGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA 152

Qy   419 CTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA 478
         |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 CTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA 92

Qy   479 TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA 538
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    91 TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA 32

Qy   539 AGGCGGGGAGTGGAGACCACCAC 560
         ||||||||||||||||| |||
Db    31 AGGCGGGAGTGGAGACCACTAC 10
```

RESULT 15
US-09-062-451-241/c
; Sequence 241, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
;   APPLICANT: Frudakis, Tony N.
;   APPLICANT: Smith, John M.
;   APPLICANT: Reed, Steven G.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;   NUMBER OF SEQUENCES: 297
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SEED and BERRY LLP
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/062,451
;   FILING DATE: 04-APR-1997
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Maki, David J.
;   REGISTRATION NUMBER: 31,392
;   REFERENCE/DOCKET NUMBER: 210121.419C2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 241:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 771 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
US-09-062-451-241

Query Match   43.1%; Score 306.2; DB 4; Length 771;
Best Local Similarity 83.7%; Pred. No. 1.6e-75;
Matches 370; Conservative   0; Mismatches 66; Indels   6; Gaps   2;

```
Qy   122 CGTGCACTGGGAGCACCTCCAACATTGGAGTTA---TGATCTACATTGGTTACCAGCAGC 178
         |||||| ||||||||||||||||||||||||||   ||||| | ||||||||||||||||
Db   448 CCTGCANTGGAACCAGCAGTGACGTTGGTGGTTATATAATAATGTCTCNTGGTACCACACAGC 389
```

CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

     Query Match   76.0%; Score 540.2; DB 19; Length 705;
     Best Local Similarity   86.1%; Pred. No. 3.2e-128;
     Matches 612; Conservative   0; Mismatches 93; Indels   6; Gaps   1;

Qy   1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTGCTGCTCTGGGTGCTCCCAGGTGCACGATGT 60
             ||||||||| ||| ||| |||| |||||| ||| ||| | || ||||||||||||||||||||
Db   1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTGCTGCTCTGGGTGCTCCCAGGTGCACGATGT 60

Qy   61 GAGTCGTCCTGACACAGCCGCCCTCAGTGTCTCGGGGCCCAGGGCAGAAGGTCACCATC 120
             || |||| ||| ||||||||| ||||| ||||| | ||||||||| ||||||| ||
Db   61 GCCTATGAACTGACTCAGCCACCCTCAGTGTCTCAGGATCCCAGGATC 120

Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
             |||||||||||||| |||||| |||||| || ||||| |||||||||||
Db   121 ACCTGTGGGGG------AGCAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAG 174

Qy   181 CCAGGAACGGCCCCAAACTCCTCATCATCTCTATGACAGCACCTCAGGAATTTCT 240
             || || ||| ||| ||| || ||| |||||||||| ||||||| ||| |||
Db   175 CCAGGCGGCCGGCCCCTATACTGGTCATCTATGATGATGATCAGGGATCCCT 234

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG 300
             ||||||||||||||||||||| |||| ||| | ||| ||||||||||| || |||
Db   235 GAGCGATTCTCTGGCTCCAAATCAGGAACAACACCGCCACCCTGACACCCTCAACGGGGTCGAG 294

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGTCTCAGGTA 360
             |||||||||||||| ||||||||||||||||| ||||| | || || || ||||||
Db   295 GCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGCAGGTAGTGATCATCCGGTC 354

Qy   361 TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT 420
             |||||||||||| |||| ||||| ||||||||||| || ||||||| |||||||||
Db   355 TTCGGAGGAGGGACCCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT 414

Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCATA 480
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   415 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCATA 474

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 534

Qy   541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   535 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC 594

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGCAGTGGAAGTCCACAGAAGCTACAGCTGCCAGGTCACG 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGCAGTGGAAGTCCACAGAAGCTCCACAGAAGCTCCACAGGTCACG 654

Qy   661 CATGAAGGGAGCCGTGGAGAAGACAGTGGCCCCTACAGAATTGTTCATGA 711
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   655 CATGAAGGGAGCCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705

RESULT 13
AAV35484
ID   AAV35484 standard; DNA; 705 BP.
XX
AC   AAV35484;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primated 7C10 light chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..705
FT   /*tag= a
FT   /product= 7C10 light chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63760.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3a; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 7C10 light chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins

Qy   541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   535 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC 594

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGCAGTGGAAGTCTACAGCTGCCAGGTCACG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGCAGTGGAAGTCTACAGCTGCCAGGTCACG 654

Qy   661 CATGAAGGGAGCCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   655 CATGAAGGGAGCCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705

RESULT 14
AAS17242
ID   AAS17242 standard; DNA; 705 BP.
XX
AC   AAS17242;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the light chain of 7C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;

KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW graft-vs-host disease; immunosuppression; organ rejection;
KW interleukin-2; IL-2; mutant; ds.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Macaca sp.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT CDS   1..705
FT   /*tag= a
FT   /product= "Light chain of 7C10 antibody"
XX
PN WO200189567-A1.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16364.
XX
PR 22-MAY-2000; 2000US-0576424.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Hanna N, Brams P;
XX
DR WPI; 2002-089895/12.
DR P-PSDB; AAU11538.
XX
PT Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy -
XX
PS Example 8; Fig 3a; 89pp; English.
XX
CC The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present nucleic
CC acid sequence encodes the light chain of 7C10, a primatised antibody
CC used in the invention to induce apoptosis and inhibit production of
CC interleukin-2 (IL-2).
XX
SQ Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match   76.0%; Score 540.2; DB 24; Length 705;
Best Local Similarity 86.1%; Pred. No. 3.2e-128;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

Qy   1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCCAGTGCACGATGT 60
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Db   1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGTGCACGATGT 60

Qy   61 GAGTCTGTGTCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120
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Db   61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGCCCCAGGGACAGACGGCCAGGATC 120

Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGAATTCACATTGGTACCAGCAGCTC 180
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Db   121 ACCTGTGGGGG-----AGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAG 174

RESULT 15
AAV11293
ID AAV11293 standard; cDNA; 651 BP.
XX
AC AAV11293;
XX
DT 27-AUG-1998 (first entry)
XX
DE Antibody HB4C5 light chain encoding cDNA.
XX
KW Antibody light chain; carboxypeptidase; bovine pancreas;
KW porcine pancreas; radioimmunoimaging; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..651
FT   /*tag= a
FT   /product= "Antibody HB4C5 light chain"
FT   /note= "the start and stop codons are not indicated"
XX
PN JP10075791-A.
XX
PD 24-MAR-1998.
XX
PF 30-AUG-1996; 96JP-0246825.
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PR 30-AUG-1996; 96JP-0246825.
XX
PA (MOMI) MORINAGA & CO LTD.
XX
DR WPI; 1998-244364/22.
DR P-PSDB; AAW40533.
XX
PT New antibody light chain or its fragment - useful for preparation of
PT therapeutic(s) or cancer radio-immuno-imaging agent(s)

Qy 181 CCAGGAACGGCCCCAAACTCCTCATCTTATGACATTAACAAGGCGACCCTCAGGAATTTCT 240
         ||| ||||||| ||||||||||||| || || |||||||| ||||||||
Db 175 CCAGCGCGGCGGGCCCCTATCTGGTCATCTATGATGATGAGTGACCGGGCCCTCAGGGATCCCT 234

Qy 241 GACCGATTCTGTGCTCCAAGTCTGGTACCGGCGGCCTTCCCTGGCCATCACTGGGCTCCAG 300
         || |||||||| || ||||| |||||| ||||||||||| ||| || |||||||||||||
Db 235 GAGCGGATTCTCTGCTCCAAATCAGGGACACACCGGAACACCCGACCATCAACGGGGTCCGAG 294

Qy 301 ACTGGAGGATGAGGCTGATTATTACTGACCAGTCTATGACAGCAGCCTGAATGTCAGTA 360
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Db 295 GCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGCTAGTGATCATCCGGTC 354

Qy 361 TTCCGGAGGAGGGACCCGGCTGACCGTCCTAGTGCAGCCAAGGTCAGCCCAGCCCCCTCACT 420
         |||||||||||||||||| ||||||||||| |||||| ||||||| ||||||| || ||||
Db 355 TTCGGAGGAGGGACCCGGGTCAGCCGTCCTAGGTCAGCCCAAGGTCAGCCCCCTCGGTCACT 414

Qy 421 CTGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
         ||||||||||||||||| || |||||| |||||| |||| |||||| ||||||||||||
Db 415 CTGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 474

Qy 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
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Db 475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 534

Qy 541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGCGGCCAGCAGC 600
         ||||||||||||||||||||||| ||||||| |||||| ||||||||||||||||||||
Db 535 GCGGGAGTGGAGACCACCACACCCTCCAAACAAACAACAACAAGTACGCGGCCAGCAGC 594

Qy 601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACGAAGTCACAGTGCCAGGTCACG 660
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Db 595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACGAAGTCACAGTGCCAGGTCACG 654

Qy 661 CATGAAGGAGGAGCACCGTGGAGAGAGACACGTGGCCCTACAGAATGTTCATGA 711
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Db 655 CATGAAGGAGGAGCACCGTGGAGAGAGACACGTGGCCCCTACAGAATGTTCATGA 705

```
XX
PS   Claim 12; Fig 9; 20pp; Japanese.
XX
CC   This cDNA encodes a antibody HB4C5 light chain. This antibody light chain
CC   or its fragment is specific for carboxypeptidase from bovine or porcine
CC   pancreas and is reactive with human cancer tissue. The antibody light
CC   chain and its fragment can be used for preparation of a cancer
CC   radioimmunoimaging reagent and therapeutic compositions.
XX
SQ   Sequence 651 BP; 160 A; 207 C; 164 G; 120 T; 0 other;

Query Match              75.0%;   Score 533.2;   DB 19;   Length 651;
Best Local Similarity    89.8%;   Pred. No. 1.9e-126;
Matches 584;   Conservative   0;   Mismatches 63;   Indels   3;   Gaps   1;

Qy    62 AGTCTGTCCTGACACAGCCGCCCTCAGTGTCTCGGGCCCCAGGCAGAAGGTCACCATCT 121
         |||||||| |||| |||| ||||||||||||||  |||||||||||||| |||||||||
Db     2 AGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGCGCCCAGGACAGAAAGTCACCATCT 61

Qy   122 CGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTCC 181
         | ||| |||| | |||| ||||||||||| | |  | ||| |||||||||||||||||||
Db    62 CCTGCTCTGGAAACAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCACCTCC 121

Qy   182 CAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCTG 241
         |||||||| |||||||||||||||| |||||| ||||  ||||||||||| || || ||
Db   122 CAGGAACAGCCCCCAAACTCCTCATTTATGACAATAATAAGCGACCCTCAAGTATTCCTG 181

Qy   242 ACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAGA 301
         |||||||||||||||||||||||| |||   |||| ||||| |||||| |||| |||||
Db   182 ACCGATTCTCTGGCTCCAAGTCTGGCACGTCTGCGCACCCTGCCACCGGCATCACCGGACTCCAGA 241

Qy   302 CTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATG---CTCAGG 358
         ||| | || ||||||||||||||||  ||  | |||||  ||||  | |   ||| ||
Db   242 CTGGGGACGAGGCCGATTATTACTGCGCAACATGGACCATCCTCCGTGTCAATTGGC 301

Qy   359 TATTCGGAGAGGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA 418
         | |||||| |||||||  ||| ||||||||||||||||||||||||||||||||||||||
Db   302 TGTTCGGCGGAGGGACTAAACTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA 361

Qy   419 CTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA 478
         ||||||||||||||| ||||||||||||||||||||||||| | ||||||||||||||||
Db   362 CTCTGTTCCCGCCCTCTCTCTGAGGAGCTTCAAGCCAACAAGAGCCACACTGGTGTGTCTCA 421

Qy   479 TAAGTGACTTCTACCCGGGAGCCGGTGACAGTGGCCTGGAAGGCAGCAGATAGCAGCCCGTCA 538
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422 TAAGTGACTTCTACCCGGGAGCCGGTGACAGTGGCCTGGAAGGCAGCAGATAGCAGCCCGTCA 481

Qy   539 AGGCGGGAGTGGAGACCACCACACCCTCCAAACAAACCAACAACAAGTACGCGGCCAGCA 598
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482 AGGCGGGAGTGGAGACCACCACACCCTCCAAACAAACCAACAACAAGTACGCGGCCAGCA 541

Qy   599 GCTACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCA 658
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542 GCTACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCA 601

Qy   659 CGCATGAAGGAGGACACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCA 708
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   602 CGCATGAAGGAGGACACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCA 651
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OM nucleic - nucleic search, using sw model

Run on: April   5, 2003, 19:13:54 ; Search time 1353.28 Seconds
                                          (without alignments)
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Title: US-09-758-173-9
Perfect score: 711
Sequence: 1 ATGAGGGGTCCCCGCTCAGCT..........CCCCTACAGAATGTTCATGA 711

Scoring table: IDENTITY_NUC
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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 9: gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
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                 13: gb_est4:*
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                 16: em_estom:*
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                 20: em_gss_pln:*
                 21: em_gss_vrt:*
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                 23: em_gss_mam:*
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                 25: em_gss_other:*
                 26: em_gss_pro:*
                 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	569.2	80.1	956	14	BQ711292	BQ711292 AGENCOURT
2	562.6	79.1	913	14	BQ708635	BQ708635 AGENCOURT
3	559	78.6	894	14	BQ708570	BQ708570 AGENCOURT
4	558.6	78.6	819	12	BG685644	BG685644 602637629 AGENCOURT
5	557.8	78.5	873	14	BQ712653	BQ712653 AGENCOURT
6	555.6	78.1	755	12	BG755185	BG755185 602714114 AGENCOURT

7	552.2	77.7	1007	14	BM920020	BM920020 AGENCOURT
8	552.2	77.7	1060	14	BM906351	BM906351 AGENCOURT
9	551.6	77.6	910	12	BG757147	BG757147 602710516
10	549.4	77.3	857	14	BQ890529	BQ890529 AGENCOURT
11	549	77.2	764	12	BG755548	BG755548 602716230
12	546	76.8	817	13	BI835917	BI835917 603085650
13	545.4	76.7	896	12	BG685967	BG685967 602638530
14	544.8	76.6	823	12	BG686957	BG686957 602650951
15	544.6	76.6	849	12	BG756887	BG756887 602710380
16	544.6	76.6	1124	14	BM918688	BM918688 AGENCOURT
17	541.8	76.2	900	12	BF663927	BF663927 602145588
18	541.6	76.2	936	14	BQ709123	BQ709123 AGENCOURT
19	539.8	75.9	832	13	BI819072	BI819072 603033425
20	539	75.8	774	12	BG398461	BG398461 602439745
21	538.6	75.8	948	12	BG757977	BG757977 602715021
22	538.4	75.7	870	12	BG684025	BG684025 602635632
23	538.2	75.7	873	12	BG686011	BG686011 602638561
24	537.4	75.6	935	12	BG755314	BG755314 602714059
25	537	75.5	868	12	BG745909	BG745909 602724089
26	535.6	75.3	701	12	BG398176	BG398176 602440022
27	535.4	75.3	947	13	BI819216	BI819216 603034633
28	532.2	74.9	864	12	BG758242	BG758242 602712422
29	532.2	74.9	902	14	BQ883560	BQ883560 AGENCOURT
30	529.8	74.5	792	12	BG760202	BG760202 602733508
31	529.6	74.5	813	12	BG755102	BG755102 602711415
32	529.4	74.5	783	13	BM007830	BM007830 603617507
33	527	74.1	894	14	BQ709510	BQ709510 AGENCOURT
34	519.8	73.1	911	12	BG398014	BG398014 602439543
35	519.6	73.1	767	13	BI836367	BI836367 603083069
36	519	73.0	695	14	BM831144	BM831144 K-EST0104
37	517.8	72.8	886	12	BG758124	BG758124 602712287
38	517.2	72.7	617	10	BE140138	BE140138 CMO-HT000
39	517.2	72.7	1030	14	BM921377	BM921377 AGENCOURT
40	516.6	72.7	856	10	BE561313	BE561313 601344452
41	515.4	72.5	918	13	BI823305	BI823305 603041212
42	514.2	72.3	823	13	BI819711	BI819711 603037886
43	510.2	71.8	842	12	BF338856	BF338856 602036112
44	510	71.7	718	12	BG759998	BG759998 602733422
45	509.8	71.7	869	10	BE562370	BE562370 601344455

ALIGNMENTS

RESULT 1
BQ711292

LOCUS   BQ711292   AGENCOURT_8353826 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278335
            956 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8353826 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278335
            5', mRNA sequence.
ACCESSION   BQ711292
VERSION   BQ711292.1   GI:21850191
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 956)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466 row: c column: 08
            High quality sequence start: 10
            High quality sequence stop: 655.
FEATURES   Location/Qualifiers

DEFINITION   AGENCOURT_8351417 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282312
5', mRNA sequence.
ACCESSION   BQ708635
VERSION   BQ708635.1 GI:21847534
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 913)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2476 row: i column: 01
High quality sequence stop: 663.

FEATURES   Location/Qualifiers
source   1..913
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/clone="IMAGE:6282312"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT   214 a   301 c   230 g   167 t   1 others
ORIGIN

Query Match   79.1%; Score 562.6; DB 14; Length 913;
Best Local Similarity 88.9%; Pred. No. 2.5e-140;
Matches 631; Conservative 0; Mismatches 75; Indels 4; Gaps 2;

Qy   4 AGGGTCCCCGCTCAGCTCCTGGGCTCCTGCTCCTCGCTCTGGCTCCCAGTGCACGATGTGAG   63
Db   36 ATGGCCTGGTCTCCTCCTCCTCACTCTTCCTCGCTCTGGCTCCCAGTGCACGATGTGAG   95

Qy   64 TCTGTCCTGACACAGCCGCGCCCTCCAGTGTCTCGGGGGCCCCAGGGCAGAAGGTCACCATCTCG   123
Db   96 TCTGTGCTAACGCAGCCGCGCCCTCCAGTGTCTCGGGGGCCCCAGGGCAGAGGGTCACCATCTCC   155

Qy   124 TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTC   180
Db   156 TGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATAATGTCACTGGTATCAGCACCTT   215

Qy   181 CCAGGAACCGCCCCCAAACTCCTCATCTCGGTACCGCGGCCTCCCTGGCTCCATCACTCGG   240
Db   216 CCAGGAACAGCCCCCAAACTCCTCATCTATGATAACAGCAATCGGCCCTCCAGGGGTCCCT   275

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCAA   300
Db   276 GACCGATTTTCTGGCTCCAAGTCTGGCCACTTCAGCCTCCTGGCCATCACTGGGCTCCAG   335

Qy   301 ACTGAGGGATGAGGCTGATTATTACTGCCAGTGTCCAGTCCTTAGGTCAGCCCCCTCAGTCACT   360
Db   336 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCAGCCTGAATGCTCAGTA   395

Qy   361 TTCCGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGTGCCCCTCCGGTCACT   420
Db   396 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGTGCCCCTCCGGTCACT   455

RESULT 2
BQ708635
LOCUS   BQ708635   913 bp   mRNA   linear   EST 16-JUL-2002

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/db_xref="taxon:9606"
/clone="IMAGE:6278335"
/clone_lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT   218 a   303 c   256 g   172 t   7 others
ORIGIN

Query Match   80.1%; Score 569.2; DB 14; Length 956;
Best Local Similarity 88.6%; Pred. No. 4.2e-142;
Matches 629; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy   3 GAGGGTCCCCGCTCAGCTCCTGGGCTCCTGCTCCTCGCTCTGGCTCCCAGTGCACGATGTGA   62
Db   22 GATGGCCTGGTCTCCTCCTCCTCACTCTTCCTCGCTCTGGCTCCCAGTGCACGATGTGA   81

Qy   63 GTCTGTCCTGACACAGCCGCGCCCTCCAGTGTCTCGGGGGCCCCAGGGCAGAAGGTCACCATCTC   122
Db   82 GTCCGTGCTGACGCAGCCGCGCCCTCCAGTGTCTGGGGGCCCCAGGGCAGGGGGTCACCATCTC   141

Qy   123 GTGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCT   179
Db   142 CTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGTACACTGGTACCAGCAGCT   201

Qy   180 CCCAGGAACCGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGGATTTC   239
Db   202 TCCAGGAACAGCCCCCAAACTCCTCATCTCTAACAACAGCAGCAATCGGCCCTCAGGGGTCCC   261

Qy   240 TGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCTCCATCACTGGGCTCCA   299
Db   262 TGACCGATTTCTCTGGCTCCAAGTCTGGCACGTCAGCCTCCCTGGCTCCATCGCTCTGGGCTCCA   321

Qy   300 GACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCAGCCTGAATGCTCAGGT   359
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Qy   360 ATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCCGGTCAC   419
Db   382 GTTCGGCGGAGGGACCAAGGCTGACCGTCCTAAGTCAGCCCAAGGCTGCCCCTCCGGTCAC   441

Qy   420 TCTGTTCCCGCCCTCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCAT   479
Db   442 TCTGTTCCCGCCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCAT   501

Qy   480 AAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAA   539
Db   502 AAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAA   561

Qy   540 GGCGGGAGTGGAGACCACCACACCCTCCAAACAAACAACAACAGTACGCGGCCAGCAG   599
Db   562 GGCGGGAGTGGAGACCACCACACCCTCCAAACAAACAACAACAGTACGCGGCCAGCAG   621

Qy   600 CTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCGTTGCCAGTCAC   659
Db   622 CTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCGTTCCCAGTCAC   681

Qy   660 GCATGAAGGAGGAGCCTGGAGAAGACAGCAGTGGCCCCTTACAGAAGAATGTTCAT   709
Db   682 GCATGAAGGGAGGAGCCTGGAGAAGACAGCAGTGGCCCCTTACAGAAGAATGTTCAT   731

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Db     65 CAGGGTCCTGGGCCAGTGTGCTGACTCAGCCACCCTCAGCCTGCGACCCCGGGGC    124
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Qy    107 AGAGGTCACCATCCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTCATT    166
          |||  |||||||||  |||| ||   | || |||||||| ||||||
Db    125 AGAGGTCACCATCTCTTGTTCTGGAAGCAGCTTCCAACATCGGAAGTAATCCTCTAAACT   184
Qy    167 GGTACCAGAGCTCCCCAGGAAACGGCCCCCCAAACTCCTCATCTATGACATTAACAGGGAC   226
          |||||||||||||||||||||||||||||||||||||||||||||||  |||| | |||| |
Db    185 GGTACCAGAGCTCCCCAGGAAACGGCCCCCCAAACTCCTCATCTATAGTTATAATCAGGGGC   244
Qy    227 CCTCAGGAATTTCTGACCGATTCTCGGCTCCAAGTCGTTGTACCGGCCTCCCTGGCCA     286
          ||||||   | |||||||||||||||||||||||||     ||| ||| ||||||||||
Db    245 CCTCAGGGGTCCCTGACCGATTCTCGGCTCCAAGTCTCGGCCACCTCAGCCTCCCTGGCCA   304
Qy    287 TCACTGGGCTCCGAGATGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC    346
          ||| ||||||||  || ||||||||||||||||||||||||  |||||| |||||||||
Db    305 TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCC    364
Qy    347 TGAATGCTCAGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTG   406
          ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 TGAATGCTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTG   424
Qy    407 CCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGTTCAAGCCAACAAGGCCACAC    466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 CCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGTTCAAGCCAACAAGGCCACAC    484
Qy    467 TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATA   526
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATA   544
Qy    527 GCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGT    586
          ||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db    545 GCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCACCACCCTCCAAACAAAGCAACAACAAGT   604
Qy    587 ACGGCGGCCAGCAGTACCTGAGCCTGACCGTGGAAGTCCCACAGAGCTACA    646
          ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    605 ACGGCGGCCAGCAGTATCTGAGCCTGACCGTGGAAGTCCCACAGAGCTACA    664
Qy    647 GCTGCCAGGTCACCCATGAAGGGAGCAGTGGCCCCTACACGAATGTT     706
          ||||||||||||||||||||||||      ||||||||||||||||
Db    665 GCTGCCAGGTCACCCATGAAGGGAGAGACAGTGGCCCCTACACGAATGTT   724
Qy    707 CAT     709
          |||
Db    725 CAT     727
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RESULT 4
BG685644

```
LOCUS       BG685644        819 bp    mRNA     linear   EST 01-MAY-2001
DEFINITION  602637629F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765518 5',
            mRNA sequence.
ACCESSION   BG685644
VERSION     BG685644.1  GI:13917041
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 819)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
```

```
Qy    421 CTGTTCCCGCCCTCCTCTGAGGAGTCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA    480
          ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db    456 CTGTTCCCGCCCTCCTCTGAGGAGTCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA    515
Qy    481 AGTGACTTCTACCCGGGAGGCCGTGACAGTGCCTGAAGGCAGATAGCAGCCCCGTCAAG     540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 AGTGACTTCTACCCGGGAGGCCGTGACAGTGCCTGAAGGCAGATAGCAGCCCCGTCAAG     575
Qy    541 GCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC    600
          ||||||||||||||||||||       |||||||||||||||||||||||||||||||||
Db    576 GCGGGAGTGGAGACCACCACCACCACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC   635
Qy    601 TACCTGAGCCTGCTGAGCGCTGAGCCGTGGAAGTCCCAGAGAAGCTACAGCTCACG      660
          ||||||||||||| ||||| |||||||||||||||||||  |||||||||||||||
Db    636 TACCTGAGCCTGCCGAGCGCTGAGCCGTGGAAGTCCCAACAAAGCTACAGCTACAGCTCCAGGTCACG   695
Qy    661 CATGAAGGGAGGAGACCGTGGAGAAGACAGTGG-CCCCTACAGAATGTTCAT      709
          ||||||||||||||||||||||||||||||||  |||||||||||||||||
Db    696 CATGAAGGGAGGAGACCGTGGAGAAGACAGTGCCCCCTACAGAATGTTCAT       745
```

RESULT 3
BQ708570

```
LOCUS       BQ708570        894 bp    mRNA     linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976221 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214845
            5', mRNA sequence.
ACCESSION   BQ708570
VERSION     BQ708570.1  GI:21847469
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2382 row: m column: 22
            High quality sequence start: 11
            High quality sequence stop: 654.
FEATURES             Location/Qualifiers
     source          1..894
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6214845"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACCAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT    209 a  291 c  217 g  168 t   9 others
ORIGIN

Query Match      78.6%;  Score 559;  DB 14;  Length 894;
Best Local Similarity  90.2%;  Pred. No. 2.3e-139;
Matches  598;  Conservative  0;  Mismatches  65;  Indels  0;  Gaps  0;

Qy     47 CAGGTGCACGATGTGAGTCTCCTGACACAGCCGCCCTCCAGTGTCTGGGGCCCCAGGGC    106
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```
RESULT 5
BQ712653
LOCUS       BQ712653                873 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7983297 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215395
            5', mRNA sequence.
ACCESSION   BQ712653
VERSION     BQ712653.1  GI:21851552
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 873)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2384 row: d  column: 20
            High quality sequence stop: 530.
FEATURES             Location/Qualifiers
     source          1..873
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6215395"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      206 a    284 c    221 g    162 t
ORIGIN
Query Match            78.5%;  Score 557.8; DB 14;  Length 873;
Best Local Similarity  88.6%;  Pred No. 4.7e-139;
Matches  628;  Conservative   0;  Mismatches  77;  Indels   4;  Gaps   2;

Qy          4 AGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCCTCCTCCTGCTCCTGCTCCCAGGTGCACCGATGTGAG   63
              ||||||  ||  |||| |||||||||||||||||||||||| || ||||||  ||||||| ||||||||||
Db         22 ATGGCCTGGTCTCCTCCTCCTCCTCCGCTCACTCTGCACAGGTCCTGGGCCCCCAGGCAGGTCCTGGGCCCAG   81

Qy         64 TCTGTCCTGACACAGCCGCCCCCTCAGTGTCTGGGGCCCCAGGGCAGGAAGGTCACCATCTCG   123
              ||||||||||||||||||||||||||||||||||||||||
Db         82 TCTGTGCTGACGCAGCCGCCCCGCCCCTCAGTGTCTGGGGCCCCAGTGTCTGGGGCCCCAGGGCAGGGCAGGGTCACCATCTCC   141

Qy        124 TGCACTGGGAGCACTTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTC   180
              ||||||||||||||||||| ||||  | || ||| ||||| ||||||||||| ||||||||
Db        142 TGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTTATGATGTACACTGGTACCAGCAGCTT   201

Qy        181 CCAGGAACGGCCCCCAAACTCCTCATCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT   240
              ||||||||  |||||||||||||||||||||||||| ||| | |||||||| || | |||||||
Db        202 CCAGGAACAGCCCCCAGACTCCTCATCATGTATGATGTAACGAGCAATCGGCCCTCAGGGGTCCCT   261

Qy        241 GACCGATTCTCTGGCTCCAAGTCTGGCCTGGGCGGAGCCGTCACACTGGCTCCAG   300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GACCGATTCTCTGGCTCCAAGTCTGGCCTGGGCTCCATCACTCTGGGCTCCAG   321

Qy        301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATG--CTCAG   357
              |||||||||||||||||||||||||||||||||||||||||||| || || |  |||||
Db        301 ACTGAGGATGAAGGGGACTGGGGAGAGAGAGAGCAGTGGGCCCCTACGAGCGCTGAATGCTGTTCAT   360
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          High quality sequence stop: 812.
FEATURES             Location/Qualifiers
     source          1..819
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4765518"
                     /clone_lib="NIH MGC 48"
                     /tissue_type="Primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit (Life Technologies).
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      178 a    264 c    225 g    152 t
ORIGIN
Query Match            78.6%;  Score 558.6; DB 139;  Length 819;
Best Local Similarity  89.3%;  Pred No. 2.8e-139;
Matches  637;  Conservative   0;  Mismatches  69;  Indels   7;  Gaps   3;

Qy          4 AGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCCTCCTCCTGCTCCTGCTCCCAGGTGCACCGATGTGAG   63
              ||||||  ||  |||| |||||||||||||||||||||||| || ||||||  |||||||
Db         36 ATGGCCTGGTCTCCTCCTCCTCCTCCGCTCACTCTGCACAGGTCCTGGGCCCCCAGGCAGGTCCTGGGCCCAG   95

Qy         64 TCTGTCCTGACACAGCCGCCCCCTCAGTGTCTGGGGCCCCAGGGCAGGAAGGTCACCATCTCG   123
              ||||| ||||| ||||||||  |||||||||||||||||||
Db         96 TCTGTGCTGACGCAGCCGCCCCGCCCCTCAGTGTCTGGGGCCCCAGTGTCTGGGGCCCCAGGGCAGGGTCACCATCTCC   155

Qy        124 TGCACTGGGAGCACTTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTC   180
              ||||||||||||||||||| ||||  | || ||| ||||| ||||||||||| ||||||||
Db        156 TGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTTATGATGTACACTGGTACCAGCAGCTT   215

Qy        181 CCAGGAACGGCCCCCAAACTCCTCATCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT   240
              ||||||||  |||||||||||||||||||||||||| ||| | |||||||| || | |||||||
Db        216 CCAGGAACAGCCCCCAGACTCCTCATCATGTATGATGTAACGAGCAATCGGCCCTCAGGGGTCCCT   275

Qy        241 GACCGATTCTCTGGCTCCAAGTCTGGCCTGGGCGGAGCCGTCACACTGGCTCCAG   300
              |||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        276 GACCGATTCTCTGGCTCCAAGTCTGGCCTGGGCTCCATCACTCTGGGCTCCAG   335

Qy        301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATG--CTCAG   357
              |||||||||||| |||||||||||||||||||||||||||||||| || || |  |||||
Db        336 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATG-CTGTTTGTG   395

Qy        358 GTATTCGGAGGAGGGACCCGGCTGACCGTGCTGGGGCTCCTGCTCCTCCTCCTGCTCCCGGTC   417
              |||||||||||||| |||||||||||||||||||||||||||||||||||
Db        396 GTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTC   455

Qy        418 ACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGGCCAACAGGCCACACTGGTGTGTCTC   477
              ||||||||||| ||||||||||||||||||||||||||
Db        456 ACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTC   515

Qy        478 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC   537
              |||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        516 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC   575

Qy        538 AAGGCCGGAGTGGAGACCACCACACCCTCCAAACAACCCAGCAGCAACAGTACGCGGCCAGC   597
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        576 AAGGCCGGAGTGGAGACCACCACACCCTCCAAACAACCCAGCAACAACAAGTACGCGGCCAGC   635

Qy        598 AGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTCACAGCTGCCAGGTC   657
              ||||||| ||||||| ||||||||||||||||||||||||||||||||||||||
Db        636 AGCTATCGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACGTACAGCTGCCAGGTC   695

Qy        658 ACGCATGAAGGGAGCACCG-TGGAGAAGACAGTGCCCCTACAGAATGTTCAT   709
              ||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        696 ACGCATGAAGGGAGCACCGTGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT   748
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Query Match   78.1%;   Score 555.6; DB 12; Length 755;
Best Local Similarity   89.5%;   Pred. No. 1.8e-138;
Matches 621; Conservative   0; Mismatches 69; Indels   4; Gaps   2;

Qy   4 AGGGTCCCGCTCAGCTCCTGGGGCTCCTGTCCTGGGGCTCCTGGCTCTGGCTCCGGTGCACGATGTGAG   63
            ||||| |||||||||||||||||||||||||||||||||||||
Db   21 ATGCCTGTCTCCTCTCCTCCGCTCCTCCTCACTCTCCTCGCTCACTGACACAGGGTCCTGGGCCCAG   80

Qy   64 TCTGTCCTGACACAGCCGCCTCCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCTCG   123
            |||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Db   81 TCTGTGCTGACGCGACCGCCCTCCAGTGTCTGGGGCCCCA-GGCAGAGGGTCACCATCTCC   139

Qy   124 TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGTC   180
            ||||||||||||||||||||||||||| |||||||||||||||| |||||||||||
Db   140 TGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGACTGTACCAGCAGCTT   199

Qy   181 CCAGGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGGACACCTCAGGAATTTCT   240
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   200 CCAGGAACAGCCCCAAACTCCTCATTCATTATGGTAACAGCAATCGGCCCTCAGGGGTCCCT   259

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGGCCTCCTGGCCATCACTGGGCTCCAG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   260 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCGCTCCTGGCCATCACTGGGCTCCAG   319

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCCTATGAATGCTCAGTA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   320 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCCTGAGTGGTTGGGTG   379

Qy   361 TTCGGAGGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCTCGGTCACT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   380 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT   439

Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   440 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA   499

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG   540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   500 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG   559

Qy   541 GCGGGAGTGGAGACCACCACCCCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   560 GCGGGAGTGGAGACCACCACCCCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC   619

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGTCGAAGTCTACAGCTGCCACG   660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   620 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGTCGAAGTCTACAGCTGCCACG   679

Qy   661 CATGAAGGGAGCACCGTGAGAAGACAGTGGCCC   694
            ||||||||||||||||||||||||||||||||||
Db   680 CATGAAGGGAGCACCGTGAGAGACACAGTGGCCC   713

RESULT 7
BM920020
LOCUS   BM920020   1007 bp   mRNA   linear   EST 12-MAR-2002
DEFINITION   AGENCOURT_6708356 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5749861
              5', mRNA sequence.
ACCESSION   BM920020
VERSION   BM920020.1 GI:19370399
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1007)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Life Technologies, Inc.

Db   322 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCCTGAGTGGGTGATG   381

Qy   361 TTCGGAGGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCTCGGTCACT   420
            ||||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   382 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCTCGGTCACT   441

Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   442 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA   501

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG   540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   502 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG   561

Qy   541 GCGGGAGTGGAGACCACCACCCCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   562 GCGGGAGTGGAGACCACCACCCCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC   621

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGTCTGCCAGGTCACG   660
            |||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Db   622 TATCTGAGCCTGACGCCTGAGCAGTGGAAATCCCA-AAAGCTACAACTGGCAGTCACG   680

Qy   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT   709
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   681 CATGAAGGGAGCACCGTGGAGAAACAGTGGCCCCTACAGAATGTTCAT   729

RESULT 6
BG755185
LOCUS   BG755185   755 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION   602714114F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854290 5',
              mRNA sequence.
ACCESSION   BG755185
VERSION   BG755185.1 GI:14065838
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 755)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM1701 row: 1 column: 03
              High quality sequence stop: 753.
FEATURES   Location/Qualifiers
     source   1..755
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4854290"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT   165 a   249 c   203 g   138 t
ORIGIN

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12779 row: o column: 14
High quality sequence stop: 712.

FEATURES
    source   1..1007
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5749861"
                    /clone_lib="NIH_MGC_120"
                    /lab_host="DH10B"
                    /note="Organ: pooled pancreas and spleen; Vector:
                    pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                    source anonymous pool of spleen and pancreas from 28 yo
                    male. Library is oligo-dT primed and directionally cloned
                    (EcoRV site is destroyed upon cloning). Average insert
                    size 1.5 kb, insert size range 1-2.5 kb. Library is
                    normalized and enriched for full-length clones and was
                    constructed by C. Gruber (Invitrogen). Research Genetics
                    tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT   253 a   336 c   232 g   173 t   13 others
ORIGIN

Query Match
Best Local Similarity   77.7%;
Matches   611;   Conservative

Score 552.2; DB 14; Length 1007;
Pred. No. 1.6e-137;
0;   Mismatches   98;   Indels   0;   Gaps   0;

Qy   1 ATGAGGGTCCCCGCTCCAGCTCCTGGGGCTCCTGCTTCTGGCTCCAGTGCACGATGT 60
Db   29 ATCATGACCTGTCCCCTCTCCTCCACCCTTCTCATTCACTGCACAGGGTCCTGGGCC 88

Qy   61 GAGTCTGTCCTGACACAGCCCCGCCCCTCAGTGTCTGGGCCCCAGAGGCAGAGAGGTCACCATC 120
Db   89 CAGTCTGTTGACGCAGCCGCCTCCTCAGTGTCTGCGGCCCCAGACAGAGAGGTCACCATC 148

Qy 121 TCGTGCACTGGGAGCACTCCAACATTGGAGGTTATGATCCTGGTATCAGCAGCTC 180
Db 149 TCCTGCTCTGGAAGGAGCTCCAACATTGGAAATAGTTGTCCTGGTATCAGCAGTTC 208

Qy 181 CCAGGAACGGCGCCCCAAACTCCTCATCTATGACAATAAACAAGGACCCTCAGGAATTTCT 240
Db 209 CCAGGACCAGCGCCCCCAACTCCTCATTTATGACAATGATAAGGACCCTCAGGGATTCCT 268

Qy 241 GACCGATTCTCTGGCTCCAAGTCCGGCACCGGCTCCCCTGGTACCGGGCTCCCATCACTGGGCTCCAG 300
Db 269 GACCGATTCTCTGGCTCCAAGTCTGGCACGTCCGCAGTCTCAGCCACCCTGGCCATCACTGGGCTCCAG 328

Qy 301 ACTGAGGATGAGGCTGATTATTACTGCAGTCCAGTCAGACAGCAGCCTGAATGCTCAGGTA 360
Db 329 ACTGAGGACGAGGCCGAATACTACTGCGGAACATGGGAATACCAGCCTGACTGCTGGGGTT 388

Qy 361 TTCGGCGGTGGGACCAGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
Db 389 TTCGGGCGGTGGGACCAAACTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 448

Qy 421 CTGTTCCCGCCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
Db 449 CTGTTCCCGCCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 508

Qy 481 AGTGACTTCTACCCGGGAGCCTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG 540
Db 509 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG 568

Qy 541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC 600
Db 569 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC 628

Qy 601 TACCTGAGCCTGACGCTGAGCAGTGAAGTCCCACAGAGTCCCAGAGAGCTACAGCTGCCAGGTCACG 660

(right column)

Db 629 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 688
Qy 661 CATGAAGGAGCACCGTGGAGAGAAGCAGTGGCCCTACCAGATGTTCAT 709
Db 689 CATGAAGGAGCACCGTGGAGAAGCAGTGGCCCCTACCAGATGTTCAT 737

RESULT 8
BM906351
LOCUS   BM906351   1060 bp   mRNA   linear   EST 12-MAR-2002
DEFINITION AGENCOURT_6620012 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590299
            5', mRNA sequence.
ACCESSION   BM906351
VERSION   BM906351.1 GI:19356730
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1060)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12364 row: g column: 04
            High quality sequence stop: 729.
FEATURES
    source   1..1060
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:5590299"
                    /clone_lib="NIH_MGC_125"
                    /lab_host="DH10B"
                    /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                    Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                    of three ovaries, from females ranging in age from 38 to
                    49 yo. Library is oligo-dT primed and directionally cloned
                    (EcoRV site is destroyed upon cloning). Average insert
                    size 2.1 kb, insert size range 1-3.5 kb. Library is
                    normalized and enriched for full-length clones and was
                    constructed by C. Gruber (Invitrogen). Research Genetics
                    tracking code 036."

BASE COUNT   257 a   338 c   259 g   204 t   2 others
ORIGIN

Query Match
Best Local Similarity   77.7%;
Matches   611;   Conservative

Score 552.2; DB 14; Length 1060;
Pred. No. 1.6e-137;
0;   Mismatches   98;   Indels   0;   Gaps   0;

Qy   1 ATGAGGGTCCCCGCTCCAGCTCCTGGGGCTCCTGCTTCTGGCTCCAGTGCACGATGT 60
Db   49 ATCATGACCTGTCCCCTCTCCTCCACCCTTCTCATTCACTGCACAGGGTCCTGGGCC 108

Qy   61 GAGTCTGTCCTGACACAGCCCCGCCCCTCAGTGTCTGGGCCCCAGAGGCAGAGAGGTCACCATC 120
Db 109 CAGTCTGTTGTTGACGCAGCCGCCTCCTCAGTGTCTGCGGCCCCAGACAGAGAGGTCACCGTC 168

Qy 121 TCGTGCACTGGGAGCAGCCCAACATTGGAGGTTATGATCCTGGTATCAGCAGCTC 180
Db 169 TCCTGCTCTGGAAGCAGCCCAACATTGGCCACATTGGGAGTAATTTAGTTTCCTGGTACCAACACCTC 228

Qy 181 CCAGGAACGGCGCCCCAAACTCCTCATCTATGACAATTAACAAGGACCCTCAGGAATTCT 240
Db 229 CCAGGGCGGCAGCCCCCATACTCCTCCTCATTTATGACAATAATAAGCGACCCTCAGGAATTCCT 288

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                                    Hong in the laboratory of Gerald M. Rubin (University of
                                    California, Berkeley) using ZAP-cDNA synthesis kit
                                    (Stratagene) and Superscript II RT (Life Technologies).
                                    Note: this is a NIH_MGC Library."

BASE COUNT      218 a      295 c      229 g      168 t
ORIGIN

Query Match    77.6%;   Score 551.6;  DB 12;  Length 910;
Best Local Similarity  88.9%;  Pred. No. 2.2e-137;
Matches 631;  Conservative  0;  Mismatches 74;  Indels  5;  Gaps  3;

Qy      4 AGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCCTGGTCCTGGCTCGCTCCCAGGTGCACGATGTGAG       63
          ||||| |||| ||||||| || ||   ||  |||  || |||||||||| ||||||
Db     36 ATGGCCTGGTCTCCTCTCCTCCCTCCACTCTCCTCGCTCACTGCAGCCCTGGGCCCAG       95

Qy     64 TCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCTCG      123
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db     96 TCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCC      155

Qy    124 TGCACTGGGAGCACCTCCAACATTGG---AGTTATGATCTACATTGGTACCAGCAGCTC      180
          |||||||||||||||| ||||||||   |||| || ||| |||| |||| ||||||||
Db    156 TGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGTTGTTCATTGTATCAGCAGCTT      215

Qy    181 CCAGGAACGGCCCCCAAACTTCCATCATCTATGACAATTAACAAGCGACCCTCAGGAATTTCT      240
          ||||||||||||||| ||||||| || |||||  || || ||||||||| |||||||||
Db    216 CCAGGAACAGCCCCCAAACTCCTCATCATGTTAACAACAATCGGCCCTCAGGGGTCCCT      275

Qy    241 GACCGATTCTCTGGCTCCAAGTCTGGTTCGGTACCGCGGCCTCCTGGCCATCACTGGGGTCCAG      300
          |||||||||||||||||||||| |||||||||||||| ||||||||| ||||||||||||
Db    276 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGCCTCCAG      335

Qy    301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCGCTGAATGCTCAGGTA      360
          ||| |||||||||||||||||||||||||||||||||||| || ||||||||||||||
Db    336 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTTCGGTG      395

Qy    361 TTCGGAGGAGGGACCCCGGCTGACCGTCCAGGTCAGCCCAGGCTCCTGCTCCTGGTCACT      420
          |||||||||||||||||||||||| |||||||||||||||||||||||||||| |||||
Db    396 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT      455

Qy    421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA      480
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    456 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA      515

Qy    481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG      540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG      575

Qy    541 GCGGGAGTGGAGACCACCACCCCATCCCAAACAAAAGCAAAGCAACAACAAGTACAGCC      600
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    576 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAAGCAAAGCAACAACAAGTACAGCGG-CAGCAGC      634

Qy    601 TACCTGAGCGTCACG--CCTGAGCAGTGGAAGTCCCAGAGTGGCCTGCCAGGTCAC      659
          ||||||||||||||  ||||||||||||||||||||||| ||||||||||||||
Db    635 TACCTGAGCCTGAGCGTGACGCCCTGAGCAGTGGAAGTCCCACAAAGCTACAGCCTGCCAGGTCAC      694

Qy    660 GCATGAAGGGAGCACCGTGGAGAAGACAGTGCCCTCTACAGAATGTTCAT      709
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    695 GCATGAAGGGAGCACCGTGGAGAAGACAGTGACCCCTACAGAATGTTCAT      744
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Qy    241 GACCGATTCTCTGGCTCCAAGTCTGGTTCGGTACCGCGGCCTCCTGGCCATCACTGGGGTCCAG      300
          |||||||||||||||||||| |  |||||||||| ||| |||||||||||||||||||||
Db    289 GACCGATTCTCTGGCTCCAAGTCTGACACGTCAGCCAGCCCTGGGCATCACTGGGGTCCAG      348

Qy    301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCCTGAATGCTGGGGGTA      360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 ACTGGGGGACGAGGGCCGATTATTACTGCGCAACATGGGATAACAGCCTGAATGCTGGGGGTA      408

Qy    361 TTCGGAGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT      420
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    409 TTCGGCGGGGGGACCAGGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT      468

Qy    421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA      480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA      528

Qy    481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG      540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG      588

Qy    541 GCGGGAGTGGAGACCACCACCCCATCCCAAACAAACAACAAGTACGGGCGGCCAGCAGC      600
          ||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Db    589 GCGGGAGTGGAGACCACCACACCCTCCAAACAAACAACAACAAGTACGGCGGCCAGCAGC      648

Qy    601 TACCTGAGCCTGAGCAGTGCAGTGCTACAGAGTCCCAGAGTCCCAGGTCACG      660
          ||||||||||||||||||||| |||||| ||||||||||||||||||||||
Db    649 TATCTGAGCCTGAGCAGTGGAAGTCCCACAGAGTCCCACAGAGTCCCAGGTCACG      708

Qy    661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTCAT      709
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    709 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTCAT      757
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AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Mark Watson
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2520 row: c  column: 19
           High quality sequence stop: 552.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT     183 a     286 c     235 g     153 t
ORIGIN
Query Match         77.3%;    Score 549.4;  DB 14;   Length 857;
Best Local Similarity   91.0%;    Pred. No. 8.5e-137;
Matches   607;  Conservative    0;  Mismatches   56;  Indels    4;  Gaps    2;

Qy          47 CAGGTGCACGATGTGAGCTCGTCTGACACAGCGCGCCCCAGTGTCTGGGGCCCCCAGGGC 106
               |||||  |||||| | | |||||||||||||| || |||||||||||||||||||||||||
Db          72 CAGGGTCCTGGGCCAGTCGTGTCGCTGACGCGGCAGCAGCGCCCCCACTGTCTGGGGCCCCCAGGGC 131

Qy         107 AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAAACATTGG---AGGTTATGATCTAC 163
               |||||||||| | | |||||| ||||||||| |||| || |||||  |||||||||||||||
Db         132 AGAGGGTACCACCATCTCCTGCACTGGGAGCAGGTCCAACATCGGGCAGGTTATGATGTAC 191

Qy         164 ATTGGTACCAGCAGCTCCAGGAACGCCCCCAGAAAACTCCTCATCTATGACATTAACAAGC 223
               ||||||||||||| || ||||||| | |||||||| |||||||||||||||| |||||||||
Db         192 AGTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAAACTCCTCATCTATGGTAGCACCAATC 251

Qy         224 GACCCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGG 283
               ||||||||||      ||| |||||  |||||||||||||||||  |||| ||||||||||
Db         252 GGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG 311

Qy         284 CCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCA 343
               |||||||||||||||| |||||||||||||| |||||||||||||| |||||||||||||
Db         312 CCATCACTGGGCTCCAGGCTGACGATGAGGCTGATTATTACTGCCAGTCCTATGACGGCA 371

Qy         344 GCCTGAATGCTCAGGTATTCGGAGGAGGGACCCGGCTGACGCTGACCGTCCTAGGTCAGCCCAAGG 403
               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db         372 GCCTGAGTGGTGTGGTATTCGGCGGAGGGACCGGAGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGG 431

Qy         404 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCA 463
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         432 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCA 491

Qy         464 CACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG 523
               ||||||||||||||| | |||| ||||||||| ||||||||||||||||||||||||||||
Db         492 CACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG 551

Qy         524 ATAGCAGCCCCGTCAAGGCGGAGTGAGAGACCACCACCCTCCAAACAAACAACACA 583
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         552 ATAGCAGCCCCGTCAAGGCGGGAGTGAGACCACCACCCTCCAAACAAAGCAACAACA 611

Qy         584 AGTACGGCGGCCAGCAGCTACCTGACGCCTGAGCAGTGGAAGTCCCAGAGAAGCT 643
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               ||||||||||||||||||||||| |||||||||||||||||||||||||||| |||||||
Db         672 ACAGCTGCCAGGTCACGCATGAGGGGAGCACCGTGGAGAGACAGCAGTGCCCCTACAGAA 731

Qy         703 TGGTCAT 709
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Db         732 TGGTCAT 738
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RESULT 11
BG755548
LOCUS       BG755548                 764 bp    mRNA     linear   EST 15-MAY-2001
DEFINITION  602716230F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856574 5',
            mRNA sequence.
ACCESSION   BG755548
VERSION     BG755548.1  GI:14066201
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 764)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1707 row: k  column: 07
            High quality sequence stop: 755.
FEATURES             Location/Qualifiers
     source          1..764
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4856574"
                     /clone_lib="NIH_MGC 48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT     177 a     243 c     203 g     141 t
ORIGIN
Query Match         77.2%;    Score 549;  DB 12;   Length 764;
Best Local Similarity   85.9%;    Pred. No. 1.1e-136;
Matches   609;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy           1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCCTCCCCAGGTGCACGGATGT 60
               ||||||||| || |||| |||||||||||||||||||||||||||||||
Db          39 ATCATGACCTGCTCCCCTCCTCCTCCACCCTTCTCATTCACTGCACCAGGGTCCTGGGCC 98

Qy          61 GAGTCTGTCCTGACACAGCCGCCCCTCCAGTGTCTGGGGCCCAGAGAGGTCACCATC 120
               ||| | |||||| | | |||  |||| ||||||||||||||| |||||||||||||||
Db          99 CAGTCGTGTTGACGCAGCCGCCGCCCCTCCAATGTCTGCGGCCGCCCCAGAGAGGTCACCATC 158

Qy         121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATGTTACATTGGTTACCAGCAGCTC 180
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Db         177
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/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT   188 a   265 c   210 g   154 t
ORIGIN

Query Match   76.8%;   Score 546;   DB 13;   Length 817;
Best Local Similarity 86.5%;   Pred. No. 6.9e-136;
Matches 614;   Conservative   0;   Mismatches 95;   Indels   1;   Gaps   1;

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Qy    1 ATGAGGGTCCCGCTCAGCTCTGGGGCTTCTGCTTCTGGCTCCTGCTTCCCAGGTGCACGATGT 60
          ||||||||||||| | ||||||||||||||||||||||||| |||||||||||||||||||
Db   30 ATCATGACCTGCTCTCCTCTCTCCTCACCCCTCTCATTCACTGCACAGGGGTCCTGGGCC 89

Qy   61 GAGTCGTCTGACACAGCGCGCCCTCAGTGTCTGGGCCCCAGGCAGAAGGTCACCATC 120
          ||||||||| |||| ||| ||||||||||||||||||||||||||||||||||||||
Db   90 CAGTCGTGTTGACGCAGCGCCCCTCAATGTCTGCGCCCCTGGACAGGAGTCTCCATC 149

Qy  121 TCGTGCACTGGAGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
          |||| |||||||||||||||| |||| ||||| |||||| | || ||||||||||||||
Db  150 TCCTGCTCTGGAAGCAGCTCCAACATTGGAATAATTATGTATCCTGGTACCAACAGGTC 209

Qy  181 CCAGGAAGGCCCCCAAACTCCTCATCATTATGACATTAACAAGGACCCTCAGGAATTCT 240
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Db  210 CCAGGAACAGCCCCCAAACTCCTCATTATGACAATAATAAGGACCCTCAGGGATTCCT 269

Qy  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCCGCCGCTCCCTGGCCATCACTGGGCTCCAG 300
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Db  270 GACCGATTCTCTGGCTCCAAGTCTGGCACGTCGGCACGTCAGCCACCCTGGCCATCTCCGGACTCCAG 329

Qy  301 ACTGGGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCATGGTGTGTGCTA 360
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Db  330 ACTGGGGACGAGGCCGATTATTATTGCGGAACATGACAGTAGCAGCCTGAGTGGTGTTGTGCTA 389

Qy  361 TTCGGAGGAGGGACCCGGCTCACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
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Db  390 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 449

Qy  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCACAAGGCCACACTGGTGTGTCTCATA 480
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Db  450 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCACAAGGCCACACTGGTGTGTCTCATA 509

Qy  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
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Db  510 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 569

Qy  541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGGCCAGCAGC 600
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Db  570 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGGCCAGCAGC 629

Qy  601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGGAAGTCCCACAGAAGCTACA-GCTGCCAGGTCAC 659
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Db  630 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGTCCCACAGAAGCTACAGGCTGCCAGGTCAC 689

Qy  660 GCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 709
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RESULT 13
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LOCUS   BG685967   896 bp   mRNA   linear   EST 01-MAY-2001
DEFINITION   602638530F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766335 5',
             mRNA sequence.
ACCESSION   BG685967
VERSION   BG685967.1   GI:13917364
KEYWORDS   EST.

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Db  159 TCCTGCTCTGGAAGCAGGTCCAACATTGGAATAATTATGTGTCCTGGTACCAGCAGCTC 218

Qy  181 CCAGGAACGGCCCCCAAACTCCTCATCATTATGACATTAACAAGGACCCTCAGGAATTTCT 240
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Db  219 CCAGGTACAGCCCCGAACTCCTCATGATCTATGAAAATAGTAAGGACCCCTCAGGGGAATCTT 278

Qy  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCCGGCGCTCCCTGGCCATCACTGGGCTCCAG 300
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Db  279 GACCGATTCTCTGGCTCCAAGTCTGGCACGTCGGCACGTCAGCCACCCTGGCCATCACCGGACTCCAG 338

Qy  301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGTTA 360
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Db  339 ACTGGGGACGAGGCCGATTATTACTGCGGGACAATGGGATGACAGCCTGGTGGTTGGGTG 398

Qy  361 TTCGGAGGAGGGACCCGGCTCACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
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Db  399 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 458

Qy  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCACAAGGCCACACTGGTGTGTCTCATA 480
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Db  459 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCACAAGGCCACACTGGTGTGTCTCATA 518

Qy  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
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Qy  541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGGCCAGCAGC 600
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Db  579 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGGCCAGCAGC 638

Qy  601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTCACGTCACG 660
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Db  639 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTCACGTCACG 698

Qy  661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 709
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Db  699 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTCCAT 747
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RESULT 12
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LOCUS   B1835917   817 bp   mRNA   linear   EST 04-OCT-2001
DEFINITION   602085650F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5224645 5',
             mRNA sequence.
ACCESSION   B1835917
VERSION   B1835917.1   GI:15947467
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 817)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM11565 row: c column: 14
             High quality sequence stop: 817.
FEATURES   Location/Qualifiers
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SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 896)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
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                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      213 a     287 c     231 g     164 t     1 others
ORIGIN

Query Match        76.7%;  Score 545.4;  DB 12;  Length 896;
Best Local Similarity   88.2%;  Pred. No. 1e-135;
Matches 628;  Conservative   0;  Mismatches   77;  Indels    7;  Gaps    3;

Qy      4 AGGGTCCCGTCAGTCCTGGGGCTCCTGTGTCTCTGGCTCTCCAGTGCACGATGTGAG 63
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Qy     64 TCTGTCTGACACAGCCACCTCCAGTGTCTGTGGGGCGCCTCAGTGTCTCGGGGGCCCGCC 123
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Db     99 TCTGTGCTGACGCAGCCGCCCTCCAGTGTCTGGGGGCAGGAGGTCAGAAGGTCACCATCTCG 158

Qy    124 TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTCATCTATGACATTAACAAG 180
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Db    159 TGCACTGGGAGCAGCAGTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTT 218

Qy    181 CCAGGAACGGCCCCAAACTCCTATCTATGACATTAACAAGGCGACCCTCAGGAATTCT 240
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Db    219 CCAGGAACAGCCCCCAAACTCCTATCTATGATGTACACTGGTACACTGGTACCAGCAGCTT 278

Qy    241 GACCGATTCTCTGGCTCCAAGTCTCGGTCCAAGTCTCGGTACCGGCGCCCTCCGGCC 300
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Db    279 GACCGATTCTCTGGCTCCAAGTCTCAGCCTCCGGCCATCACTGGGCTCCAG 338

Qy    301 ACTGAGGATGAGGCTGATTATTACTGCGCCAGTCCTATGACAGCAGCCTGAATGCTCA---G 357
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Db    339 GCTGAGGATGAGGCTGATTATTACTGCGCCAGTCCTATGACAGCAGCAGCTGGTGGTCATGTG 398

Qy    358 GTATTCGGAGGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGGCTGCCCCCTCGGTC 417
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Db    399 GTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGGCTGCCCCCTCGGTC 458

Qy    418 ACTCTGTTCCGCCCTCCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTC 477
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Db    459 ACTCTGTTCCGCCCTCCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTC 518

Qy    478 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC 537
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Db    519 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC 578

Qy    538 AAGGCGGGAGTGGAGACCACCACACCTCCAAACAAAGCAACACAACAGTACGCGGCCAGC 597
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Db    579 AAGGCGGGAGTGGAGACCACCNAACCTCCAAACAAAGCAAACAAGCAACAAGTACGCGGCCAGC 638

Qy    598 AGTACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGTACAGTGCCAGTC 657
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Db    639 AGTATCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGTACAGTGCCAGGTC 698

Qy    658 ACGCATGAAGGAGGAGCACCGTGGAAGACAGTGGCCCTACAGAGAATGTTCAT 709
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Db    699 ACGCATGAAGGAGGAGCACCGTGAGAAGAACCCGTGG-CCCTACAGAGAATGTTCAT 749

RESULT 14
BG686957
LOCUS       BG686957                823 bp     mRNA        linear    EST 01-MAY-2001
DEFINITION  602650951F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763148 5',
            mRNA sequence.
ACCESSION   BG686957
VERSION     BG686957.1  GI:13918354
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 823)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1618 row: f  column: 13
            High quality sequence stop: 808.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      198 a     261 c     213 g     151 t
ORIGIN

Query Match        76.6%;  Score 544.8;  DB 12;  Length 823;
Best Local Similarity   91.0%;  Pred. No. 1.4e-135;
Matches 590;  Conservative   0;  Mismatches   57;  Indels    1;  Gaps    1;

Qy     62 AGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCT 121
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Db     17 AGTCTGTGCTGACTCAGCCACCCTCAGCCGTCTGGGACCCCGGGCCAGGAGGGTCACCATCT 76
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/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT   202 a   280 c   213 g   154 t
ORIGIN

Query Match   76.6%; Score 544.6; DB 12; Length 849;
Best Local Similarity 87.2%; Pred. No. 1.6e-135;
Matches 620; Conservative 0; Mismatches 89; Indels 2; Gaps 2;

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Qy   61 GAGTCTGTCCTGACACAGCCGCCCGCCCTCAGTGTCTGGGGCCCCAGGAAGGTCACCATC  120
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Db   89 CAGTCTGTGTTGACGCAGCGCCCTCAGTGTCTGCGGCCCCAGGACAGCAGAAGGTCACCATC  148

Qy  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC  180
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Db  149 TCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAACTC  208

Qy  181 CCAGGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGGCACCCTCAGGAATTTCT  240
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Db  209 CCAGGAACAGCCCCCAAACTCCTCATCTATGAAAATAATAAGCGACCCTCAGGGATTCCT  268

Qy  241 GACCGATTCTCTGGCT-CCAAGTCTGGTACCGCGGCTCCCCTGGCCATCACTGGGCTCCA  299
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Db  269 GACCGATTCTCTGCTCCCAAGTCTGGCACGTCAGCCATCACCGGGCTCCA  328

Qy  300 GACTGAGGATGAGGCTGATTATTACTGCGGAACATGGGATAGCAGCCTGAATGCTCAGGT  359
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Db  329 GACTGGGGGACGAGGCCGATTATTATTACTGCGGAACATGGGATAGCAGCCTGAGTGCTGGGGT  388

Qy  360 ATTCGGAGGAGGGACCCGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCAC  419
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Qy  480 AAGTGACTTCTACCCGGGAGAGCCGGTGACAGTGGGCCTGGAAGGCAGCAGCGATAGCAGCCCCGTCAA  539
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Db  509 AAGTGACTTCTACCCGGGAGAGCCGGTGACAGTGGGCCTGGAAGGCAGCAGCGATAGCAGCCCCGTCAA  568

Qy  540 GGCGGGAGTGGAGACCACCACACCCTCCAAACAGCAGTCAGCAACAACAAGTACGCGGCAGCAG  599
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Db  569 GGCGGGAGTGGAGACCACCACACCCTCCAAACAGCAGTCAGCAACAACAAGTACGCGGCCAGCAG  628

Qy  600 C-TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGAGCAAGCTCACAGTCACAGGTCA  658
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Db  629 CTTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAAAGTCACAGTCACCAGGTCA  688

Qy  659 CGCATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT  709
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Db  689 CGCATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT  739
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Search completed: April 6, 2003, 06:20:40
Job time : 1357.28 secs

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Qy  182 CAGGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGGCACCCTCAGGAATTTCTG  241
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Qy  302 CTGAGGATGAGGCTGATTATTACTGCCGAGTCTCATGCACGTCCTATGACAGCAGCCTGAGTGGTGGTAT  361
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Db  257 CCGAGGATGAGGCTGATTATTCCTGTGCAGCGATGACCCCAAGGGCTGCCCCTCGAGTGGTGGTAT  316

Qy  362 TCGGAGGAGGGACCCGCTGACCGTCCTAGGTCAGCCCCCAAGGCTGCCCCTCGGTCACTC  421
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Db  317 TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCCCAAGGCTGCCCCTCGGTCACTC  376

Qy  422 TGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAA  481
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Db  377 TGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAA  436

Qy  482 GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGCAGATAGCAGCCCCGTCA  541
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Db  437 GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGCAGATAGCAACAACCGTCA  496

Qy  542 CGGGAGTGGAGACCACCACACCCTCCAAACAGCAGTCAGCAACAAGTACGCGGCCAGCAGCT  601
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Db  497 CGGGAGTGGAGACCACCACACCCTCCAAACAGCAGTCAGCAACAACAAGTACGCGGCCAGCT  556

Qy  602 ACCTGAGCCTGAGCGCTGGAAGTCCCACAGCTACAGCGTCAGCTGCCAGTCACGC  661
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Qy  662 ATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT  709
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RESULT 15
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LOCUS   BG756887   849 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602710380F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850923 5',
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ACCESSION   BG756887
VERSION   BG756887.1 GI:14067540
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 849)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1692 row: o column: 20
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FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"

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              GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:    April 5, 2003, 18:12:24 ; Search time 195.124 Seconds
                                       (without alignments)
                            8205.894 Million cell updates/sec

Title:          US-09-758-173-9
Perfect score:  711
Sequence:       1 ATGAGGGTCCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 711

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters:    4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_101002:*
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       2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	711	100.0	711	19	AAV35488	Macaque primatized
2	711	100.0	711	24	AAS17246	DNA sequence of a
3	709.4	99.8	711	18	AAT62512	Primatised anti-hu
4	582.6	81.9	935	22	AAC66525	Human immune syste
5	571.4	80.4	884	11	AAQ03609	Sequence encoding
6	565.2	79.5	762	22	AAC84209	Plasmid Glambda-1B
7	558.8	78.6	5679	22	AAC84207	Plasmid Glambda-1A
8	558.2	77.7	768	22	AAX06953	Monoclonal antibod
9	552.6	77.7	768	20	AAX06954	Monoclonal antibod
10	547	76.9	654	14	AAQ49835	Anti-HIV-1 recombi
11	546.2	76.8	810	23	AAS87270	DNA encoding novel
12	540.2	76.0	705	18	AAT62509	Primatised anti-hu
13	540.2	76.0	705	19	AAV35484	Macaque primatized
14	540.2	76.0	705	24	AAS17242	DNA sequence of a
15	533.2	75.0	651	19	AAV11293	Antibody HB4C5 lig
16	533.2	75.0	708	22	AAH47902	Human type antihum
17	532.2	74.9	915	24	ABN97248	Gene #3746 used to
18	532.2	74.9	915	24	ABK64815	Human benign prost
19	532.2	74.9	915	24	ABL65478	Lung cancer relate
20	530.2	74.6	895	22	AAC66530	Human immune syste
21	523.6	73.6	708	22	AAH47904	Human type antihum
22	522.8	73.5	1845	24	ABL49526	Plasmid scFv(CC046
23	518.8	73.0	708	22	AAH47898	Human type antihum
24	510.6	71.8	891	22	AAC66528	Human immune syste
25	509.2	71.6	763	23	AAS83480	DNA encoding novel
26	502.6	70.7	902	14	AAQ35100	Antibody D lambda
27	499.4	70.2	889	23	AAS77073	DNA encoding novel
28	498.6	70.1	906	22	AAK51914	Human polynucleoti
29	496.4	69.8	951	23	AAS90539	DNA encoding novel
30	494.4	69.5	783	23	AAS83483	DNA encoding novel
31	494.4	69.5	876	23	AAS83478	DNA encoding novel
c 32	493.8	69.5	888	21	AAA95786	Human immune syste
c 33	487.4	68.6	1636	23	ABV22585	Human prostate exp
34	487.4	68.6	1636	23	ABV28405	Human prostate exp
35	486.6	68.4	756	23	AAS83477	DNA encoding novel
36	484.2	68.1	885	19	AAV34321	Human secreted pro
37	482.6	67.9	879	19	AAV34304	Human secreted pro
38	480.6	67.6	1636	23	ABV22585	Human prostate exp
39	480.6	67.6	1636	23	ABV28405	Human prostate exp
40	477	67.1	926	20	AA224427	Human bladder tumo
41	475.2	66.8	807	23	AAS83484	DNA encoding novel
42	470.4	66.2	872	9	AAN81655	VDJC regions of hu
43	468.4	65.9	702	18	AAT62867	Ant-CD4 monkey-hum
44	466	65.5	1027	24	ABQ54438	Human ovarian anti
c 45	465.6	65.5	849	22	AAH99186	Human EST-derived

ALIGNMENTS

```
RESULT 1
AAV35488
ID   AAV35488 standard; DNA; 711 BP.
XX
AC   AAV35488;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 16C10 light chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH            Location/Qualifiers
FT   Key
FT   CDS        1..711
FT              /*tag= a
FT              /product= 16C10 light chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
```

XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63764.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5a; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 16C10 light chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. Mab's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match   100.0%;   Score 711;   DB 19;   Length 711;
Best Local Similarity   100.0%;   Pred. No. 8.5e-172;
Matches   711; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCCTGGCTCCCGGATGT 60

Qy   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGG 120

Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGAGGTTATGATCTACATTGGTACC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCGTGCACTGGGAGCACCTCCAACATTGAGGTTATGATCTACATTGGTACC 180

Qy   181 CCAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAAGGCACCCTC 240
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Db   181 CCAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAAGGCACCCTC 240

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCTCCCCTGGCCATCACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCTCCCCTGGCCATCACT 300

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCATGATGACAGCAGCAGCC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCATGATGACAGCAGCAGCC 360

Qy   361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCTG 420

Qy   421 CTGTTCCCGCCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGT 480
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Db   421 CTGTTCCCGCCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGT 480

Qy   481 AGTGACTTCTACCCGGGAGAGTGCCGTGACAGTGGCCTGGAAGGCAGATAG 540
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Db   481 AGTGACTTCTACCCGGGAGAGTGCCGTGACAGTGGCCTGGAAGGCAGATAG 540

Qy   541 GCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGCCAGCAGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGCCAGCAGC 600

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCAGAAGTCCAGAAGTCTACAGCTGCCAGGTCACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCAGAAGTCCAGAAGTCTACAGCTGCCAGGTCACG 660

Qy   661 CATCAAGGGAGCACCGTGGAGAAGACAGTGGCCCTACAGAATGTTCATGA 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CATCAAGGGAGCACCGTGGAGAAGACAGTGGCCCTACAGAATGTTCATGA 711

RESULT 2
AAS17246
ID   AAS17246 standard; DNA; 711 BP.
XX
AC   AAS17246;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the light chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Location/Qualifiers
FT   Key
FT   CDS   1..711
FT   /*tag= a
FT   /product= "Light chain of 16C10 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11645.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 5a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or

Left column:

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CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present nucleic
CC   acid sequence encodes the light chain of 16C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match          100.0%;  Score 711;  DB 24;  Length 711;
Best Local Similarity 100.0%;  Pred. No. 8.5e-172;
Matches  711;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGACGATGT 60
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Db    1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGACGATGT 60

Qy   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120

Qy  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGTTATGATCTACATTGGTACCAGCAGCTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGTTATGATCTACATTGGTACCAGCAGCTC 180

Qy  181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAGGCGACCCTCAGGAATTTCT 240
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Db  181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAGGCGACCCTCAGGAATTTCT 240

Qy  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCCGGCTCCTGGGGCTCCATCACTGGGCTCCAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCCGGCTCCTGGGGCTCCATCACTGGGCTCCAG 300

Qy  301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360

Qy  361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420

Qy  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480

Qy  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540

Qy  541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAGTACGCGGCCAGCAGC 600
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Db  541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAGTACGCGGCCAGCAGC 600

Qy  601 TACCTGAGCCTGACCCTGACGAGTGGAGAGCTACAGTCTGCCAGTCACG 660
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Db  601 TACCTGAGCCTGACCCTGACGAGTGGAGAGCTACAGTCTGCCAGTCACG 660

Qy  661 CATGAAGGGAGCAGACAGTGCCCCTACAGAATGTTCATGA 711
          ||||||||||||||||||||||||||||||||||||||||
Db  661 CATGAAGGGAGCAGACAGTGCCCCTACAGAATGTTCATGA 711

RESULT 3
AAT62512
ID   AAT62512 standard; DNA; 711 BP.
XX
AC   AAT62512;
XX
DT   25-MAY-1997 (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 light chain DNA.
```

Right column:

```
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US10053.
XX
PR   07-JUN-1995;   95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01821.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 11; Fig 10A; 81pp; English.
XX
CC   2 DNA sequences (AAT62512 and AAT62513) respectively code for
CC   primatised forms (AAW01821 and AAW01822) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   16C10.  Cloned 16C10 light and heavy variable genes are inserted
CC   into an expression vector (pref. NEOSPLA) which contains human light
CC   and heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells.  Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressant for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 711 BP; 161 A; 226 C; 193 G; 131 T; 0 other;

Query Match          99.8%;  Score 709.4;  DB 18;  Length 711;
Best Local Similarity 99.9%;  Pred. No. 2.2e-171;
Matches  710;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGACGATGT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGACGATGT 60

Qy   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120

Qy  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGTTATGATCTACATTGGTACCAGCAGCTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGTTATGATCTACATTGGTACCAGCAGCTC 180

Qy  181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAGGCGACCCTCAGGAATTTCT 240
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Db  181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAGGCGACCCTCAGGAATTTCT 240

Qy  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCCTCCTGGGGCTCCATCACTGGGCTCCAG 300
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Db  301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360
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Query Match   81.9%;   Score 582.6;   DB 22;   Length 935;
Best Local Similarity   89.8%;   Pred. No. 5.2e-139;
Matches 637;   Conservative   0;   Mismatches 69;   Indels   3;   Gaps   1;

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Qy      4  AGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCTCGTCTCCTCGCTCCAGTGCACGATGTGAG    63
           |||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||
Db     74  ATGGCCTGGTCGTCCTCTCCTCACTCTCCTCGCTCCAGTGCACAGCAGGGTCCTGGGCCCAG   133

Qy     64  TCTGTCCGACACAGCGCCGCCCCTCCAGTGTCTCGGGCCCCAGGGCGAGAGGTCACCATCTCG   123
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    134  TCTGTGCTGACGGCAGCGCCGCCCAGTGTCTCGGGCCCCAGGGCCAGGGGGTCACCATCTCC    193

Qy    124  TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTC    180
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Db    194  TGCACTGGGAGCAGCTCCAACATCGGGGCAGGGGGTTATGATGTACACTGGTACCAGCAGCTT   253

Qy    181  CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTCT    240
           |||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    254  CCAGGAACAGCCCCCCAAACTCCTCATCTATGTAGTAGAAATCGGCCCTCAGGGGTCCCT    313

Qy    241  GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCCTCCCTGGCCATCAGTCTGGCTCCAG    300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314  GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTCTGGCTCCAG    373

Qy    301  ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAATGCTCAGGTA    360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374  GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAGTGTGTGGTA    433

Qy    361  TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT    420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434  TTCGGCGGGGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT    493

Qy    421  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA    480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA    553

Qy    481  AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGAATAGCAGCCCGTCAAG    540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554  AGTGACTACTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGAATAGCAGCCCGTCAAG    613

Qy    541  GCGGGAGTGGAGACCACCACACCCTCCAAACAACCTCAAAACAACAAGTACGCGGCCAGCAGC    600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614  GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGCAGC    673

Qy    601  TACCTGAGCCTGAGCGTCCAGAGTGGAAGTCCCACAGAAGTCACAGTTGCCAGGTCACG    660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674  TACCTGAGCCTGAGCGTCGACAGTGGAAGTCCCACAGAAGTCACAGTTACCAGGTCACG    733

Qy    661  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT    709
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT    782
```

RESULT 5
AAQ03609
ID   AAQ03609   standard;   cDNA;   884 BP.
XX
AC   AAQ03609;
XX
DT   06-AUG-1989   (first entry)
XX
DE   Sequence encoding 4G12 monoclonal antibody (MAb) L chain.
XX
KW   4G12 MAb; human lung cancer; oesophageal carcinoma; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   25..729
FT   /*tag= a
FT   /product=4G12 L
FT   misc_feature   25..375
FT   /*tag= b

```
Qy    361  TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT    420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT    420

Qy    421  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA    480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA    480

Qy    481  AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGAATAGCAGCCCGTCAAG    540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AGTGACTACTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGAATAGCAGCCCGTCAAG    540

Qy    541  GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGC    600
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGC    600

Qy    601  TACCTGAGCCTGAGCGTCCAGAGTGGAAGTCCCACAGAAGTCACAGTTGCCAGGTCACG    660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TACCTGAGCCTGAGCGTCGACAGTGGAAGTCCCACAGAAGTCACAGTTGCCAGGTCACG    660

Qy    661  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA    711
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA    711
```

RESULT 4
AAC66525
ID   AAC66525   standard;   cDNA;   935 BP.
XX
AC   AAC66525;
XX
DT   15-FEB-2001   (first entry)
XX
DE   Human immune system associated protein HISAP-7 coding sequence.
XX
KW   Human; immune system associated protein; HISAP-7; immune disorder;
KW   infection; autoimmune disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   US6135941-A.
XX
PD   24-OCT-2000.
XX
PF   27-MAR-1998;   98US-0049672.
XX
PR   27-MAR-1998;   98US-0049672.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI   Hillman JL, Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   P-PSDB; AAB36209.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing
PT   immune or cell proliferative disorders or infections -
XX
PS   Claim 3; Column 83-84; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAPs). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ   Sequence 935 BP; 216 A; 299 C; 248 G; 172 T; 0 other;

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FT    misc_feature      /label=V region
FT                      376..414
FT                      /*tag= c
FT    misc_feature      /label=J region
FT                      415..729
FT                      /*tag= d
FT    polyA_signal      /label=C region
FT                      835..840
FT                      /*tag= e
FT                      /number=1
FT    polyA_signal      856..861
FT                      /*tag= f
FT                      /number=2
XX
PN    JP0204628 9-A.
XX
PD    15-FEB-1990.
XX
PF    05-AUG-1988;    88JP-0196647.
XX
PR    05-AUG-1988;    88JP-0196647.
XX
PA    (YOSH ) YOSHITOMI PHARM. IND. KK.
XX
DR    WPI; 1990-094983/13.
DR    P-PSDB;AAR05555.
XX
PT    DNA base sequence coding for 4G12 monoclonal antibody - which reacts
PT    specifically with human lung cancer and oesophageal carcinoma.
XX
PS    Disclosure; Page 549; 9pp; Japanese.
XX
CC    Sequence is cloned and synthetic DNA/RNA of human Ab L chain C regions
CC    is used as probe to obtain sequences coding for 4G12 MAb.
CC    See also AAQ03607-Q03610.
XX
SQ    Sequence 884 BP; 219 A; 286 C; 212 G; 166 T; 1 other;

Query Match             80.4%;  Score 571.4;  DB 11;  Length 884;
Best Local Similarity   87.9%;  Pred. No. 3.7e-136;
  Matches   623;  Conservative    0;  Mismatches   .86;  Indels    0;  Gaps    0;

Qy      1 ATGAGGGTCCCCGCTCAGCTCCTGGGGGCTCCTGCTGCTCCTGGCTCCCAGGTGCACGATGT  60
          ||||||| |||||||||||||||||||   ||||||  |||||||||||| |||||||
Db     22 ATCATGACCTGCTCCCCTCTCCTCACCCTTCTCATTCACTGCACGGGTCTCTGGGCC  81

Qy     61 GAGTCTGTCCTGACACAGCCGCCGCCCCTCAGTGTCTGGGGCCCCCAGGGCAGAAGGTCACCATC 120
          |||||  ||||||||||||   |||||||||||||||||||||||||||||||||||||
Db     82 CAGTCTGTGTTGACGCAGCCGCCCCCCTCAGTGTCTGCGGCCCCCAGGACAGAAGGTCACCATC 141

Qy    121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACAGCAGCTC 180
          |||||  || ||||||||||||||||  ||||||||||||||  |||||||
Db    142 TCCTGCTCTGGAAGCAGCTCCAACATTGGAATAATTATGTATCCTGGTACCAGCAGCTC 201

Qy    181 CCAGGAACGGCCCCCAAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT 240
          ||||||  ||  |||| |||   ||| |||||| ||||| ||| ||| |||||||  |
Db    202 CCAGGAACAGCAGCCCCAAACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCT 261

Qy    241 GACCGATTCTCTGGCTCCAAGTCTGGCTACCGCGGCCTCCCTGGCTCACTGGGCTCCAG 300
          |||||||||||||| ||||||||||||||   |||  ||| |||| |||||||||||
Db    262 GACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAG 321

Qy    301 ACTGAGGATGAGGCTGATTATTACTGCACAGCTCCTATGACAGCAGCTGAATGCTCAGGTA 360
          |||||||||||  ||||||||||||||  |||||||||||  ||||| ||| |||||||
Db    322 ACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGAGTGCTGGGGTA 381

Qy    361 TTCGGAGGAGGGACCCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
          |||||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Db    382 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 441

Qy    421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 501
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Qy    481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 561

Qy    541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGGCGGCCAGCAGC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGGCGGCCAGCAGC 621

Qy    601 TACCTGAGCCTGACGCCTGAGAGTGAAGTCCCAGAGAGTCACAGTGCTGCCAGGTCACG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    622 TACCTGAGCCTGACGCCTGAGAGTGAAGTCCCAGAGAGTCACAGTGCTGCCACGTCACG 681

Qy    661 CATGAAGGAGGACACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 709
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    682 CATGAAGGAGGACACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 730
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```
RESULT 6
AAC84209
ID   AAC84209 standard; DNA; 762 BP.
XX
AC   AAC84209;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Plasmid Glambda-1Bpcn DNA sequence.
XX
KW   Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
KW   Glambda-1; human; virucide; RSV propagation; ds.
XX
OS   Homo sapiens.
XX
XX
PN   WO200069462-A1.
XX
PD   23-NOV-2000.
XX
PF   18-MAY-2000;  2000WO-US13694.
XX
PR   18-MAY-1999;  99US-0134702.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Gross MS,  Sweet RW,  Taylor G;
XX
DR   WPI; 2001-024947/03.
XX
PT   Human monoclonal antibody and functional fragments, useful for
PT   therapeutic and/or prophylactic treatment of respiratory syncytial
PT   virus infection, is specifically reactive with the F protein epitope of
PT   the virus -
XX
PS   Claim 3, 6; Fig 11; 102pp; English.
XX
CC   The invention provides a human monoclonal antibody (I) and its functional
CC   fragments specifically reactive with an F protein epitope of respiratory
CC   syncytial virus (RSV), and capable of neutralizing infection by the virus
CC   such as Glambda-1A or Glambda-1B. The antibody can be expressed by
CC   standard recombinant methodology. (I) is useful for detecting RSV by
CC   contacting a source suspected of containing RSV with (I) and determining
CC   whether (I) binds to the source. (I) is also useful for providing passive
CC   immunotherapy prophylactically, to RSV disease in a human. (I) is useful
CC   for therapeutic and/or prophylactic treatment of RSV infection in human
CC   patients, particularly infants and young children. (I) is also useful
CC   as a diagnostic reagent for the determination of RSV mediated disorders
CC   or for tracking progress of treatment of the disorders. The present
CC   sequence represents the continuous DNA sequence of the coding region of
CC   the light chain of plasmid Glambda-1Bpcn.
XX
SQ   Sequence 762 BP; 174 A; 241 C; 195 G; 152 T; 0 other;

Query Match             79.5%;  Score 565.2;  DB 22;  Length 762;
Best Local Similarity   91.6%;  Pred. No. 1.4e-134;
```

```
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Gross MS,   Sweet RW,   Taylor G;
XX
DR   WPI; 2001-024947/03.
XX
PT   Human monoclonal antibody and functional fragments, useful for
PT   therapeutic and/or prophylactic treatment of respiratory syncytial
PT   virus infection, is specifically reactive with the F protein epitope of
PT   the virus -
XX
PS   Claim 6; Fig 9A-E; 102pp; English.
XX
CC   The invention provides a human monoclonal antibody (I) and its functional
CC   fragments specifically reactive with an F protein epitope of respiratory
CC   syncytial virus (RSV), and capable of neutralizing infection by the virus
CC   such as Glambda-1A or Glambda-1B. The antibody can be expressed by
CC   standard recombinant methodology. (I) is useful for detecting RSV by
CC   contacting a source suspected of containing RSV with (I) and determining
CC   whether (I) binds to the source. (I) is also useful for providing passive
CC   immunotherapy prophylactically, to RSV disease in a human. (I) is useful
CC   for therapeutic and/or prophylactic treatment of RSV infection in human
CC   patients, particularly infants and young children. (I) is also useful
CC   as a diagnostic reagent for the determination of RSV mediated disorders
CC   or for tracking progress of treatment of the disorders. The present
CC   sequence represents the continuous DNA sequence of the expression plasmid
CC   Glambda-1Apcn containing the RSV neutralising human Glambda-1 mAb for the
CC   light chain.
XX
SQ   Sequence 5679 BP; 1339 A; 1489 C; 1483 G; 1368 T; 0 other;

Query Match              78.6%;  Score 558.8;  DB 22;  Length 5679;
Best Local Similarity    91.0%;  Pred No. 9.4e-133;
Matches  606;  Conservative   0;  Mismatches  57;  Indels  3;  Gaps  1;

Qy         47 CAGGTGCACGATGTGAGTCGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
              ||||||  ||| | ||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 CAGGTGCCACTCCCAGTCTGTGTTGACGGCAGCCGCCCTCAGTCTCTGCGGGCCCCAGGAC 1111

Qy        107 AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTAC 163
              ||||||||||||||||||||||||||||||||||||||||||    |||||||||||||||
Db       1112 AGAAGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACCTCACCGGGGCAGGTTATGATGTTC 1171

Qy        164 ATTGGTACCAGCAGCTCCAGGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGC 223
              ||||||||||||||||||||| ||||||||||||||||||||||||||||| |||||||
Db       1172 ACTGGTACCGGCAACTTCCAGGACAGCAGCCCCAAACTCCTCATCTATGATAACAACAATC 1231

Qy        224 GACCCTCAGGAATTCTGACCGATTCTCTGGCTCCAAGTCTGGCTACCGGCCTCCCTGG 283
              ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1232 GGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCTCCAAGTCTCCCTGG 1291

Qy        284 CCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCA 343
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1292 CCATCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCA 1351

Qy        344 GCCTGAATGCTCAGGTATTCGGAGGAGGCACCGGCTGACCGTCCTAGGTCAGCCCAAGG 403
              ||||||| |||||||  ||||||||||||||||| ||||||||||||||||||||||||||
Db       1352 GCCTGAATGGTTATGTCTTCGGAACTGGGACCAGGTCACCGTCCTAGGTCAGCCCAAGG 1411

Qy        404 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCA 463
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1412 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCA 1471

Qy        464 CACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1472 CACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAA 1531

Qy        524 ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCCTCCAAACAAGCAACACA 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1532 TTAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCCTCCAAACAAGCAACAACA 1591

Qy        584 AGTACGCGCGGCCAGCTACCTGAGCGCTGACGCCTGAGCGCAGTGGAAGTCCCAGGAGCT 643
```

RESULT 7
```
AAC84207
ID   AAC84207 standard; DNA; 5679 BP.
XX
AC   AAC84207;
XX
DT   19-MAR-2001   (first entry)
XX
DE   Plasmid Glambda-1Apcn DNA sequence.
XX
KW   Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
KW   Glambda-1; human; virucide; RSV propagation; ds.
XX
OS   Homo sapiens.
XX
XX
PN   WO200069462-A1.
XX
PD   23-NOV-2000.
XX
PF   18-MAY-2000; 2000WO-US13694.
XX
PR   18-MAY-1999; ' 99US-0134702.
XX
```

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Matches  610;  Conservative   0;  Mismatches  53;  Indels  3;  Gaps  1;

Qy         47 CAGGTGCACGATGTGAGTCGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
              ||||||  ||| | ||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CAGGTGCCACTCCCAGTCTGTGTTGACGGCAGCCGCCCTCAGTCTCTGCGGGCCCCAGGAC 129

Qy        107 AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTAC 163
              ||||||||||||||||||||||||||||||||||||||||||    |||||||||||||||
Db        130 AGAAGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACCTCACCGGGGCAGGTTATGATGTTC 189

Qy        164 ATTGGTACCAGCAGCTCCAGGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGC 223
              ||||||||||||||||||||| ||||||||||||||||||||||||||||| |||||||
Db        190 ACTGGTACCGGCAACTTCCAGGACAGCAGCCCCAAACTCCTCATCTATGATAACAACAATC 249

Qy        224 GACCCTCAGGAATTCTGACCGATTCTCTGGCTCCAAGTCTGGCTACCGGCCTCCCTGG 283
              ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCTCCAAGTCTCCCTGG 309

Qy        284 CCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCA 343
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        310 CCATCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCA 369

Qy        344 GCCTGAATGCTCAGGTATTCGGAGGAGGCACCGGCTGACCGTCCTAGGTCAGCCCAAGG 403
              ||||||| |||||||  ||||||||||||||||| ||||||||||||||||||||||||||
Db        370 GCCTGAATGGTTATGTCTTCGGAACTGGGACCAGGTCACCGTCCTAGGTCAGCCCAAGG 429

Qy        404 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCA 463
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCA 489

Qy        464 CACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 CACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAA 549

Qy        524 ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCCTCCAAACAAGCAACACA 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TTAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCCTCCAAACAAGCAACAACA 609

Qy        584 AGTACCGGCGGCCAGCTACCTGAGCGCTGACGCCTGAGCAGTGGAAGTCCCAGAAGCT 643
              |||||| ||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        610 AGTACCGGCGGCCAGCTATCTGAGCCTGAGCAGTGGGAAGTCCCACAGAAGGT 669

Qy        644 ACAGCTGCCAGGTCAGCCATGAAGGGAGACAGTGGCCCCTACAGAAT 703
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 ACAGCTGCCAGGTCAGCCATGAAGGGAGACAGTGGCCCCTACAGAAT 729

Qy        704 GTTCAT 709
              ||||||
Db        730 GTTCAT 735
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CC        astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
CC        primitive neural ectodermal tumour (PNET), pancreatic ductal
CC        adenocarcinoma, small and large cell lung adenocarcinomas,
CC        squamous cell carcinoma, bronchoalveoarcarcinoma, epithelial
CC        adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
CC        breast tumours such as ductal and lobular adenocarcinoma, squamous
CC        and adenocarcinomas of the uterine cervix, uterine and ovarian
CC        epithelial carcinoma, prostatic adenocarcinoma, transitional
CC        squamous cell carcinoma of the bladder, B and T cell lymphoma
CC        (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC        malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
XX
SQ        Sequence 768 BP; 169 A; 256 C; 202 G; 141 T; 0 other;

Query Match             77.7%;   Score 552.6;  DB 20;  Length 768;
Best Local Similarity   89.6%;      Pred. No. 2.2e-131;
Matches  594;        Conservative   0;  Mismatches  69;  Indels  0;  Gaps  0;

Qy     47 CAGTGCACGATGTGAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
          |||  ||| ||   ||  || | ||||||||||| ||||||||||||||||||||||||
Db     62 CAGGGTCCTGGGCCCAGTCTGTGTGCACTCAGCCACCCTCAGCCTCTGCCCCCCGGGC 121

Qy    107 AGAAGGTCACCATCTGTGCACTGGGACGCACCTCCAACATTGGAGGTTATGATCTACATT 166
          |||  |||||||||||  | ||||| ||||||||||||||||||||||||||||||||
Db    122 AGAGGGTCACCATCTCTTGTTCTGGAAGCAACTCCAACATCGGAAGTAAGACTGTAAACT 181

Qy    167 GGTACCAGCAGCTCCCAGGAACGGCCCCCAAAACTCCTCATCTATGACATTAACAAGGCGAC 226
          |||||||||||||  |||||| |||||||  |||  |  ||||||||| ||| ||||||||
Db    182 GGTACCAGCAACTCCCAGGAACGGCCCCCAAATTTCTCATCTATAGTAATAATCAGCCGGC 241

Qy    227 CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGGGCCTCCCTGGCCA 286
          ||||| || |||||||||||||||||||||||||||||||||| ||| ||||||||||
Db    242 CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTCGGCACCTCAGCCTCCCTGGCCA 301

Qy    287 TCACTGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCATGTCTATGACAGCAGCC 346
          ||| |||||||| |||||||||| ||| ||| ||| ||||||||| ||| ||||||| |||
Db    302 TCAGTGGGCTCCAGTCTGAGGATGAGGCTTATTACTGTGCAGCATGGGATGACAGCC 361

Qy    347 TGAATGCTCAGGTATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTG 406
          |||||||||||||||||||||||||||||||||||||||| ||||  |||||||||||||
Db    362 TGAATGGTTGGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTGGGTCAGCCCAAGGCTG 421

Qy    407 CCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCAACAAGGCCACAC 466
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCAACAAGCCCACAC 481

Qy    467 TGGTGTCTCATAAGTGACTTCACCGGGACCAGTGGCCTGGAAGGCAGATA 526
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 TGGTGTCTCATAAGTGACTTCACCGGGACCAGTGGCCTGGAAGGCAGATA 541

Qy    527 GCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGT 586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 GCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGT 601

Qy    587 ACGCGGCCAGCAGTACCTGAGCCTGAGCGCTGAGCAGTGGAAGTCCCACAGAAGCTACA 646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602 ACGCGGCCAGCAGTACCTGAGCCTGAGCGCTGAGCAGTGGAAGTCCCACAGAAGCTACA 661

Qy    647 GCTGCCAGGTCACGCATGAAGGAGCAGTGGCCCCTACAGAATGTT 706
          |||||||||||||||||||||||||||||||||||||||||||||
Db    662 GCTGCCAGGTCACGCATGAAGGAGCAGTGGCCCCTACAGAATGTT 721

Qy    707 GTTCAT 709
          ||||||
Db    722 GTTCAT 724
```

```
RESULT 9
AAX06954/c
ID   AAX06954 standard; DNA; 768 BP.
XX
AC   AAX06954;
XX
```

```
Db   1592 AGTACCGGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGGT 1651
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    644 ACAGCTGCCAGGTCACGCATGAAGGAGCAGTGGCCCCTACAGAAT 703
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1652 ACAGCTGCCAGGTCACGCATGAAGGAGCAGTGGCCCCTACAGAAT 1711

Qy    704 GTTCAT 709
          ||||||
Db   1712 GTTCAT 1717
```

```
RESULT 8
AAX06953
ID   AAX06953 standard; DNA; 768 BP.
XX
AC   AAX06953;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Monoclonal antibody 4B5 light chain variable region DNA.
XX
KW   Antigen binding fragment 4B5; monoclonal antibody; cancer;
KW   neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
KW   sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
KW   GD2 antigen; human; ds.
XX
OS   Homo sapiens.
XX
FH                    Location/Qualifiers
FT   CDS              19..726
FT                    /*tag=  a
XX
PN   WO9902545-A2.
XX
PD   21-JAN-1999.
XX
PF   08-JUL-1998;  98WO-IB01046.
XX
PR   08-JUL-1997;  97US-0051945.
XX
PA   (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI   Dan MD;
XX
DR   WPI; 1999-120769/10.
DR   P-PSDB; AAW88465.
XX
PT   New antibody 4B5 polynucleotides and polypeptides - used to develop
PT   products for the diagnosis and treatment of cancers and for
PT   prophylactic therapy to reduce risk of recurrence
XX
PS   Claim 4; Page 80; 83pp; English.
XX
CC   This is the DNA sequence of a polynucleotide that encodes the light
CC   chain variable region (see AAW88465) of the recombinant human
CC   monoclonal antibody (MAb) 4B5.  4B5 recognises antibodies specific
CC   for GD2 antigen antibodies. Antibodies specific for GD2 recognise
CC   various cancers including glioblastoma, neuroblastoma, malignant
CC   and/or metastatic melanoma, breast adenocarcinoma, lung
CC   adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC   prostate adenocarcinoma.  The invention encompasses 4B5 derivatives
CC   with immunologic specificity for antibodies specific for GD2. These
CC   derivatives, or antigen binding fragments, comprise regions of the
CC   4B5 VDJ junction and regions spanning the 4B5 CDRs.  Other
CC   derivatives include Fab, F(ab')2, Fab', scFv and isolated heavy and
CC   light chains.  Polynucleotide fragments (see AAX06951-54), both
CC   coding and complementary strands, encoding 4B5 antibody V regions
CC   are also provided, as well as therapeutic plasmids and vectors,
CC   including vaccinia virus vectors, comprising these polynucleotides.
CC   4B5 has been shown to mimic GD2, and is particularly useful in
CC   generating a host immune response to cancer.  Products of the
CC   invention can be used in the detection and treatment of e.g.
```

```
DT   10-MAY-1999 (first entry)
XX
DE   Monoclonal antibody 4B5 light chain variable region DNA.
XX
KW   Antigen binding fragment 4B5; monoclonal antibody; cancer;
KW   neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
KW   sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
KW   GD2 antigen; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            complement (43..750)
FT                  /*tag= a
XX
PN   WO9902545-A2.
XX
PD   21-JAN-1999.
XX
PF   08-JUL-1998; 98WO-IB01046.
XX
PR   08-JUL-1997; 97US-0051945.
XX
PA   (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI   Dan MD;
XX
DR   WPI; 1999-120769/10.
DR   P-PSDB; AAW88465.
XX
PT   New antibody 4B5 polynucleotides and polypeptides - used to develop
PT   products for the diagnosis and treatment of cancers and for
PT   prophylactic therapy to reduce risk of recurrence
XX
PS   Claim 6; Page 80; 83pp; English.
XX
CC   This is the complementary strand of a DNA sequence (see also
CC   AAX06953) that encodes the light chain variable region (see AAW88465)
CC   of the recombinant human monoclonal antibody (MAb) 4B5. 4B5
CC   recognises antibodies specific for GD2 antigen antibodies. Such
CC   antibodies recognise various cancers including glioblastoma,
CC   neuroblastoma, malignant and/or metastatic melanoma, breast
CC   adenocarcinoma, small cell lung carcinoma,
CC   colon adenocarcinoma and prostate adenocarcinoma. The invention
CC   encompasses 4B5 derivatives with immunologic specificity for
CC   antibodies specific for GD2. These derivatives, or antigen binding
CC   fragments, may comprise regions of the 4B5 VDJ junction and regions
CC   spanning the 4B5 CDRs. Other derivatives include Fab, F(ab')2,
CC   Fab', scFv and isolated heavy and light chains. Polynucleotide
CC   fragments (see AAX06951-54), both coding and complementary strands,
CC   encoding 4B5 antibody V regions are also provided, as well as
CC   therapeutic plasmids and vectors, including vaccinia virus vectors,
CC   comprising these polynucleotides. 4B5 mimics GD2, and is useful in
CC   generating a host immune response to cancer. Products of the
CC   invention can be used in the detection and treatment of e.g.
CC   astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
CC   primitive neural ectodermal tumour (PNET), pancreatic ductal
CC   adenocarcinoma, small and large cell lung adenocarcinomas,
CC   squamous cell carcinoma, bronchoalveoarcarcinoma, epithelial
CC   adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
CC   breast tumours such as ductal and lobular adenocarcinoma, squamous
CC   and adenocarcinomas of the uterine cervix, uterine and ovarian
CC   epithelial carcinoma, prostatic adenocarcinoma, transitional
CC   squamous cell carcinoma of the bladder, B and T cell lymphoma
CC   (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC   malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
XX
SQ   Sequence 768 BP; 141 A; 202 C; 256 G; 169 T; 0 other;

Query Match     77.7%;  Score 552.6;  DB 20;  Length 768;
Best Local Similarity   89.6%;  Pred. No. 2.2e-131;
Matches 594;  Conservative 0;  Mismatches 69;  Indels 0;  Gaps 0;
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```
Qy   47  CAGGTGCACGATGTGAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGC  106
             ||| | ||||||||||||||   |||||||| |||  |||||||||| ||||||||||
Db  707  CAGGGTCCTGGGCCCAGTCTGTGCTGACTCAGCCACCTCAGCCATCCAGCCTCCCAGGGC  648

Qy  107  AGAAGGTCACCATCTCGTGCACTGGGAGCACTCCACATTGGAGGTTATGATCTACATT  166
             ||| ||||||||||||  ||||  |||||||||||  |||||||| ||||  |||
Db  647  AGAGGGTCACCATCTCTGTTGGGAGCAACTCCAACATCCGGAAGTAAGACTGTAAACT  588

Qy  167  GGTACCAGCAGCTCCCAGGAACGGCCCCAAACTCCTCATCCATGACATTAACAAGGGAC  226
             |||||||||||  |||||||||||||||||    ||||||| |||  |||   |||||
Db  587  GGTACCAGCAGCAACTCCCAGGAACGGCCCCAAATTTCTCATCTATAGTAATAATCAGCGGC  528

Qy  227  CCTCAGGAATTTCTGACCGATTCTGGCTCCAAGTCTGGTACGGCGCCTCCCTGGCCA  286
             |||||| | ||||| |||||||||| ||||||||||||| |||| |||||||||||||
Db  527  CCTCAGGGTCCCTGACCGATTCTGCTGCTCCAAGTCTGGTCACCTGCCCTCAGCCTCCCTGGCCA  468

Qy  287  TCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC  346
             |||  ||||||||| |||||||||||||||||||||||||  |||  ||||| |||||||
Db  467  TCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGATGACAGCAGCC  408

Qy  347  TGAATGCTCAGTATTCGGAGGAGGACACCCGGCTGACCGTCCTAGGTCAGCCCCAAGGCTG  406
             |||||| | |||  |||  |||||| |||| | ||||||||||||| ||||||||||||||
Db  407  TGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTGGGTCAGCCCCAAGGCTG  348

Qy  407  CCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCCACAC  466
             |||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||
Db  347  CCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGCCCCACAC  288

Qy  467  TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATA  526
             |||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db  287  TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCAGTGACAGTGGCCTGGAAGGCAGATA  228

Qy  527  GCAGCCCCGTCAAGGCGGGAGTGGAGAGCACCACCACACCTCCAAACAAAGCAACAACAAGT  586
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  227  GCAGCCCCGTCAAGGCGGGAGTGGAGAGCACCACCACACCCTCCAAACAAAGCAACAACAAGT  168

Qy  587  ACGGGCCAGCAGTCACTACCTGAGCCTGAGCGCCTGAGCGTGGAAGTCCCACAGAAGCTACA  646
             ||||||||||||||||||||||||||||||||   |||||||| |||||||||||||||||
Db  167  ACGGGCCAGCAGTCACTACCTGAGCCTGAGCGTGAAGTCCCACAGAAGCTACA  108

Qy  647  GCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTT  706
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  107  GCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTT  48

Qy  707  CAT  709
             |||
Db   47  CAT  45
```

```
RESULT 10
AAQ49835
ID   AAQ49835 standard; cDNA; 654 BP.
XX
AC   AAQ49835;
XX
DT   27-APR-1994 (first entry)
XX
DE   Anti-HIV-1 recombinant antibody 447-52D light chain coding sequence.
XX
KW   Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW   HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW   acquired immune deficiency syndrome; chimeric antibody;
KW   surface glycoprotein gp120; V3 loop; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..654
FT                  /*tag= a
FT                  /note= "encodes recombinantly modified 447-52D
FT                  light chain"
XX
PN   WO9319785-A.
```

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XX
PD   14-OCT-1993.
XX
PF   23-MAR-1993;  93WO-US02629.
XX
PR   01-APR-1992;  92US-0861701.
XX
PA   (MERI ) MERCK & CO INC.
PA   (JOHN/) JOHNSON L S.
PA   (PFAR/) PFARR D S.
XX
PI   Conley AJ,  Emini EA,  Johnson LS,  Mark GE,  Pfarr DS;
XX
DR   WPI; 1993-336600/42.
DR   P-PSDB; AAR42163.
XX
PT   New recombinant human antibody - with HIV neutralising activity
PT   against at least two isolates, useful for preventing or treating
PT   infection in diagnosis, etc.
XX
PS   Example 9; Fig 2B; 154pp; English.
XX
CC   EBV-transformed cell lines and mouse-human heterohybridomas
CC   producing human MAbs specific for the gp120 V3 loop of HIV-1 MN
CC   isolate were obtained. MAb 447-52D was found to recognise the
CC   tetrapeptide motif GPGR, i.e. the Principal Neutralising
CC   Determinant common to the V3 loop of different HIV isolates.
CC   A recombinant Ab was produced in which the L chain V region was
CC   derived from 447-52D and to which a signal sequence and a L chain
CC   intronic sequence are appended, fused to a fragment contg. a short
CC   intronic segment of the human lambda 2 C region and the human
CC   lambda 2 constant encoding domain.
XX
SQ   Sequence 654 BP; 156 A; 199 C; 178 G; 121 T; 0 other;

Query Match             76.9%;  Score 547;  DB 14;  Length 654;
Best Local Similarity   91.1%;  Pred. No. 5.7e-130;
Matches  593;  Conservative    0;  Mismatches   55;  Indels    3;  Gaps     1;

Qy       62 AGTCTGTCTGACACAGCCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCT 121
            ||||||   |||  ||||||||||| ||||||||||  |||||||| |||||||||||||
Db        2 AGTCTGTTGACGGACGCGCCCCTCAGTGTCTGCGGTCTGCGGGCCCCAGGAGAAGGTCACCATCT 61

Qy      122 CGTGCACTGGGAGCACTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTCC 181
            | |||||||||||||  |||  |||||||||| ||| ||  ||| |||||||||||||
Db       62 CCTGCTCTGGAAGCAGTCCAACATTGGGAATAATTATGTATTGTGTACCAGCAGTTCC 121

Qy      182 CAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAAGGACCCTCAGGAATTCTG 241
            |||||  |||||||||||||| |||  |||||| ||| |||||||||||||||  ||||
Db      122 CAGGAACAGCGCCCCCAAACTCCTCATTTATTGGCAATAATAAGGCACCCTCAGGGATTCCTG 181

Qy      242 ACCGATTCTCTGGCTCCAAGTCTGGTACCCGGGCCTCCCTGGCCATCACTGGGCTCCAGA 301
            |||||||||||||||||| |  ||||||| || ||||  |||||||||| |||| |||||
Db      182 ACCGATTCTCTGGCTCCAAGTCTGGCACGCACGTCAGCCCACCCTGGGCATCACCGGACTCCAGA 241

Qy      302 CTGAGGATGAGGCTGATTATTACTGGCAGTCCTATGACAGCAGCCAGCGAATGCTCA--GG 358
            |||| |||||||||||||| |||||  |||||  ||||| |||||||| |||||
Db      242 CTGGGGACGAGGCCGATTATTCTCGCCAACATGGGATAGCGGCCCAAGGCGGCCTGAGTGCTGATTGGG 301

Qy      359 TATTCCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCAAGGCTGCCCCTCGGGTCA 418
            || ||||| |||||||||||  |||||||| |||||||||||  |||||  ||||| ||
Db      302 TGTTCGGCGAGGAGGGGACCAAGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGGTCA 361

Qy      419 CTCTGTTCCCGCCCTCTCCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCA 478
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||
Db      362 CTCTGTTCCCGCCCTCTCCTGAGGAGCTTCAAGGCAGCCAACAGGGCCACACTGGTGTGTCTCA 421

Qy      479 TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA 538
            |||||||||||||||| |||||||| ||  |||||||||||||||||| |||||||||||
Db      422 TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA 481

Qy      539 AGGCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAGTACGCGGCCAGCA 598
            ||||||||||||||||||||||||||||||||||||||||||
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```
Db      482 AGGCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAGTACGCGGCCAGCA 541

Qy      599 GCTACCTGAGCCTGAGCGCTGAGCTGAGTCCCAGAGAAGCTACAGCTCCAGTCA 658
            |||| ||||||||||||||||||||||| |||||||||| ||||| |||||||
Db      542 GCTATCTGAGCCTGAGCCTGAGCAGTCAGCAGTCCCACAGAAGCTACAGCTGCCAGTCA 601

Qy      659 CGCATGAAGGAGCACCGTGAGAAGACAGTGGCCCTACAGAATGTTCAT 709
            |||||||||||||||||||||||||| ||||||||||||||||||||
Db      602 CGCATGAAGGGAGGGAGACAGTGTGCCCTACAGAAATGTTCAT 652
```

```
RESULT 11
AAS87270
ID   AAS87270 standard; cDNA; 810 BP.
XX
AC   AAS87270;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #23074.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG23083.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 23074; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 810 BP; 176 A; 275 C; 211 G; 148 T; 0 other;
```

PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US10053.
XX
PR   07-JUN-1995;   95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01817.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 7; Fig 8A; 81pp; English.
XX
CC   2 DNA sequences (AAT62509 and AAT62510) respectively code for
CC   primatised forms (AAW01817 and AAW01818) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   7C10. Cloned 7C10 light and heavy variable genes are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match   76.0%; Score 540.2; DB 18; Length 705;
Best Local Similarity 86.1%; Pred. No. 3.2e-128;
Matches 612; Conservative   0; Mismatches   93; Indels   6; Gaps   1;

Qy   1 ATGAGGGTCCCCGTCCAGCTCTGGGGGCTCCTGCTGCTCCTGGCTCCCTGGGCTCCACGATGT   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1 ATGAGGGTCTCCCGTCCAGCTCTGGGGGCTCCTGCTGCTCTGCTCCCTGGGCTCCACGATGT   60

Qy   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120
          |||||||||||||||| |||||||| |||||||||||||||||||||||||||||||||||
Db   61 GCCTATGAACTGACTCAGCCACCCTCCGTGTCCCGGTCAGTGTCCCCAGGACAGACGGCCAGGATC 120

Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
          |||||||||||||||||||||||||||| ||||||| |||||||||||||||||
Db   121 ACCTGTGTGGGG------AGACAACAGTAGAAATGAATATGTCCACTGTCCACTGTCCAGCAGAAG 174

Qy   181 CCAGGAACGGCGCCCCAAACTCCTCATCCATGACATTAACAAGGACCCTCAGGAATTTCT 240
          |||| ||||||||||||||||||||||||| ||||||||| |||||||||||||||||
Db   175 CCAGCGCGGCGGCCCCTATACTGGTCATCTATGATGATGATAGTGACCGGCCCTCAGGGATCCCT 234

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGCCTCCTGCTCCCAGTGCCACGATGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACGGCTACCCTGACCATCAACAACGGGGTCGAG 294

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   295 GCCCGGGATGAGGCTGACTATTACTGTCAGTGGGACAGCAGCCTAGTGATCATCCGGTC 354

Qy   361 TTCGGAGGAGGGACCCCGGCTGACCGGTCCTAGGTCAGCCCAAGGCTGCCCCCGGTCACT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   355 TTCGGAGGAGGGACCCGGGCTGACCGGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 414

Qy   421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 474

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG 534

Query Match   76.8%; Score 546.2; DB 23; Length 810;
Best Local Similarity 89.0%; Pred. No. 9.7e-130;
Matches 590; Conservative   0; Mismatches   73; Indels   0; Gaps   0;

Qy   47 CAGGTGCACGATGTGAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
          ||||| |||||||||||||||||||||||| || ||||||||||||||||||||||||
Db   49 CAGGGTCCTGGGCCCCAGTCTGTACTGACGCGCCAGCCCTCAGCGTCTGGGACCCCCGGGC 108

Qy   107 AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATT 166
          |||||||| | |||||| || ||||| ||||||||||||| ||||||||||||
Db   109 AGAGGGTCACAATCTCTTGTTCTGGCAGCTTCAGTGGCAGCTCCTAATGTGTATACT 168

Qy   167 GGTACCAGCAGCTCCCAGGAACGGCGCCCCAAACTCCTCATCCATGACATTAACAAGGAC 226
          ||||||||||||||||||||||||||||||||||||||||||| | ||| ||| ||||
Db   169 GGTACCAGCAACTCACAGAACGCCCCAAACTCCTCATCTATAGGAATAATCAGCGGC 228

Qy   227 CCTCAGGAATTTCTGGCTCCAAGTCTGGTACCGCGGCTCCCTGCTCCCTGGCCA 286
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Qy   287 TCACTGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC 346
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Qy   347 TGAATGCTCAGGTATTCGGCGGAGGGACCAAGGCTG 406
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Qy   407 CCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACAC 466
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Qy   467 TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATA 526
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Db   469 TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATA 528

Qy   527 GCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGT 586
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Db   589 ACGCGGCGGCCAGCAGCTATCTGAGCGCTGAGCAGTGGAAGTCCCACAGAAGCTACA 648

Qy   647 GCTGCCAGGTCACGCATGAAGGAGAGCACCGTGCAGAAGACAGTGGCCCCTACAGAATGTT 706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 GCTGCCAGGTCACGCATGAAGGGAGAGCACCGTGCAGAAGACAGTGGCCCCTACAGAATGTT 708

Qy   707 CAT 709
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Db   709 CAT 711

RESULT 12
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ID   AAT62509 standard; DNA; 705 BP.
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AC   AAT62509;
XX
DT   25-MAY-1997 (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX

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                    GenCore version 5.1.3
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       April 5, 2003, 19:47:34 ; Search time 32.1002 Seconds
                                         (without alignments)
                                         6735.375 Million cell updates/sec

Title:        US-09-758-173-1
Perfect score: 705
Sequence:     1 ATGGAGGGTCCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 705

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:     441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:    882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued Patents NA:*
           1: /cgn2_6/ptcdata/1/ina/5A_COMB.seq:*
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           3: /cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
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           5: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
           6: /cgn2_6/ptcdata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	705	100.0	705	3	US-08-487-550-1	Sequence 1, Appli
	2	585.2	83.0	702	3	US-08-523-894-5	Sequence 5, Appli
	3	540.2	76.6	711	3	US-08-487-550-9	Sequence 9, Appli
	4	473	67.1	935	3	US-09-049-672A-20	Sequence 20, Appl
	5	457	64.8	902	3	US-08-378-939-11	Sequence 11, Appl
	6	456	64.7	895	3	US-09-049-672A-25	Sequence 25, Appl
	7	455.4	64.6	891	3	US-09-049-672A-23	Sequence 23, Appl
	8	435.6	61.8	885	3	US-09-152-060-47	Sequence 47, Appl
	9	434	61.6	879	4	US-09-152-060-29	Sequence 29, Appl
c	10	432.2	61.3	928	4	US-09-152-060-46	Sequence 46, Appl
	11	425.4	60.3	919	4	US-09-049-672A-24	Sequence 24, Appl
	12	407.4	57.8	716	4	US-08-793-450-5	Sequence 5, Appli
c	13	306.6	43.5	584	4	US-09-404-879A-268	Sequence 268, App
c	14	273.2	38.8	771	4	US-08-991-789A-241	Sequence 241, App
c	15	273.2	38.8	771	4	US-09-062-451-241	Sequence 241, App
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	17	267.2	37.9	387	1	US-08-379-072A-20	Sequence 20, Appl
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	19	267.2	37.9	387	1	US-08-481-869-20	Sequence 20, Appl
	20	267.2	37.9	387	1	US-08-476-349A-109	Sequence 109, App
	21	267.2	37.9	387	1	US-08-476-237-16	Sequence 16, Appl
	22	267.2	37.9	387	3	US-08-523-894-3	Sequence 3, Appli
	23	260.4	36.9	327	1	US-09-202-181-1	Sequence 1, Appli
	24	259.4	36.8	408	4	US-09-025-769B-169	Sequence 169, App
	25	249.8	35.4	642	2	US-08-634-783A-4	Sequence 4, Appli
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	27	246.2	34.9	346	2	US-08-761-277A-50	Sequence 50, Appl
	28	246	34.9	333	2	US-08-477-553A-44	Sequence 44, Appl
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	40	202.2	28.7	314	4	US-09-370-838-13	Sequence 13, Appl
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                              ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;     STREET: 699 Prince Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/487,550
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Teskin, Robin L.
;     REGISTRATION NUMBER: 35,030
;     REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703-836-6620
;     TELEFAX: 703-836-2021
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 705 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: not relevant
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 1..705
;     FEATURE:
;       NAME/KEY: mat_peptide
;       LOCATION: 1..705
US-08-487-550-1

Query Match             100.0%;   Score 705;   DB 3;   Length 705;
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Best Local Similarity 100.0%; Pred. No. 3.4e-186; Indels 0; Gaps 0;
Matches 705; Conservative 0; Mismatches 0;

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Qy    121 ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG  180
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Qy    481 TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGA  540
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/523,894
  FILING DATE: 06-SEP-1995
  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
  NAME: Teskin, Robin L.
  REGISTRATION NUMBER: 35,030
  REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 703-836-6620
  TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 702 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  ORIGINAL SOURCE:
    ORGANISM: Homo sapiens
  POSITION IN GENOME:
    CHROMOSOME/SEGMENT: lambda variable and constant domains in
    CHROMOSOME/SEGMENT: CE9.1
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..702
  FEATURE:
    NAME/KEY: mat_peptide
    LOCATION: 1..702

US-08-523-894-5

Query Match 83.0%; Score 585.2; DB 3; Length 702;
Best Local Similarity 89.6%; Pred. No. 5e-153;
Matches 629; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy    124 TGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGCGG  183
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Db    181 GCCCCTGTCGTGTCATCTATGTGTGCACAGCGGAACGGCCCTCAGGGATTCCTGAGCGATTC  240

Qy    244 TCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGAT  303
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Db    421 CCCTCCTTCTGAGGAGGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC  480

Qy    484 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG  543
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RESULT 2
US-08-523-894-5
; Sequence 5, Application US/08523894
; Patent No. 6136310
GENERAL INFORMATION:
  APPLICANT: Hanna, Nabil
  APPLICANT: Newman, Roland A.
  APPLICANT: Reff, Mitchell E.
  TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
  TITLE OF INVENTION: Therapy
  NUMBER OF SEQUENCES: 59
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22314-3187
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible

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Qy 604 CTGACCGCCTGAGCAGTGGAAGTCCCAGAGAGCTACAGCTGCCAGGTCACGCAGGG 663
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Qy 664 AGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCATGA 705
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Db 661 AGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCATGA 702

RESULT 3
US-08-487-550-9
; Sequence 9, Application US/0487550
; Patent No. 6113898
GENERAL INFORMATION:
  ;   APPLICANT: Anderson, Darrell R.
  ;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
  ;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
  ;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
  ;   TITLE OF INVENTION: IMMUNOSUPRESANTS"
  ;   NUMBER OF SEQUENCES: 12
  ;   CORRESPONDENCE ADDRESS:
  ;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
  ;   STREET: 699 Prince Street
  ;   CITY: Alexandria
  ;   STATE: VA
  ;   COUNTRY: USA
  ;   ZIP: 22314
  ;   COMPUTER READABLE FORM:
  ;   MEDIUM TYPE: Floppy disk
  ;   COMPUTER: IBM PC compatible
  ;   OPERATING SYSTEM: PC-DOS/MS-DOS
  ;   SOFTWARE: PatentIn Release #1.0, Version #1.30
  ;   CURRENT APPLICATION DATA:
  ;   APPLICATION NUMBER: US/08/487,550
  ;   FILING DATE: 07-JUN-1995
  ;   CLASSIFICATION: 435
  ;   ATTORNEY/AGENT INFORMATION:
  ;   NAME: Teskin, Robin L.
  ;   REGISTRATION NUMBER: 35,030
  ;   REFERENCE/DOCKET NUMBER: 012712-131
  ;   TELECOMMUNICATION INFORMATION:
  ;   TELEPHONE: 703-836-6620
  ;   TELEFAX: 703-836-2021
  ;   INFORMATION FOR SEQ ID NO: 9:
  ;   SEQUENCE CHARACTERISTICS:
  ;   LENGTH: 711 base pairs
  ;   TYPE: nucleic acid
  ;   STRANDEDNESS: not relevant
  ;   TOPOLOGY: linear
  ;   MOLECULE TYPE: peptide
  ;   FEATURE:
  ;   NAME/KEY: CDS
  ;   LOCATION: 1..711
  ;   FEATURE:
  ;   NAME/KEY: mat_peptide
  ;   LOCATION: 1..711
US-08-487-550-9

Query Match   76.6%; Score 540.2; DB 3; Length 711;
Best Local Similarity   86.1%; Pred. No. 1.5e-140;
Matches 612; Conservative   0; Mismatches 93; Indels   6; Gaps   1;

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Qy 121 ACCTTGTGGGG------AGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAG 174
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Qy 175 CCAGCGCGGGCCCCTATACTGTCATCATGATGATAGTGACCGGCCCTCAGGGATCCCT 234
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Db 181 CCAGGAACGGCCCCGGCTGACCCTCAAACTCCTCATCATGACTACAAGGCGACCCTCAGGAATTTCT 240

Qy 235 GAGCGATTCTCTGGCTCCAAATCAGGAACACCGCCACCCTGACCATCAACGGGGTCGAG 294
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Qy 295 GCCGGGATGAGGTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTC 354
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Db 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGAGACGAGCAGCCTGAATGCTCAGGTA 360

Qy 355 TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTGCCGTCCAGGTGCCCCTCCGGTCACT 414
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Db 361 TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAGGTGCCCCTCCGGTCACT 420

Qy 415 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 474
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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540

Qy 535 GCGGGAGTGGAGACGACCACCACCCTCCAAACAAAGCAACAACAACAAGTACGCGGCCAGCAGC 594
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GCGGGAGTGGAGACGACCACCACCCTCCAAACAAAGCAACAACAACAAGTACGCGGCCAGCAGC 600

Qy 595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGAGAGCTACAGCTGCCAGGTCACG 654
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACG 660

Qy 655 CATGAAGGAGGCACCGTGGAGAAGACAGTGCCCCCTACAGAATGTTCATGA 705
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CATGAAGGAGGCACCGTGGAGAAGACAGTGCCCCCTACAGAATGTTCATGA 711

RESULT 4
US-09-049-672A-20
; Sequence 20, Application US/09049672A
; Patent No. 6135941
GENERAL INFORMATION:
  ;   APPLICANT: Hillman, Jennifer L.
  ;   APPLICANT: Lal, Preeti
  ;   APPLICANT: Tang, Y. Tom
  ;   APPLICANT: Yue, Henry
  ;   APPLICANT: Au-Young, Janice
  ;   APPLICANT: Corley, Neil C.
  ;   APPLICANT: Guegler, Karl J.
  ;   APPLICANT: Baughn, Mariah R.
  ;   TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
  ;   NUMBER OF SEQUENCES: 28
  ;   CORRESPONDENCE ADDRESS:
  ;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
  ;   STREET: 3174 Porter Drive
  ;   CITY: Palo Alto
  ;   STATE: CA
  ;   COUNTRY: USA
  ;   ZIP: 94304
  ;   COMPUTER READABLE FORM:
  ;   MEDIUM TYPE: Diskette
  ;   COMPUTER: IBM Compatible
  ;   OPERATING SYSTEM: DOS
  ;   SOFTWARE: FastSEQ for Windows Version 2.0
  ;   CURRENT APPLICATION DATA:
  ;   APPLICATION NUMBER: US/09/049,672A
  ;   FILING DATE: HEREWITH
  ;   CLASSIFICATION: 536

us-09-758-173-1.rnl

```
        PRIOR APPLICATION DATA:
          APPLICATION NUMBER:
          FILING DATE:
        ATTORNEY/AGENT INFORMATION:
          NAME:  Cerrone, Michael C
          REGISTRATION NUMBER:  39,132
          REFERENCE/DOCKET NUMBER:  PF-0497 US
        TELECOMMUNICATION INFORMATION:
          TELEPHONE:  650-855-0555
          TELEFAX:  650-845-4166
          TELEX:
    INFORMATION FOR SEQ ID NO:  20:
        SEQUENCE CHARACTERISTICS:
          LENGTH:  935 base pairs
          TYPE:  nucleic acid
          STRANDEDNESS:  single
          TOPOLOGY:  linear
        IMMEDIATE SOURCE:
          LIBRARY:  ADRETUT05
          CLONE:  2492122
    US-09-049-672A-20
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Query Match        67.1%;    Score 473;    DB 3;    Length 935;
Best Local Similarity  80.4%;    Pred. No. 6.5e-122;
Matches 570;    Conservative    0;    Mismatches 130;    Indels    9;    Gaps    1;

Qy      4  AGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCAGGTGCACGATGTGCC   63
           ||||||||   ||||| |||    |||||
Db     74  ATGGCCTGGTCTCCTCCTCACTCTCCTCGCTCACTGCACAGGTCCTGGGCCCAG  133

Qy     64  TATGAACTGACTCAGCCACCCTCCGGTGTCCCAGGACAGACGGCCAGGATCACC  123
           |||| ||||||| ||||| ||||||  |||||||| |||| |||||||||||||
Db    134  TCTGTGCTGACGGCCGCCCTCAGTGTCTGGGCGTCTGGGCCAGGAGGGTCACCATCTCC  193

Qy    124  TGTGGGGAG--------ACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAG  174
           ||||||||         ||||||| || || |||||  ||||||||||||| ||| ||
Db    194  TGCACTGGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTT  253

Qy    175  CCAGCCGCGGGCCCCTATACTGGTCATCTATGATGATGATGAGTGACCGGCCCTCAGGGATCCCT  234
           |||  |||||| |||||  |||  ||||||||| |||||| |||||||
Db    254  CCAGGACAGCCCCCAAACTCCTCATCTATGGTAGTAGAAATCGGCCCCTCAGGGGTCCCT  313

Qy    235  GAGGCGATTCTCTGGCTCCAAATCAGGGAACACCGCACCCTGACCATCAACGGGGTCGAG  294
           || ||||||||||||||||| |||| |||||||||||||| ||||||||| || |||||
Db    314  GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCTGGCCATCACTGGGCTCCAG  373

Qy    295  GCCGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACACAGGGCTAGTGATCATCCGGTC  354
           |||||||||| |||||||||||||||||| ||||||||||||||
Db    374  GCTGAGGATGAGGCTGATTATTACTGCCAGTCTCCAGTCCTATGACAGCAGCCTGAGTGGTGTGGTA  433

Qy    355  TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGGTCACT  414
           ||||| ||||||||||  ||||||||||||||||  || ||||||| ||||||||||
Db    434  TTCGGCGGAGGGACCAAGCTGACCGTCCTCGGTCAGCCCAAGGCTGCCCCCTCGGTCACT  493

Qy    415  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGGCCACACTGGTGTGTCTCATA  474
           ||||||||||||||||||||||||||||||||||||||||||
Db    494  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGGCCACACTGGTGTGTCTCATA  553

Qy    475  AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  534
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||| ||||
Db    554  AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  613

Qy    535  GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGCGGCCAGCAGC  594
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    614  GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGCGGCCAGCAGC  673

Qy    595  TACCTGAGCCTGACGCTGAGCAGTGAAGTCCCACGAGCTACAGCTGCCAGGTCACG  654
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674  TACCTGAGCCTGACGCTGAGCAGTGAAGTCCCACGAGCTACAGCTGCCAGGTCACG  733

Qy    655  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTCACAGAATGTTCAT  703
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTCACAGAATGTTCAT  782
```

RESULT 5
US-08-378-939-11
; Sequence 11, Application US/08378939
; Patent No. 5876961
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GENERAL INFORMATION:
  APPLICANT:  CROWE, JAMES SCOTT
  APPLICANT:  LEWIS, ALAN PETER
  TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
  NUMBER OF SEQUENCES:  46
  CORRESPONDENCE ADDRESS:
    ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
    STREET:  555 THIRTEENTH ST. N.W.
    CITY:  WASHINGTON
    STATE:  D.C.
    COUNTRY:  U.S.
    ZIP:  20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE:  Floppy disk
    COMPUTER:  IBM PC compatible
    OPERATING SYSTEM:  PC-DOS/MS-DOS
    SOFTWARE:  PatentIn Release #1.0,  Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/378,939
    FILING DATE:
    CLASSIFICATION:  435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 07/952640
    FILING DATE:  01-DEC-1992
  ATTORNEY/AGENT INFORMATION:
    NAME:  ERNST, BARBARA G
    REGISTRATION NUMBER:  30,377
    REFERENCE/DOCKET NUMBER:  1808-118
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (202) 783-6040
    TELEFAX:  (202) 783-6031
INFORMATION FOR SEQ ID NO:  11:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  902 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  both
    TOPOLOGY:  linear
  MOLECULE TYPE:  cDNA
  HYPOTHETICAL:  NO
  ANTI-SENSE:  NO
  FEATURE:
    NAME/KEY:  CDS
    LOCATION:  32..739
  FEATURE:
    NAME/KEY:  mat_peptide
    LOCATION:  89..739
  FEATURE:
    NAME/KEY:  sig_peptide
    LOCATION:  32..86
US-08-378-939-11
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Query Match        64.8%;    Score 457;    DB 2;    Length 902;
Best Local Similarity  80.0%;    Pred. No. 1.7e-117;    Indels   12;    Gaps    2;
Matches 567;    Conservative    0;    Mismatches 130;

Qy      4  AGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCAGGTGCACGATGTGCC   63
           ||||||||   ||||| |||    |||||
Db     32  ATGGCCTGGTCTCCTGCTCCTCACCCTCCTCACTCAGGACACAGGGTCCTGGGCCCAGC   91

Qy     64  TATGAACTGACTCAGCCACCCTCCGGTGTCCCAGGACAGACGGCCAGGATCACC  123
           |||| ||||||| |||  || ||  |||||||| |||| |||||||||||||
Db     92  TCTGTGCTGACTCAGCCGTCCTCGGTGTCCGGGTCTCCGGGACAGTCGATCACCATCTCC  151

Qy    124  TGTGGGGGAGCAACAGT--------AGAAATGAATATGTCCACTGGTACCAGCAGAAG  174
           |||| ||| || ||||          |||||| |||| ||||||||||||||||||||
Db    152  TGCACTGGGACCAACAATGATGTTGGAGGTTATAACCTTGTCTCCTGGTACCAGCAGCAC  211
```

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;      REGISTRATION NUMBER: 39,132
;      REFERENCE/DOCKET NUMBER: PF-0497 US
;   TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:    650-845-4166
;      TELEX:
; INFORMATION FOR SEQ ID NO:  25:
;   SEQUENCE CHARACTERISTICS:
;      LENGTH: 895 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;      LIBRARY: LUNGTUT13
;      CLONE: 3116314
; US-09-049-672A-25

Query Match             64.7%;  Score 456;  DB 3;  Length 895;
Best Local Similarity   82.8%;  Pred. No. 3.3e-117;
Matches  535;  Conservative   0;  Mismatches  105;  Indels   6;  Gaps   1;

Qy     64 TATGAACTGACTCAGCCACCCTCGGTGTCCCAGGACAGACGGCCAGGATCACC 123
          |||||| |||||| |||| ||||||||||  |||||||||| ||||||||
Db     97 TCTGTGCTGACTCAGCCCCCCTCAGCGTCTGGGACCCCGGGCAGAGGTCACCATCTCT 156

Qy    124 TGTGGGGGAGA------CAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCA 177
          |||||||||        ||| |||| ||| ||   |||| ||||||||||||||||
Db    157 TGTTCTGGAACCACCTCCAACATCGCAAGTAATTCTGTGCATTGGTACCAATTAGTTCCA 216

Qy    178 GGCGGGCCCCTATACTGGTCATCTATGATGATAGTGAC 237
          |||| |||||||||||| ||| |||||| |||| ||
Db    217 GGCGGCGCCCCCAAACTCCTCATCTATCTATGCTAATGATAGTGAC 237

Qy    238 CGATTCTCTGCTCCAAATCAGGGAACACCGCCACCCTGCCCCTGCTCCTGGCCATCAGTGTGGGCTCCCTG 297
          ||||||||||||||| ||||| |||| |||||||||||||| ||||||||  |||||||
Db    277 CGATTCTCTGGCTCCAAGTCTGGCACCCGGTCACAAGCTGCTCCTGGCCATCAGTGTCCCTGACCAGCCTGAGGCC 336

Qy    298 GGGGATGAGCTGACTATTACTGTCAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTC 357
          ||| |||||| |||||||||||| |||||||   |||||||
Db    337 GAGGATGAAACTGATTATTACTGTCAACATGGGATGACAGTGTCAGTGGTTGGATGTTC 396

Qy    358 GGAGGGAGGACCCGGGTGACCGTCCTAGGTCAGCCAACAGCTACCTG 417
          |||||||||||||| ||||||||||||||||||||  |||| ||||||
Db    397 GGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCAACAGCTACCTG 456

Qy    418 TTCCCGCCCTCCTCTGAGGAGTTCAAGCAACAAGGCCACACTGGTGTGTCTCATAAGT 477
          ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    457 TTCCCACCCTCCTCTGAGGAGTTCAAGCAACAAGGCCACACTGGTGTGTCTCATAAGT 516

Qy    478 GACTTCTACCCGGGAGCCGTGACAGTGCCTGACAGTGGCCTGAAGGCAGAATAGCAGCCCCGTCAAGGCG 537
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    517 GACTTCTACCCGGGAGCCGTGACAGTGCCTGACAGTGGCCTGAAGGCAGCAGATAGCAGCCCCGTCAAGGCG 576

Qy    538 GGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAGTACGGCCAGCAGCTAC 597
          |||||||||||||||||||||||||| |||| ||||||||||||||||||||||||
Db    577 GGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAGTACGGCCAGCAGCTAC 636

Qy    598 CTGAGCCTGACGCCTGACGCTGGAGAAGTCCCAGCAGTGCCCTTACAGAGTTCACGCAT 657
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    637 CTGAGCCTGACGCCTGACGCTGGAGAAGTCCCACAAAAGTCCCAGCAGTGCCCTTACAGAGTTCACGCAT 703

Qy    658 GAAGGGAGCACCCGTGGAGAAGACAGTGCCCCTACAGTTCACGCAT 696
          |||||||||||||||||||||||||||||||||||||||||||||
Db    697 GAAGGGAGCACCCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 742

RESULT 7
US-09-049-672A-23
; Sequence 23, Application US/09049672A
; Patent No. 6135941
;   GENERAL INFORMATION:
;      APPLICANT: Hillman, Jennifer L.
;      APPLICANT: Lal, Preeti
```

```
Qy    175 CCAGCGCGGGGCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCCTCAGGGATCCCT 234
          ||||  ||||||   ||||||||||||  ||||   ||||||   |||||||||||  ||
Db    212 CCAGGCAAAGCCCCCAAAATCATGATTTATGAGGTCAGTAAGCGGCCCCTCAGGGGTTTCT 271

Qy    235 GAGCGGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCACCCTCCGACATCTCGGGCTCCAG 294
          ||||| ||||||||||||||||| |||||||||||  ||  |||||||    |||||
Db    272 AATCGCTTCTCTGGCTCTGGCTCCGAGTCTGGCAACACGGCTCCCTGCAACATCTCTGGGCTCCAG 331

Qy    295 GCCGGGATGAGGCTGACTATTACTGTCAGTGTGGGACAGGGCTAGTGATCATCCGGTC 354
          || |||||  ||||   |  |||||||| ||||||||
Db    332 GCTGAGGACGAGGCTGATTATTACTG---CTGCTCATATGCAGGTAGTTACACTGTGGTT 388

Qy    355 TTCGGACGAGGGGACCCGGTGACCGTCCTAGGTCAGCCAACAAGGCTGCCCCTGCCTCACT 414
          |||||| | |||||||||||||||||||||||||||||||||||||||||||||||  |||
Db    389 TTCGGCGCAGGGACCAAACTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCTGCCTCACT 448

Qy    415 CTGTTCCCGCCCTCCTCTGAGGAGTTCAAGCCAACAAGGCCAACACTGGTGTGTCTCATA 474
          ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Db    449 CTGTTCCCGCCCTCCTCTGAGGAGTTCAAGGCCAACAAGGCCACACTGGTGTGTCTCATA 508

Qy    475 AGTGACTTCTACCCGGGAGCCGTGACAGTGCCTGACAGTGGCCAGCCCCGTCAAG 534
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    509 AGTGACTTCTACCCGGGAGCCGTGACAGTGCCTGACAGTGGCCAGCAGCCCCGTCAAG 568

Qy    535 GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGCAACAACAGTACGGCCAGCAGC 594
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    569 GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGCAACAACAGTACGGCCAGCAGC 628

Qy    595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGTGCCCAGGTCACG 654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    629 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGTGCCCAGGTCACG 688

Qy    655 CATGAAGGGAGCACCCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 703
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 CATGAAGGGAGCACCCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 737

RESULT 6
US-09-049-672A-25
; Sequence 25, Application US/09049672A
; Patent No. 6135941
;   GENERAL INFORMATION:
;      APPLICANT: Hillman, Jennifer L.
;      APPLICANT: Lal, Preeti
;      APPLICANT: Tang, Y. Tom
;      APPLICANT: Yue, Henry
;      APPLICANT: Au-Young, Janice
;      APPLICANT: Corley, Neil C.
;      APPLICANT: Guegler, Karl J.
;      APPLICANT: Baughn, Mariah R.
;   TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Incyte Pharmaceuticals, Inc.
;      STREET: 3174 Porter Drive
;      CITY: Palo Alto
;      STATE: CA
;      COUNTRY: USA
;      ZIP: 94304
;   COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/049,672A
;      FILING DATE: HEREWITH
;      CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;      NAME: Cerrone, Michael C
```

```
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Yue, Henry
;  APPLICANT: Au-Young, Janice
;  APPLICANT: Corley, Neil C.
;  APPLICANT: Guegler, Karl J.
;  APPLICANT: Baughn, Mariah R.
;  TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;  NUMBER OF SEQUENCES: 28
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Incyte Pharmaceuticals, Inc.
;  STREET: 3174 Porter Drive
;  CITY: Palo Alto
;  STATE: CA
;  COUNTRY: USA
;  ZIP: 94304
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette
;  COMPUTER: IBM Compatible
;  OPERATING SYSTEM: DOS
;  SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/049,672A
;  FILING DATE: HEREWITH
;  CLASSIFICATION: 536
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:
;  FILING DATE:
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Cerrone, Michael C
;  REGISTRATION NUMBER: 39,132
;  REFERENCE/DOCKET NUMBER: PF-0497 US
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 650-855-0555
;  TELEFAX: 650-845-4166
;  TELEX:
;  INFORMATION FOR SEQ ID NO: 23:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 891 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  IMMEDIATE SOURCE:
;  LIBRARY: THYRNOT10
;  CLONE: 2872705
US-09-049-672A-23

Query Match          64.6%;  Score 455.4;  DB 3;  Length 891;
Best Local Similarity 79.8%;  Pred. No. 4.8e-117;
Matches  566;  Conservative   0;  Mismatches 131;  Indels  12;  Gaps  2;

Qy    4 AGGGTCCCCGCTCAGCTCCTGGGGCTTCTGCTCCTGCTCCCAGGTGCACGATGTGCC      63
          || |  |   |||||  ||||  ||    |||||||||||||| ||| |||||||||
Db   34 ATGGCCTGGCCTCTGCTATTCCTCACCCTCCACTCAGGCACAGGGTCCTGGGCCCAG      93

Qy   64 TATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGCCAGGACCAGGATCACC  123
          |  |||||||||||||  ||| ||||||| | |||| |||||| | ||  |  | || ||
Db   94 TCTGCCCTGACTCAGCCTGCCTCCGTGTCCTGGGTCTCCTGGACAGTGACATCACCATCTCC  153

Qy  124 TGTGGGGGAGCAACAGTA-------GAAATGAATATGTCCACTGGTACCAGCAGAAG      174
          ||   || | |||| |         ||  |  || ||| || ||||||| ||||
Db  154 TGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAGTCC   213

Qy  175 CCAGGCGCGGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCT    234
          |||||| |||  ||  || || ||| | || || || | ||| |||||||||||  | |
Db  214 CCAGGCACGGCCCCCAAACTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCT     273

Qy  235 GAGCGATTCTCGGCTCCAAATCAGGAGAACACCGCCACCCTGACCATCAACGGGGTCGAG    294
          || ||||||| |||||||| | ||| | ||| |||| |||||||||||  ||| |  |||
Db  274 AATCGGTTCTCTGGCTCCAAGTCTGGCACACGGCCTCCCTGACCATCTCTGGGCTCCAG    333

Qy  295 GCCGGGGATGAGGCTGACTATTACTGCAGGTGTGGGACAGGGCTAGTCATCATCCGGTC     354
          || || ||||| ||||| ||||||||    ||  |  ||| | || ||  |   |   |
Db  334 GCTGAGGACGAGGCTGATTATTACTG-----CAGCTCATATATGTAGGCAACAACATTGTGGTA  390
```

```
Qy  355 TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT     414
          |||||  ||||||||   ||||||||||||||||||||||||||||||||| |||||||||
Db  391 TTCGGCGGAGGGACCAAGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT      450

Qy  415 CTGTTCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA      474
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  451 CTGTTCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA      510

Qy  475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG     534
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  511 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG     570

Qy  535 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGCAGTACGCGGCCAGCAGC  594
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  571 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGCAGTACGCGGCCAGCAGC  630

Qy  595 TACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG      654
          || |||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  631 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG     690

Qy  655 CATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT      703
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  691 CATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT      739
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RESULT 8
US-09-152-060-47
;  Sequence 47, Application US/09152060
;  Patent No. 6648230
;  GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 28 Human Secreted Proteins
;  FILE REFERENCE: PZ003P1.US
;  CURRENT APPLICATION NUMBER: US/09/152,060
;  CURRENT FILING DATE: 1998-09-11
;  EARLIER APPLICATION NUMBER: PCT/US98/04858
;  EARLIER FILING DATE: 1998-03-12
;  EARLIER APPLICATION NUMBER: 60/040,762
;  EARLIER FILING DATE: 1997-03-14
;  EARLIER APPLICATION NUMBER: 60/040,710
;  EARLIER FILING DATE: 1997-03-14
;  EARLIER APPLICATION NUMBER: 60/050,934
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,100
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,357
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,189
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/057,765
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/068,368
;  EARLIER FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 47
;  LENGTH: 885
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-152-060-47

Query Match          61.8%;  Score 435.6;  DB 4;  Length 885;
Best Local Similarity 81.2%;  Pred. No. 1.5e-111;
Matches  520;  Conservative   0;  Mismatches 114;  Indels  6;  Gaps  1;

Qy   70 CTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGCAGCGGCCAGGATCACCTGTGGG    129
          ||||||||||| ||||| ||||| |  |    |||||| ||||| | |  ||   ||| |||
Db   87 CTGACTCAGCCCCCCTCCGTGTCCAAGGACTTGAGACGACTTCACCTGCACC      146

Qy  130 GGAGACAACAGTAGAAATG-----AATATGTCCACTGGTACCAGCAGAAGCCAGCCGGG    183
          || | |||||  |  || ||     ||||||||| |||||||||||||||
Db      (continued)
```

```
Db   147 GGAACAACAACAATGTTGGCGACCAAGGAGCAGCTTGGCTGCAGCAGCACCAGGGCCAC 206
             ||||||||        ||              |||    ||||||||    |
Qy   184 GCCCCTATACTGGTCATCTATGATGATGAGTAGTGACCGGCGATCCCTGAGCGATTC 243
             ||||||||||    ||||  ||    |||||||||||      ||||||  ||||
Db   207 CCTCCCAAACTCCTGTCCTACAGGAATAATAACCGGCCCTCAGGGATCTCAGAGAGATTA 266
             ||||  ||      ||||||||||||||              |||    |||
Qy   244 TCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
             ||||        ||||||||||||||||||||  ||||||||||
Db   267 TCTGCATCCAGGTCAGGAGGAGCCACATCCTCCTGACCATTACTGGCTTCAGCCTGAGGAC 326
             |||     ||||||||||||              |||||||  |||
Qy   304 GAGGCTGACTATTACTGCGGTGTGGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA 363
             |||||||||||||||      |||||||
Db   327 GAGGCTGACTATTACTGCGCAGCATATGACAGCAGCCTTCGCAGTTTGGATGTTCGGCGGA 386
             ||||||||||||||        ||||||||||||||||||||
Qy   364 GGGACCCGGGGTGACCGTCCTAGGTCAGGCTGCCCCAAGGCTGCCCCCTCGGTCACTCTT 423
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   387 GGGACCAAGCTGACCGTCCTAGGTCAGCCACGGCTGCCCCAAGGCTGCCCCCTCGGTCACTCTT 446
             |||||||||||||||||||||||||||
Qy   424 CCCTCCTCTGAGGAGCTTCAAGCCACAGAGGCCACACTGGTGTGTCTCATAAGTGACTTC 483
             ||||||||||||||||||||||||||||
Db   447 CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCTCATAAGTGACTTC 506
             ||||||||||||||||||||||||
Qy   484 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG 543
             ||||||||||||||||||||||||||||||||
Db   507 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG 566
             ||||||||||||||||||||
Qy   544 GAGACCACCACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGC 603
             |||||||||||||||
Db   567 GAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGC 626
             ||||||||||||||||||||
Qy   604 CTGACGCCTGAGCAGTGGAAGAGCTACAGCTGCCAGTTCACGCATGAAGGG 663
             |||||||||||||||||||||||||
Db   627 CTGACGCCTGAGCAGTGGAAGAGCTACAGCTGCCAGTTCACGCATGAAGGG 686
             |||||||||||||||||||||||||
Qy   664 AGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 703
             ||||||||||||||||||||||
Db   687 AGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 726
```

RESULT 9
US-09-152-060-29
; Sequence 29, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

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;   LENGTH: 879
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-152-060-29

      Query Match             61.6%;   Score 434;  DB 4;   Length 879;
      Best Local Similarity   81.1%;   Pred. No. 4e-111;
      Matches  519;   Mismatches  115;   Indels  6;   Gaps  1;
      Conservative   0;

Qy    70 CTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGGACGGGCCAGGATCACCTGTGGG 129
            |||||||||||||||||||||||||||||||||||||||||||||  |||||  ||
Db    79 CTGACTCAGCCCCCCTCGGTGTCCAAGGACTTGACAGCAGCCCACACTCACCTGCACC 138
            ||||||||||                      |||||||||||||||||||||||
Qy   130 GGAGACAACAGTAGAAATG------AATATGTCCACTGGTACCAGCAGAAGCCAGCGCGCG 183
            |||||||||||||          |||||||||||||||||||||||||||||||||||
Db   139 GGGAACAACAACAATGTTGGCGACCAAGGAGCAGCTTGGCTGCAGCACCAGGGCCCAC 198
            ||||||||||||||||||||||||||||||||||||||
Qy   184 GCCCCTATACTGGTCATCTATGATGATGAGTAGTGACCGGCCCTCAGGGATCCCTGAGCGATTC 243
            ||||||||||||||||||||||||||||||||
Db   199 CCTCCCAAACTCCTGTCCTACAGGAATAATAACCGGCCCTCAGGGATCTCAGAGAGATTA 258
            ||||||||||||||||||||
Qy   244 TCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
            ||||||||||||||||||||||||||||||
Db   259 TCTGCATCCAGGTCAGGAGGGAGCCACATCCTCCTGACCATTACTGGCTTCAGCCTGAGGAC 318
            |||||||||||||||||||||||||||||
Qy   304 GAGGCTGACTATTACTGTGCAGGTGTGGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA 363
            ||||||||||||||      |||||||||||||||||||||||||||||||||
Db   319 GAGGCTGACTATTACTGCGCAGCATATGACAGCAGCCTCCGCAGTTTGGATGTTCGGCGGA 378
            |||||||||||||||||||||||||||||||
Qy   364 GGGACCCGGGGTGACCGTCCTAGGTCAGGCTGCCCCAAGGCTGCCCCCTCGGTCACTCTT 423
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   379 GGGACCAAGCTGACCGTCCTAGGTCAGCCACGGCTGCCCCAAGGCTGCCCCCTCGGTCACTCTT 438
            |||||||||||||||||||||||||
Qy   424 CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC 483
            |||||||||||||||||||||||||||||||||||||
Db   439 CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCTCATAAGTGACTTC 498
            ||||||||||||||||||||||||||||||||
Qy   484 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG 543
            |||||||||||||||||||||||||||||||||||||||||||||
Db   499 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG 558
            ||||||||||||||||||||
Qy   544 GAGACCACCACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGC 603
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   559 GAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGC 618
            ||||||||||||||||||||||||
Qy   604 CTGACGCCTGAGCAGTGGAAGAGCTACAGCTCCCAGAAGAGCTGCCAGGTCACGCATGAAGGG 663
            ||||||||||||||||||||||||||
Db   619 CTGACGCCTGAGCAGTGGAAGAGCTACAGCTACCAGTGCCAGGTCACGCATGAAGGG 678
            |||||||||||||||||||||||||||
Qy   664 AGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 703
            |||||||||||||||||||||||
Db   679 AGCACCGTGGAGAAGACAGGTGCCCCTACAGAATGTTCAT 718
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RESULT 10
US-09-152-060-46/c
; Sequence 46, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100

Db   481 ACARAGCAACAACAAGTACGGCGGCCAGCAGCTACCTGAGCCTGACGCCYGAGCAGTGGAA 422

Qy   524 GTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAGGAGCACCGTGGAGAAGACAGT 683

Db   421 GTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAGGAGCACCGTGGAGAAGACAGT 362

Qy   684 GGCCCTACAGAATGTTCAT 703

Db   361 GGCCCTACAGAATGTTCAT 342

RESULT 11
US-09-049-672A-24
; Sequence 24, Application US/09049672A
; Patent No. 6115941
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Yue, Henry
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Baughn, Mariah R.
;   TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/049,672A
;   FILING DATE: HEREWITH
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Cerrone, Michael C
;   REGISTRATION NUMBER: 39,132
;   REFERENCE/DOCKET NUMBER: PF-0497 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX:
; INFORMATION FOR SEQ ID NO: 24:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 919 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: LNODNOT08
;   CLONE: 3056213
US-09-049-672A-24

Query Match   60.3%;   Score 425.4;   DB 3;   Length 919;
Best Local Similarity   81.0%;   Pred. No. 9.8e-109;
Matches   524;   Conservative   0;   Mismatches   111;   Indels   12;   Gaps   2;

Qy   66 TGAACTGACTCAGCCACCCTCGGTGTCCCAGGACAGAGCGGCCAGGATCACCTG 125
      |||||| |||||||| |||||||||| ||||| |||||||||||||||||| ||||
Db   125 TGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCCCTGGAGGGACCAGTCACACTCACTTG 184

Qy   126 TGG-------GGGGAGCAACAGTAGAAATGAATAGTGTCCACTGGTACCAGCAGAAGCC 176

EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
;   LENGTH: 928
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (49)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (78)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (148)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (163)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (532)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-46

Query Match   61.3%;   Score 432.2;   DB 4;   Length 928;
Best Local Similarity   85.7%;   Pred. No. 1.3e-110;
Matches   480;   Conservative   17;   Mismatches   61;   Indels   2;   Gaps   2;

Qy   145 AATGAATAGTCCACTGGTACCAGCAGAAGCCAGGCCAGCCTAT-ACTGGTCATCTA 203
      |||||| ||||||||||||||||| |||||||||||| || | ||||||||||||||
Db   900 AAGAAATATGTWTATTGTACCAMCAGAAGTCAGGCCAGCGCCCTGTGCCTGGTCATCTA 841

Qy   204 TGATGATAGTGACCGGCCCTCAGGGATCCTGAGCGATTCTCTGGCTCCAAATCAGGGAA 263
      ||| |||| ||||||||||||||::|| |||||||||| |||||||||||||
Db   840 TGAGGACAACAAACGACCCTCC-GGATCCCTSAGAGATTCYTGGCTCCAGYTCAGGGAC 782

Qy   264 CACCGCCACCTTGACCATCAACGGGGTCGAGGCCGGGATGAGGGCTGACTATTACTGTCA 323
      |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   781 AGTGGCCACCTTGACTATCAGTGGGGCCCAGGTGAGGATGCGGCTGACTACTACTGTTA 722

Qy   324 GGTGTGGGACAGGGCTAGTAGTGATCATCCGGTCTTCGGAGGAGGGACCGGGTGACCGTCCT 383
      |||||| ::|||||||||||||||||||||||||||||||| |||||||||||||||||
Db   721 CTCAACAGACAGCAGTGGTAATCATGGKGTCTTCGGAACTGGGACCAAGGTCACCGTCCT 662

Qy   384 AGTCAGCCCAAGGTCACCGGTCGTCCGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCA 443
      |||| | |||||||::||| |||||||||||||||||||||||||||||||||||||
Db   661 AGGTCAGCCCAAGGCYRMCCCCWCKGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTYCA 602

Qy   444 AGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGCACAGT 503
      |||||||||||||||| ||||||::|||::|:|||||||||||||||||||||||||||
Db   601 AGCCAACAAGGCCACACTRGTGTGTCTSATMAGTGACTTCTACCCGGGAGCCYGTGACAGT 542

Qy   504 GGCCTGGAAGGCAGATAGCAGCCCGTCAAGCGGGAGTGGAGACCACCACACCCTCCAA 563
      |||||||||| ||||| |||||||||||||| ||||||||||:|||::|||||||||||
Db   541 GGCCTGGAANGCAGATRGCAGCCCCGTCAAGCGGGAGTGGAGACCACCAMACCCTCCAA 482

Qy   564 ACAAAGCAACAACAAGTACGCCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAA 623
      |||:|||||||||||| ||| |||||||||||||||||||||||||||||||||||||||

RESULT 12
US-08-793-450-5
Sequence 5, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10556
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 716 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..716
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..57
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..716
; OTHER INFORMATION: /product= "IMMUNOGLOBIN, LIGHT
; OTHER INFORMATION: CHAIN"

US-08-793-450-5

Query Match   57.8%;   Score 407.4; DB 4;   Length 716;
Best Local Similarity 78.0%;   Pred. No. 8.7e-104;
Matches 536; Conservative 0; Mismatches 106; Indels 45; Gaps 2;

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Qy   47 CAGGTGCCACGATGTCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGAC  106
         |||||| ||  ||  |||| ||| | ||||| ||    ||||| |||| || ||| |||
Db   44 CAGGTGTCCACTCCGACACATCCGAGCTCAGCTCACTCAGGAACCTCGTGTCTGTGGCCTTGTGGGAC  103

Qy  107 AGACGGCCAGGATCACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACC  166
         |||| |||||||||| |||| ||| ||||| ||   ||     |  ||||| ||||||||
Db  104 AGACAGTCAGGATCACATGCCAAGGACAGCAGCCTATTATGCAAGCTGGTACC  163

Qy  167 AGCAGAAGCCAGGCCAGGCGGGACCCGGGCCCTATACTTGTCATCTATGATGATAGTAGTGACCGGCCCTCAG  226
         ||||||||| |||| |||| |||| |||| || |||||||||||||| 
Db  164 AGCAGAAGCCAGGACAGGCAACAGGCACCTGTACTTGTCATCTATGGTAAAAACAACCGGCCCTCAG  223

Qy  227 GGATCCCTGAGCGATTCTCTGGCTCCAAATCAGTGAACTGACTCAGCCACCCTGACCATCAACG  286
         ||||||  ||||||||||||||||| |   ||  |  ||  ||| |||||||||||||||| ||
Db  224 GGATCCCAGACCGATTCTCTGGCTCCAGCTCAGGAAACACAGCTTCCTGACCATCACTG  283

Qy  287 GGGTCGAGGCCGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATC  346
         ||| | ||||| | |||||||||||||||   ||                 |  ||  ||
Db  284 GGGCTCAGGCGGAAGATGAGGCTGACTATTTCTGTAA------------CAGCCGTG  328

Qy  347 ATCCGGTCTTCGGACAGGGGACCAAGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCT  406
                  |||||| | |||||||||||||||||||||||||||||||||||||||||
Db  329 GGAAGGTGTTCGGCGGAGGGACCAAGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCT  388

Qy  407 CGGTCACTCTGTTCCCGCCCTCC------------TCTGAGG  436
         ||||||||||||||||||||| 
Db  389 CGGTCACTCTGTTCCCGCCCTCTGAGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAGG  448

Qy  437 AGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCG  496
         |||||||||||||||||||||||| ||||||||| || |||| 
Db  449 AGCTTCAAGCCAACAAGGCCACACTAGTGTGTCTGATCAGTGGCGGGTGGAGACCGGGAGCTG  508

Qy  497 TGACAGTGCCTGAAGGCAGCAGATAGCCCCGTCAAGGCGGGAGTGGAGACCACACAC  556
         |||| |||| | ||||| ||||  ||  |||||||||||||||||||||||||  | 
Db  509 TGACATTGGCTTCGGAAGGCAGGATGGCAGGCCCGTCAAGGCGGGAGTGGAGACCAACAAAC  568

Qy  557 CCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTACCTGAGCCTGAGC  616
         ||||  ||| | |||||||||||||||||||||||||||||||||||||||||| 
Db  569 CCTCAAACAGAGCAACAACAAGTACGGCGGCCAGCAGCTACCTGAGCCTGAGCCCCCAGC  628

Qy  617 AGTGGAAGTCCACAGAAGCTACAGTCCCAGGTGCCATGAAGGGAGCACCGTGTGGAGA  676
         ||||||||||||||||||||||||||||||||||||| |||||||||||| | ||||
Db  629 AGTGGAAGTCCACAGAAGCTACAGTCCCAGGTGCCATGAAGGGAGCACTGCAGAGA  688
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(continuation alignment)

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Db  185 TCGCTTGAGCTCTGGCTCAGTCTCTCTACTAGTAACTACCCCAGCTGGTACCAGCAGACCCC  244
Qy  177 AGCGCGGCCCTATACTGGTCATCTATGATGATGAGTAGTGACCGGGATCCCTGA  236

Db  245 AGCGCCAGGCTCCACGCACGCTCATATACGGCACAAGTGTTGTTCTTCTTCTGGAGTCCCTGA  304
Qy  237 GCGATTCTCTGGCTCCAAATCAGGAACCATCAACCGACCCTCACCATCAACGGGGTCGAGGC  296

Db  305 TCGCTTCTCTGGCTCCATCCTGGGAACAAAGCCGGCCTCACCATCACGGGGGCCCAGGC  364
Qy  297 CGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGCGGCTAGTGATCATCCGGTCTT  356

Db  365 AGATGATGAATCTGATTATTATTGT---GTCCTATATAGGCGTAGTGGCGTCTTGGGTGTT  421
Qy  357 CGGACAGGGGACCAAGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCT  416

Db  422 CGGCGGAGGGACCAAGCTGTCGGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCT  481
Qy  417 GTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAG  476

Db  482 GTTCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAG  541
Qy  477 TGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC  536

Db  542 TGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC  601
Qy  537 GGGAGTGGAGACCACCACAGCCACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTA  596

Db  602 GGGAGTGGAGACCACCACAGCCACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTA  661
Qy  597 CCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGTCCCAGAGCTGCCAGGTCACGCGCA  656

Db  662 CCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAAAAGCTACAGTCCCAGGTCACGTCA  721
Qy  657 TGAACGGAGCACCGTGGAGAAGACAGTGGAGAAGACAGTGCCGCCCCTACAGAATGTTCAT  703

Db  722 TGAAGGGAGCACCGTGGAGAAGACAGTGGAGAAGACAGTGCCGCCCCTACAGAATGTTCAT  768
```

APPLICANT: Frudakis, Tony N.
             Smith, John M.
             Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
                    TREATMENT AND DIAGNOSIS OF BREAST CANCER
;
;
;
NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
        ADDRESSEE: Seed IP Law Group
        STREET: 701 Fifth Avenue, Suite 6300
        CITY: Seattle
        STATE: Washington
        COUNTRY: USA
        ZIP: 98104-7092
COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/991,789A
        FILING DATE: 11-Dec-1997
        CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
        NAME: Potter, Jane E. R.
        REGISTRATION NUMBER: 33,332
        REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
        TELEPHONE: (206) 622-4900
        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 241:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 771 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: cDNA
    ORIGINAL SOURCE:
        ORGANISM: Homo sapiens
    SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-991-789A-241

Query Match   38.8%;   Score 273.2; DB 4; Length 771;
Best Local Similarity 79.2%;   Pred. No. 1.3e-66;
Matches 336; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

Qy   131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGGGGCCCCTA 190
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Db   430 GTGACGTTGGTGGTTATAATAATGTCTNTGGTACCAACAGCACCCAGGCAAAGCCCCCA 371

Qy   191 TACTGGTCATCTATCATGATGATAGTGACCGGCCCTGAGGGATTCCTCTGGCT 311
         |||||||| ||||||||||| ||||||||| |||| ||| || ||||||||||
Db   370 AATTCATGATTTATGAGGTCGGTAATCGGCCCCAGGGGTTTCTAATCGCTTCTCTGGCT 311

Qy   251 CCAAATCAGGAACACCCGCCACCTGACCATCAACGGGTCGAGGCCGGGGATGAGGCTG 310
         ||||||||||||| | | |||||||||||| || ||||||| ||||| ||||||||||
Db   310 CCAAGTNTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTG 251

Qy   311 ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGACACCC 370
         |||||||| || | ||||||||||||||| ||||||||||| || || ||||||||||
Db   250 ATTATTACTG---CAGCTCATATACAAGCAGCAGCCAGCACTCTCGTGTTTGGCGGAGGGACCA 194

Qy   371 GGGTGACCGTCCTAGGTCAGCCCAGGCTGCCCCGTGACTCTGGCCT 430
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Db   193 AGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCGTGACTCTGGCCT 134

Qy   431 CTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCATAAGTGACTTCTACCCGG 490
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Db   133 CTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG 74

Qy   491 GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA 550
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Qy   677 AGACAGTGGCCCCTACAGAATGTTCAT 703
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Db   689 AGACGGTGGCCCCTGCAGAATGTTCAT 715

RESULT 13
US-09-404-879A-268/c
; Sequence 268, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
;   APPLICANT: Mitcham, Jennifer L.
;   APPLICANT: King, Gordon E.
;   APPLICANT: Algate, Paul A.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;   TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
;   FILE REFERENCE: 210121.462C2
;   CURRENT APPLICATION NUMBER: US/09/404,879A
;   CURRENT FILING DATE: 1999-09-24
;   NUMBER OF SEQ ID NOS: 393
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 268
;   LENGTH: 584
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(584)
;   OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-268

Query Match   43.5%;   Score 306.6; DB 4; Length 584;
Best Local Similarity 85.0%;   Pred. No. 6.7e-76;
Matches 367; Conservative 0; Mismatches 57; Indels 8; Gaps 2;

Qy   215 ACCGGGCCCTCAGGGATCCTGAGCGATTCTCGGCTCCAAATCAGGG-----AACACCGC 269
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Db   449 AGCGGGCCCTCAGGGGTCCCTGATCGCTTNTCGGCTTCCAAGTCTTGGCAAACACGGGCC 390

Qy   270 CACCCTGACCATCAACGGGTCGAGGCCGGGGATGAGGCTGACTATTACTGTCAGGTGTG 329
         |||||||||||||||| | |||||||||| |||||||||||| |||||||||||||||
Db   389 TCCCTTGACNGTCTCTGGCTCTCAGGCTGAGGATGAGGCTGATTATTATTACTGCAGCTCATA 330

Qy   330 GGACAGGGCTAGTGATCATCCGGTCTTCGGAGGAGGAGGACCCGGTGACCGTCCTAGGTCA 389
         ||||||||| ||||||| |||||| || |||||||| || |||||| |||||| ||||||
Db   329 TGCAGGCAACA--ACAATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCA 273

Qy   390 GCCCAGGCTGCCCCGTGTTCCGCCCTCTTCTGAGGAGCTTCAAGCCAA 449
         ||||||||| ||||||| |||| |||| ||| |||||||||||||||||
Db   272 GCCCAAGGCTGCCCCGTGTTCCCACCCTCTCTGAGGAGCTTCAAGCCAA 213

Qy   450 CAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACCAGTGGCCTG 509
         ||||||||||||||||| || |||||||||||||||| |||||||||| ||||||||||
Db   212 CAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACCAGTGGCCTG 153

Qy   510 GAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACACACCCTCCAAACAAAG 569
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Db   152 GAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCGGGAGCCACCACCCTCCANCAAAG 93

Qy   570 CAACAACAAGTACGCGCCGCCAGCAGCCTGAGCCTGAGCAGTGGAAGTCCCA 629
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Db   92 CAACAACAAGTACGCGCCGCCAGCAGCCTACCTGAGCCTGAGCCGTGGAAGTCCCA 33

Qy   630 CAGAAGCTACAG 641
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RESULT 14
US-08-991-789A-241/c
; Sequence 241, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:

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Qy    551  CCAC  554
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Db     13  CTAC  10
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RESULT 15
US-09-062-451-241/c
; Sequence 241, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SEED and BERRY LLP
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104-7092
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/062,451
;   FILING DATE: 04-APR-1997
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Maki, David J.
;   REGISTRATION NUMBER: 31,392
;   REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 241:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 771 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
US-09-062-451-241

Query Match   38.8%; Score 273.2; DB 4; Length 771;
Best Local Similarity   79.2%; Pred. No. 1.3e-66;
Matches 336; Conservative   0; Mismatches   85; Indels   3; Gaps   1;

Qy   131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGCGGCGCCCTA 190
             | ||| || || | |||| ||||| ||| ||||||| |||| | || ||||
Db   430 GTGACGTTGGTGTGGTTATATAATGTCTCNTGGTACCAACAGCACCCAGCAAAGCCCCCA 371

Qy   191 TACTGGTCATCTATGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250
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Db   370 AATTCATGATTTATGAGGTCGGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCT 311

Qy   251 CCAAATCAGGGAACACCGCACCCTGACCATCAACGGGTCGAGGCCCGGGATGAGGCTG 310
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Db   310 CCAAGTNTGCAACACGACGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTG 251

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Db   193 AGCTGACCCGTCCTAGGTCAGCCCAAGGTGCCCCCTCCGGTGCCCCTCGGTCACTCGTTCCCACCCTCCT 134
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Qy   431  CTGAGGAGCTTCAAGCCACCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG 490
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   133  CTGAGGAGCTTCAAGCCACCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG 74

Qy   491  GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    73  GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA 14

Qy   551  CCAC 554
              | |
Db    13  CTAC 10
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Search completed: April 6, 2003, 06:25:10
Job time : 34.1002 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: April 5, 2003, 19:13:05 ; Search time 2231 Seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-9
Perfect score: 711
Sequence: 1 ATGGAGGTCCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1455140287B residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	711	100.0	711	6	AR108866	AR108866 Sequence
2	582.6	81.9	935	6	AR135362	AR135362 Sequence
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4	573	80.6	870	9	HSIGLV	X14583 Human mRNA
5	571.2	80.3	903	9	BC020233	BC020233 Homo sapi
6	570.6	80.3	827	9	AB064143	AB064143 Homo sapi
7	566.6	79.7	800	9	AB064188	AB064188 Homo sapi
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9	566	79.6	815	9	AB064149	AB064149 Homo sapi
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14	560	78.8	747	9	HSIGVL006	X57806 Human rearr
15	558	78.5	821	9	AB064141	AB064141 Homo sapi
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31	548.4	77.1	831	9	AB064224	AB064224 Homo sapi
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33	546.2	76.8	810	9	HSIGVL025	X57815 Human rearr
34	546.2	76.8	816	9	AB064178	AB064178 Homo sapi
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36	545	76.7	789	9	AB064205	AB064205 Homo sapi
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45	533.2	75.0	708	6	BD013339	BD013339 Novel pep

ALIGNMENTS

RESULT 1
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LOCUS   AR108866   711 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION   Sequence 9 from patent US 6113898.
ACCESSION   AR108866
VERSION   AR108866.1 GI:12825142
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 711)
AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE   Human B7.1-specific primatized antibodies and transfectomas
                expressing said antibodies
JOURNAL   Patent: US 6113898-A 9 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

Left column (RESULT 2)

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     source       1..711
                  /organism="unknown"
BASE COUNT     160 a    226 c    193 g    132 t
ORIGIN

Query Match        100.0%;    Score 711;  DB 6;  Length 711;
Best Local Similarity  100.0%;  Pred. No. 4.9e-174;
Matches  711;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy    61 GAGTCTGTCCTGACACAGCCGCCGCTCAGTGTCTCGGGGCCCCAGGGCAGAAGGTCACCATC   120
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Qy   181 CCAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT   240
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Db   181 CCAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT   240

Qy   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGCCTCCCTGGCCATCACTGGGCTCCAG   300
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Db   241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGCCTCCCTGGCCATCACTGGGCTCCAG   300

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAAATGCTCAGGTA   360
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Db   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAAATGCTCAGGTA   360

Qy   361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT   420
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Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA   480
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Db   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA   480

Qy   481 AGTGACTTCTACCCGGGAGCCGTGAACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAG   540
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Db   541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC   600

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG   660
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Db   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG   660

Qy   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA   711
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Db   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA   711
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RESULT 2
AR135362
LOCUS   AR135362   935 bp   DNA   linear   PAT 16-JUN-2001
DEFINITION Sequence 20 from patent US 6135941.
ACCESSION   AR135362
VERSION   AR135362.1 GI:11476034
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 935)
  AUTHORS   Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J.,
            Corley,N.C., Guegler,K.J. and Baughn,M.R.
  TITLE   Human immune system associated molecules

Right column (RESULT 3)

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JOURNAL     Patent: US 6135941-A 20 24-OCT-2000;
FEATURES          Location/Qualifiers
     source       1..935
                  /organism="unknown"
BASE COUNT     216 a    299 c    248 g    172 t
ORIGIN

Query Match        81.9%;    Score 582.6;  DB 6;  Length 935;
Best Local Similarity  89.8%;  Pred. No. 1.1e-140;
Matches  637;  Conservative  0;  Mismatches  69;  Indels  3;  Gaps  1;

Qy     4 AGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAG    63
         ||||||||||||||||||||||  ||  ||  |||||||||||||||||||||| ||
Db    74 ATGGCCTGGTCTCCTCTCCTCCTCACTCTCCTCACTGCTCCTCACTCCTCGGGCCCCAG   133

Qy    64 TCTGTCCTGACACAGCCGCCGCCCTCAGTGTCTCGGGGCCCCAGGGCAGAAGTCACCATCTCG   123
         ||||||  |||||  |||  ||| ||||||||||||||||||||||||||||||||| |||
Db   134 TCTGTGTCGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCC   193

Qy   124 TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTC   180
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Qy   181 CCAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT   240
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         ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   314 GACCGATTCTCTGGCTCCAAGTCTGGTACCTCGGCCTCCCTGGCCATCACTGGGCTCCAG   373

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAAATGCTCAGGTA   360
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   374 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAGTGTGGTGGTA   433

Qy   361 TTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT   420
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Db   434 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT   493

Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA   480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   494 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA   553

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAG   540
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   554 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAG   613

Qy   541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   614 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGC   673

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   674 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG   733

Qy   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT   709
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Db   734 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT   782
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RESULT 3
AB064208
LOCUS   AB064208   790 bp   mRNA   linear   PRI 02-JUL-2002
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L68.
ACCESSION   AB064208
VERSION   AB064208.1 GI:21669622
KEYWORDS   .
SOURCE   Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L68.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1

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Db   428  CTCTGTTCCCACCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA  487
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Qy   479  TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGAAGGCAGCAGATAGCAGCCCGTCA  538
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488  TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGAAGGCAGCAGATAGCAGCCCGTCA  547

Qy   539  AGGCGGGAGTGGAGACCAACAACCTCCAAACAACAAGCAACAACAAGTACGCGGCCAGCA  598
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   548  AGGCGGGAGTGGAGACCAACAACCTCCAAACAACAAGCAACAACAAGTACGCGGCCAGCA  607

Qy   599  GCTACCTGAGCCTGAGCGCCGTGACGTGGAAGTCCCAGAAGACTACAGTCTGCCAGGTCA  658
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   608  GCTACCTGAGCCTGAGCGCCGTGACGTGGAAGTCCCAGAAAGCTACAGTCTGCCAGGTCA  667

Qy   659  CGCATGAGGGAGGGAGGAGACAGTGCCCCTACAGAATGTTC  707
               ||||||||||||||||||||||||||||||||||||||||
Db   668  CGCATGAGGGAGGGAGGAGACAGTGCCCCTACAGAATGTTC  716
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RESULT 4
HSIGLV
LOCUS        HSIGLV                    870 bp    mRNA        linear   PRI 27-NOV-1995
DEFINITION   Human mRNA for Ig lambda-chain.
ACCESSION    X14583
VERSION      X14583.1   GI:33394
KEYWORDS     Ig light chain; immunoglobulin; lambda-immunoglobulin.
SOURCE       Homo sapiens
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 870)
  AUTHORS    Kishimoto,T.
  TITLE      Direct Submission
  JOURNAL    Submitted (03-MAR-1999) Kishimoto T., Yoshitomi Pharmaceutical
             Industries Ltd, Research Labs, 7-25 Koyata 3-chome, Iruma Shi,
             Saitama, 358 Japan
REFERENCE    2  (bases 1 to 414)
  AUTHORS    Kishimoto,T., Okajima,H., Okumoto,T. and Taniguchi,M.
  TITLE      Nucleotide sequences of the cDNAs encoding the V-regions of H- and
             L-chains of a human monoclonal antibody with broad reactivity to
             malignant tumor cells
  JOURNAL    Nucleic Acids Res. 17 (11), 4385 (1989)
  MEDLINE    89296497
  PUBMED     2500644
COMMENT      hybridoma; clone=4G12 L6
             Data kindly reviewed (03-JUL-1989) by Kishimoto T.
FEATURES             Location/Qualifiers
     source          1..870
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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     CDS             25..732
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                     SSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGD
                     EADYYCGTWDSSLSAGVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS
                     DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQV
                     THEGSTVEKTVAPTECS"
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     misc_feature    85.. .375
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                     /note="J region"
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                     /note="C region"
BASE COUNT     206 a    285 c    213 g    166 t
ORIGIN
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AUTHORS    Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
           Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
           Miura,K. and Kurosawa,Y.
TITLE      Construction and characterization of antibody libraries: isolation
           of therapeutic human antibodies and application to functional
           genomics
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 790)
  AUTHORS  Kurosawa,Y.
  TITLE    Direct Submission
  JOURNAL  Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
           Comprehensive Medical Science, Fujita Health University;
           Kutsukake-cho, Toyoake 470-1192, Japan
           (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT    Please visit our web site
           URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1..790
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                     /db_xref="taxon:9606"
                     /clone="L68"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
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                     /gene="IGL"
     CDS             1..>790
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                     /codon_start=1
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                     /protein_id="BAC01836.1"
                     /db_xref="GI:21669623"
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                     CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSY
                     SCQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVN"
     sig_peptide     1..66
                     /gene="IGL"
                     /note="pelB signal peptide"
BASE COUNT     176 a    250 c    213 g    151 t
ORIGIN

Query Match             80.9%;  Score 575.4;  DB 9;  Length 790;
Best Local Similarity   94.0%;  Pred. No. 8.3e-139;
Matches   610;  Conservative    0;  Mismatches   36;  Indels    3;  Gaps    1;
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Qy    62  AGTCTGTCCTGACAGCCGCCCTCCAGTGTCTGGGGCCCCAGGGCAGGAGAAGGTCACCATCT  121
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Db    68  AGTCTGTGTTGACGGCCGCCGCCCTCCAGTGTCTGGGGCCCCAGGGCAGGAGAGGGTCACCATCT  127

Qy   122  CGTGCACTGGGAGACACCTCCAACATTGG--AGGTTATGATCACATTGGTACCAGCAGC  178
               |||||||||||||||||||||||||||   ||||||||| || |||||||||||||||
Db   128  CCTGCACTGGGAGCAGCTCCAACATCGGGGCTGGGTATGTGACACTGGTACCAGCAGC  187

Qy   179  TCCCAGGAACGGCCCCCAAAACTCCTCATCTATGATGACAATAACAGGCGACCCTCAGGAATT  238
               |||||||||||| |||||||||||||||||||| ||||| ||| |||||||||||||||
Db   188  TTCCAGGAACAGCGCCCCAAAACTCCTCATCTATGTGAACAGCAATAACAGGCGACCCTCAGGGTCC  247

Qy   239  CTGACCGATTCTGGCTCCAAGTCTGGTACCGGCGGCCTTCCCTGGCCATCACTGGGCTCC  298
               ||||||||||||||||||||||||| |||  |||||||||||||||||| |||||||||
Db   248  CTGACCGATTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCC  307

Qy   299  AGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGG  358
               ||||||||||||||||||||||||||||| ||||| || |||||||||||||| |||||
Db   308  AGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTGTGG  367

Qy   359  TATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA  418
               ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   368  TATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA  427

Qy   419  CTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA  478
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Query Match
Best Local Similarity 80.6%;   Score 573; DB 9; Length 870;
Matches 624; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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Qy     1 ATGAGGGTCCCGCTCAGCTCCGGGGCTCCTGCTCCTCCTCCTGCTGGCTCCCAGTGCACGATGT  60
           |||||||||||||| ||||||||||  ||||||
Db    22 ATCATGACCTGTCCCCTCTCCTCCTCACCCTTCATTCACTGCACAGGGTCCTGGGCC  81

Qy    61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGCCCCAGGGCAGAAGGTCACCATC  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    82 CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGTCACCATC  141

Qy   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC  180
           |||||||||  ||||||  |||||||||||||||||  |||||||||||||||||||
Db   142 TCCTGCTCTGGAAGCAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGCTC  201

Qy   181 CCAGGAACGGGCCCCAAACTCCTCATCTATGACAATAACAAGCGACCCTCAGGAATTTCT  240
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Db   202 CCAGGAACAGCCCCCCAAACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCT  261

Qy   241 GACCGATTCTCGGCTCCAAGTCTGTACCGGGCCTCCCTGGCCATCACTGGGCTCCAG  300
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Db   262 GACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAG  321

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA  360
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Db   322 ACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGAGTGCTGTGGGGTA  381

Qy   361 TTCGGAGGAGGGACCCGGCTACCGTCCTAGTCAGCCCCAAGGCTGCCCCCTCGGTCACT  420
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Db   382 TTCGGCGGAGGGACTAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCATCGGTCACT  441

Qy   421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  480
           |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db   442 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  501

Qy   481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   502 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG  561

Qy   541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAAGTACGGCCGGCCAGCAGC  600
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   562 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAAGTACGGCCGGCCAGCAGC  621

Qy   601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG  660
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Db   622 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG  681

Qy   661 CATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT  709
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Db   682 CATGAAGGGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT  730
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RESULT 5
BC020233
LOCUS   BC020233   903 bp   mRNA   linear   PRI 03-JAN-2002
DEFINITION Homo sapiens, clone MGC:31936 IMAGE:4765518, mRNA, complete cds.
ACCESSION   BC020233
VERSION   BC020233.1 GI:18044240
KEYWORDS   MGC.
SOURCE   Homo sapiens.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 903)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (19-DEC-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 40 Row: h Column: 5
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction, Similarity but not identity
            to protein.

FEATURES   Location/Qualifiers
     source   1..903
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                     /db_xref="taxon:9606"
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                     /lab_host="DH10B-R"
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     CDS   35..748
                     /codon_start=1
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BASE COUNT   216 a   293 c   227 g   167 t
ORIGIN

Query Match
Best Local Similarity 80.3%;   Score 571.2; DB 9; Length 903;
Matches 638; Conservative 0; Mismatches 68; Indels 6; Gaps 2;

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Qy     4 AGGGTCCCGCTCAGCTCCGGGGCTCCTGCTCCTCCTCCTGCTGGCTCCCAGTGCACGATGTGAG  63
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Db    35 ATGGGCTGGTCTCCGCTCCTCCTCACTCTCCTCGCTCACTGCACAGGGTCCTGGGCCCAG  94

Qy    64 TCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGCCCCAGGGCAGAAGGTCACCATCTCG  123
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    95 TCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGCCCCAGGGCAGAAGGTCACCATCTCC  154

Qy   124 TGCACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTC  180
           |||||||||||||||||||||||||   |||| | ||| |||| ||||||||||||||
Db   155 TGCACTGGGAGCAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTT  214

Qy   181 CCAGGAACGGGCCCCCAAACTCCTCATCTATGACAATAACAAGCGACCCTCAGGAATTTCT  240
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Db   215 CCAGGAACAGCCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCT  274

Qy   241 GACCGATTCTCGGCTCCAAGTCTGTACCGGGCCTCCCTGGCCATCACTGGGCTCCAG  300
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Db   275 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAG  334

Qy   301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCT---CAG  357
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Db   335 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTGGTTTGTG  394
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CLISDFYPGAVTVAWKADSSPVVAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSY
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               /note="pelB signal peptide"
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BASE COUNT    174 a    260 c    231 g    162 t
ORIGIN
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Query Match                80.3%;  Score 570.6;  DB 9;  Length 827;
Best Local Similarity       93.5%;  Pred. No. 1.5e-137;
Matches 607;  Conservative   0;  Mismatches 39;  Indels   3;  Gaps   1;

Qy    62  AGTCTGTCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCT  121
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Db    68  AGTCTGTGTTGACCAGCCGCCCCTCACTGTCTGGGGCCCCAGGGCAAAGGGTCACCATCT  127

Qy   122  CGTGCACTGGGACGCAGCCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGC  178
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Db   128  CCTGCACTGGGACGAGCTTCCAACATCGGGACAGCAGGCAGGTTATGATGTACACTGGTACCAGCAGC  187

Qy   179  TCCCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTT  238
          ||||||||||||||||||||||||||||||||||||     |          |||||||||
Db   188  TTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTGACATCAATCAATCGGCCCTCAGGGGTCC  247

Qy   239  CTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCTCCTGGCCATCACTGGGCTCC  298
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Db   248  CTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCTCCTGGCCATCACTGGGCTCC  307

Qy   299  AGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAATGCTCAGG  358
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Db   308  AGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAGTGGTTCGG  367

Qy   359  TATTCGGAGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCCCAAGGCTGCCCCCGGTCA  418
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Db   368  TATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCCCAAGGCTGCCCCCGGTCA  427

Qy   419  CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA  478
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Db   428  CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA  487

Qy   479  TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGGAAGGCAGATAGCAGCCCCGTCA  538
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Db   488  TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA  547

Qy   539  AGGCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGGCGGCCAGCA  598
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Db   548  AGGCGGGGGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCA  607

Qy   599  GCTACCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCA  658
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Db   608  GCTATCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTAA  667

Qy   659  CGCATGAAGGAGCACGGTGGAGAAGACAGTGGCCCCTACGAATGTTC  707
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Db   668  CGCATGAAGGAGCACGGTGGAGAAGACAGTGGCCCCTACGAATGTTC  716
```

```
RESULT 7
AB064188
LOCUS       AB064188           800 bp     mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L48.
ACCESSION   AB064188
VERSION     AB064188.1  GI:21669582
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L48.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
```

Qy   358 GTATTCGGAGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCCCAAGGCTGCCCCCTCGGTC 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   395 GTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCCCAAGGCTGCCCCCTCGGTC 454

Qy   418 ACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTC 477
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Db   455 ACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTC 514

Qy   478 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC 537
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Db   515 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC 574

Qy   538 AAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGGCGGCCAGC 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   575 AAGGCGGGGGTGGAGAGCACCACCACACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGC 634

Qy   598 AGCTACCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTC 657
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Db   635 AGCTATCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTC 694

Qy   658 ACGCATGAAGGAGCACGGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT 709
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Db   695 ACGCATGAAGGAGCACGGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT 746

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RESULT 6
AB064143
LOCUS       AB064143           827 bp     mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L3.
ACCESSION   AB064143
VERSION     AB064143.1  GI:21669492
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L3.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 827)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1..827
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="L3"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1..827
                     /gene="IGL"
     CDS             1..>827
                     /gene="IGL"
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                     /product="immunoglobulin lambda light chain VLJ region"
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                     /db_xref="GI:21669493"
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                     TGSSSNIGAGYDVHWYQQLPGTAPKLLIYGDINRPSGVPDRFPSGSKSGTSASLAITGL
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Qy   483  TGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC  542
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Db   492  TGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC  551

Qy   543  GGGAGTGGAGACCACCACCACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTA  602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   552  GGGAGTGGAGACCACCACCACCCTCCAAACAAGGCAACAACAAGTACGGCGGCCAGCAGCTA  611

Qy   603  CCTGAGCCTGAGCGCTGAGGAGTGGAGTCCCAGAGACTCAGCTGCCAGGTCACCGA  662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   612  CCTGAGCCTGAGCGCTGAGGAGTGGAGTCCCACAAAAGCTACAGTCACCGCTGCCAGGTCACCGCA  671

Qy   663  TGAAGGGAGCACCGTGGAAGACAGTGGCCCCTACAGAATGTTC  707
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Db   672  TGAAGGGAGCACCGTGGAGAGACACAGTTGCCCCCTACAGAATGTTC  716
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RESULT 8
BC022098
LOCUS       BC022098                 919 bp    mRNA    linear   PRI 28-JAN-2002
DEFINITION  Homo sapiens, clone MGC:31944 IMAGE:4878869, mRNA, complete cds.
ACCESSION   BC022098
VERSION     BC022098.1  GI:18380971
KEYWORDS    MGC.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 40 Row: n Column: 11
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction. Similarity but not identity to protein.
FEATURES             Location/Qualifiers
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                     /note="Vector: pOTB7"
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        Miura,K. and Kurosawa,Y.
TITLE   Construction and characterization of antibody libraries: isolation
        of therapeutic human antibodies and application to functional
        genomics
JOURNAL Unpublished
REFERENCE   2  (bases 1 to 800)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT   Please visit our web site
          URL:http://www.fujita-hu.ac.jp/~immunity/.
FEATURES             Location/Qualifiers
     source          1..800
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="L48"
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                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1..800
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                     QAEDEADYYCQSYDSSLSGWVFGGGTKLTVPGQPKAAPSVTLFPPSSEELQANKATLV
                     CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQGNNKYAASSYLSLTPEQWKSHKSY
                     SCQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSDLPQPPVNAGGG"
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                     /gene="IGL"
                     /note="pelB signal peptide"
BASE COUNT    176 a    256 c    217 g    151 t
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Best Local Similarity  91.5%;   Pred. No. 1.6e-135;
Matches  603;   Conservative    0;   Mismatches   39;   Indels    3;   Gaps    1;
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Qy    66  TGTCCTGACACAGCCGCCCAGTGTCTGGGGCCCCCAGGCCAGAAGGTCACCATCTCGTG  125
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Db    72  TATACTGACTCAACCGCCCCAGTGTCTGGGGCCCCCAGGCCAGAGGGTCACCATCTCCTG  131

Qy   126  CACTGGGAGCACCTCCAACATTGG---AGGTTATGATCTACATTGGTACCAGCAGCTCCC  182
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Db   132  CACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTTCC  191

Qy   183  AGGAACAGGCCCCAAACTCCTCATCTATGACATTAACAGAGCGACCCTCAGGAATTTCTGA  242
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Qy   243  CCGATTCTCTGGCTCCAAGTCTGGTACCCGGGCCTCCCTGGCCATCACTGGGCTCCAGGAC  302
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Db   252  CCGATTCTCTGGCTCCAAGTCTGGCACCTCAGGCTCCCTGGCCATCACTGGGCTCCAGGC  311

Qy   303  TGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCAGCCTGAATGCTCAGGTATT  362
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Db   312  TGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTCAGCGGGGTGGTTGGGTGTT  371

Qy   363  CGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGTCACTCT  422
          |||  ||||| |||||| |||||||| |||||||||| ||||||||||| |||||||| |
Db   372  CGGCGGAGGGACCAAGTTGACCGTCCCAGGTCAGCCCAAGGCTGCCCCCTCCGTCACTCT  431

Qy   423  GTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTTGTGTCTCATAAG  482
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Db   432  GTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTTGTGTCTCATAAG  491
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REFERENCE   1
AUTHORS     Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
TITLE       Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 815)
AUTHORS     Kurosawa,Y.
TITLE       Direct Submission
JOURNAL     Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="L9"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1..815
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                     /protein_id="BAC01777.1"
                     /db_xref="GI:21669505"
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                     LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYS
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Left column:

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Qy   482  GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGG 541
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Db   488  GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGG 547

Qy   542  CGGGAGTGGAGACACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCT 601
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Db   548  CGGGAGTGGAGACACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCT 607

Qy   602  ACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGC 661
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Qy   662  ATGAAGGAGCACCGTGGAGAGACACAGTGGCCCCTACAGAATGTTC 707
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RESULT 10
AB064148

LOCUS   AB064148   812 bp   mRNA   linear   PRI 02-JUL-2002
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L8.
ACCESSION   AB064148
VERSION   AB064148.1 GI:21669502
KEYWORDS   .
SOURCE   Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L8.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE   Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 812)
  AUTHORS   Kurosawa,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT   Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES   Location/Qualifiers
     source   1..812
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="L8"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
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     CDS   1..>812
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                     /codon_start=1
                     /product="immunoglobulin lambda light chain VLJ region"
                     /protein_id="BAC01776.1"
                     /db_xref="GI:21669503"
                     /translation="MKYLLPTAAGLLLLAAQPAMAQSVLTQPPSVSAAPGQKVTISC
                     SGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQ
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                     LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYS
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BASE COUNT  183 a  253 c  220 g  156 t
ORIGIN

Query Match                   Score 562.8;  DB 9;  Length 812;
Best Local Similarity  79.2%;  Pred. No. 1.6e-135;
Matches  594;  Conservative  0;  Mismatches  52;  Indels  0;  Gaps  0;

Qy    62  AGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGCCCCAGGGCAGGAAGGTCACCATCT 121
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Db    68  AGTCTGTGTGACGGCAGCCCCCTCAGTGTCTGCGGCCCCAGGGCAGGAAGGTCACCATCT 127

Qy   122  CGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTCC 181
          |||| ||||||||||||||||| || ||||||||| ||||| || |||||||||||||||
Db   128  CCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGCTCC 187

Qy   182  CAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAAGGACCCCTCAGGATTTCTG 241
          |||||||||||||| |||| |||||  || || || ||| |||||||||||||| |||||
Db   188  CAGGAACAGCGCCCCAAACTCCTCATTTATGACAATAATAAGGACCCCTCAGGGATTCCTG 247

Qy   242  ACCGATTCTCTGGCTCCAAGTCTGTACCGCGCGTCAGCCACCCTGGGCATCACCGGACTCCAGA 301
          |||||||||||||| |||||||| || ||| || |||||||||||||||||||| |||||||||
Db   248  ACCGATTCTCTGGCTCCAAGTCTGGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGA 307

Qy   302  CTGAGGATGAGGCTGATTATTACTGCACAGCCTATGACAGCAGCTGAATGCTCAGGTAT 361
          |||||| |||| |||||||| || |||||||||| || || |||||| |||||||||||
Db   308  CTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGAGTGCTCGGCGTGT 367

Qy   362  TCGGAGGAGGGACCCGGCTACCGGCTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTC 421
          |||| || ||| |||||||||| |||||||||||||| ||||| |||||||||||||||||
Db   368  TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTC 427

Qy   422  TGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAA 481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428  TGTTCCCGCCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAA 487

Qy   482  GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGG 541
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Db   488  GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGG 547

Qy   542  CGGGAGTGGAGACACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCT 601
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Db   548  CGGGAGTGGAGACACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCT 607

Qy   602  ACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGC 661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   608  ACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGT 667

Qy   662  ATGAAGGAGCACCGTGGAGAGACACAGTGGCCCCTACAGAATGTTC 707
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Db   668  ATGAAGGAGCACCGTGGAGAGACACAGTGGCCCCTACAGAATGTTC 713
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RESULT 11
AB064147

LOCUS   AB064147   816 bp   mRNA   linear   PRI 02-JUL-2002
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L7.
ACCESSION   AB064147
VERSION   AB064147.1 GI:21669500
KEYWORDS   .
SOURCE   Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L7.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE   Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 816)

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Db   548  CGGGAGTGGAGACCACCACACCCTCCAAACAACAAAGCAACAACAGTACGCGGCCAGCAGCT  607
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Qy   602  ACCTGAGCCTGAGCGCTGAGCAGTGGAGTCCCACAGAGACTACAGTCGCCAGTCACGC  661
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Db   608  ATCTGAGCCTGAGCGCTGAGCAGTGGAGTCCCACAGAGAGCTACAGTCGCCAGTCACGA  667
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Qy   662  ATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC  707
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Db   668  ATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC  713
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RESULT 12
AB064219
LOCUS        AB064219               827 bp    mRNA     linear    PRI 02-JUL-2002
DEFINITION   Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
             region, partial cds, clone:L79.
ACCESSION    AB064219
VERSION      AB064219.1  GI:2169644
KEYWORDS     .
SOURCE       Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L79.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
             Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
             Miura,K. and Kurosawa,Y.
TITLE        Construction and characterization of antibody libraries: isolation
             of therapeutic human antibodies and application to functional
             genomics
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 827)
AUTHORS      Kurosawa,Y.
TITLE        Direct Submission
JOURNAL      Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
             Comprehensive Medical Science, Fujita Health University;
             Kutsukake-cho, Toyoake 470-1192, Japan
             (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT      Please visit our web site
             URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
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Qy    62  AGTCTGTCCTGACACAGCCGCCCCCCAGTGTCTGGGCCCCCAGTGTCTGGGCCCCCAGTGTCTGGGCCCCCAGTGTCACCATCT  121
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AUTHORS      Kurosawa,Y.
TITLE        Direct Submission
JOURNAL      Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
             Comprehensive Medical Science, Fujita Health University;
             Kutsukake-cho, Toyoake 470-1192, Japan
             (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT      Please visit our web site
             URL:http://www.fujita-hu.ac.jp/immunity/.
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Matches  594;  Conservative   0;  Mismatches   52;  Indels   0;  Gaps   0;

Qy    62  AGTCTGTCCTGACACAGCCGCCCTCCAGTGTCTGGGCCCCCAGTGTCTGGGCCCCCAGTGTCACCATCT  121
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Db    68  AGTCTGTGTGACGCAGCCGCCCTCCAGTGTCTGCGGCCCCAGTGTCACCATCT  127

Qy   122  CGTGCACTGGAGACACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTCC  181
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Db   128  CCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGCTCC  187

Qy   182  CAGGAACGGCGCCCCAAACTCCTCATCTATGACATTAACAACGACCCTCAGGAATTCTG  241
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Db   188  CAGGAACAGCGCCCCAAACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTG  247

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Db   248  ACCGATTCTCTGGCTCCAAGTCTGGCACGTCGGCATCAGCCACGCTGGCCATCACCGGACTCCAGA  307

Qy   302  CTGAGGATGAGGCTGATTATTACTGCAGTCCTCCTATGACAGCCTGAATGCTCAGGTAT  361
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Db   308  CTGGGGACGAGGCCGATTATTACTGCGGAACATGGGACAGTGCCTGGTGCCTGAGTGGTAT  367

Qy   362  TCGGAGGAGGACCCGGCTGACCGTCCTAGGTGACAGCTTCAGCGCAAGGTCTGCCCCTCACTC  421
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Db   368  TCGGCGGAGGACCCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTC  427

Qy   422  TGTTCCCGCCCTCTTCTGAGGAGCTTCAAGCGCCAACAAGGCCACACTGGTGTGTCTCATAA  481
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Db   428  TGTTCCCGCCCTCTTGAGGAGCTTCAAGCGCCAACAAGGCCACACTGGTGTGTCTCATAA  487

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Db         98  AGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGTAAACT  157

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Db        158  GGTACCAGCAGCTCCCAGGAACGGCGCCCCCCAAACTCCTCATCTATCGTAATAATCAGCGGC  217

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Qy        287  TCACTGGGCTCCAGACTGAGGATGAAGGCTGATTATTACTGGCAGTGATGACGACAGCC  346
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Db        338  TGAATGGTGGTATTCGGTATTCGGAGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTG  397

Qy        407  CCCCCCTCGGTCACTCGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACAC  466
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Db        398  CCCCCTCGGTCACTCGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACAC  457

Qy        467  TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGGCAGATA  526
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Db        458  TGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGGCAGATA  517

Qy        527  GCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCCCAAACAAAGCAACAACAAGT  586
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Db        518  GCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACCCCCAAACAAAGCAACAACAAGT  577
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Db         68  AGGCTGCTCACTCAGCCGTCCTCAGTGTCTGGGCCCCAGGGCAGAGGGTCACCATCT   127
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Db        128  CCTGACCGATTCTGGCTCCAAGTCGGGGCAGGTTATGATCTACATTGGTACCAGCAGC   187
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Qy        179  TCCCAGGAACGGCGCCCCCAAACTCCTCATCTATGACATTAACAAGGCGACCCTCAGGAATTT   238
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Qy        357  -GGTATTCGGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGG   415
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Db        548  TCAAGGCGGGGAGTGGAGACCACCACCCCCAAACAAAGCAACAACAAGTACGCGGCCA   607
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Qy        596  GCAGCTACCTGAGCGCCTGAGCCGTGAGCAGTGGAAGTCCCACAGAGCTCCACAGAGCTACAGCTGCCAGG   655
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Db        608  GCAGCTATCGTGGGTCCCTGAGCGCCTGAGCCGTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGG   667
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Qy        656  TCACGCATGAAGGAGCACCGTGGCCCCTACAGATGTTC   707
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LOCUS       HSIGVL027      750 bp    mRNA       linear   PRI 20-JUL-1995
DEFINITION  Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION   X57817
VERSION     X57817.1   GI:33733
KEYWORDS    Ig lambda light chain; immunoglobulin.
SOURCE      Homo sapiens
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 750)
  AUTHORS   Klobeck,H.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
            Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
            Muenchen, Schillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE   2  (bases 338 to 384)
  AUTHORS   Combriato,G. and Klobeck,H.G.
  TITLE     V lambda and J lambda-C lambda gene segments of the human
            immunoglobulin lambda light chain locus are separated by 14 kb and
            rearrange by a deletion mechanism
  JOURNAL   Eur. J. Immunol. 21 (6), 1513-1522 (1991)
   MEDLINE   91257162
   PUBMED    1904362
COMMENT     , for overlapping sequences see: X51754-55; J00252-54; M15641-42.
FEATURES             Location/Qualifiers
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Qy   647  GCTGCCAGGTCACGCATGAAGGAGGAGCACCGTGGACAGCAGTGGCCCCTACAAGTGTT 706
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DEFINITION   Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION   X57806
VERSION   X57806.1 GI:33709
KEYWORDS   Ig lambda light chain; immunoglobulin.
SOURCE   Homo sapiens
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 747)
  AUTHORS   Klobeck,H.G.
  TITLE   Direct Submission
  JOURNAL   Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
             Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
             Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE   2 (bases 335 to 381)
  AUTHORS   Combriato,G. and Klobeck,H.G.
  TITLE   V lambda and J lambda-C lambda gene segments of the human
             immunoglobulin lambda light chain locus are separated by 14 kb and
             rearrange by a deletion mechanism
  JOURNAL   Eur. J. Immunol. 21 (6), 1513-1522 (1991)
  MEDLINE   91257162
  PUBMED   1904362
COMMENT   for overlapping sequences see: X51754-55; J00252-54; M15641-42.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="22"
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                     /cell_type="B-cell"
                     /tissue_type="spleen"
                     /clone_lib="phage library cML"
     gene   1..747
                     /gene="immunoglobulin lambda light chain"
     mRNA   1..747
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     sig_peptide   <1..48
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     misc_feature   49..379
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                     /note="variable region; V(lambda)I"
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Best Local Similarity    87.8%;    Pred. No. 8.4e-135;
Matches   611;   Conservative    0;   Mismatches   85;   Indels    0;   Gaps    0;

Qy    14  CTCAGCTCCTGGGGCTCCTGCTGCTGCTCCGGCTCCCAGGTGCACGATGTGAGTCTGTCCTGA 73
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Db     2  CCCCTCTCCTCCTCCACCCTTCTCATTCACTGACGCACAGGTGCACGATGTGAGTCTGTTGA 61

Qy    74  CACAGCGCCTCAGTGTCTGGGCCCCAGGGCAGAAGTCACCATCTGTGCACTGGGA 133
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Db    62  CGCAGCCGCCGCCCAGTGTCTGCGGCCCCCAGGACAGAAGGTCACCATCTCCTGCTCTGGAA 121

Qy   134  GCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTCCCAGGAACGGCCC 193
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Db   122  GCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGCTCCCGGGAAGGGCCC 181

Qy   194  CCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCTGACGGATTCTCTG 253
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Db   182  CCAAACTCCTCATCTTTGAAATAATAAGGCGACCCTCAGCCATTTCCTGACGGATTCTCTG 241

Qy   254  GCTCCAAGTCTGGTACCCGGCGCTCCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGG 313
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Db   242  GCTCCAAGTCTGGCGACGTGCGGCATCAGCCACCCTGGGGATCGGCGGGCTCCAGACTGAGGACGAGG 301

Qy   314  CTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGCTCAGGTATTCGGAGGAGGGA 373
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Db   302  CCGATTATTATTGCGGAACATGGGACAGCAGCCTGACTGATGTGGTTTTCGGCGGAGGGA 361

Qy   374  CCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCT 433
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Db   362  CCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCT 421

Qy   434  CCTCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 493
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Db   422  CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 481

Qy   494  CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGGCCCCGTCAAGGGCGGAGTGGAGA 553
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Db   482  CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA 541

Qy   554  CCACCACACCCTCCAAAACAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGA 613
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Db   542  CCACCACCCCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGA 601

Qy   614  CGCCTGAGCAGTGGAAGTCCCACAGCTGCACGCATGAAGGGAGCA 673
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Db   602  CGCCTGAGCAGTGGAAGTCCCACAGCTGCACGCATGAAGGGAGCA 661

Qy   674  CCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTCAT 709
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Db   662  CCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTCAT 697
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RESULT 15
AB064141
LOCUS   AB064141   821 bp   mRNA   linear   PRI 02-JUL-2002
DEFINITION   Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
             region, partial cds, clone:L1.
ACCESSION   AB064141
VERSION   AB064141.1 GI:21669488
KEYWORDS   .
SOURCE   Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L1.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,

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            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
TITLE       Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 821)
AUTHORS     Kurosawa,Y.
TITLE       Direct Submission
JOURNAL     Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
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                     peripheral blood and bone marrow"
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ORIGIN

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Best Local Similarity 91.5%;  Pred. No. 2.8e-134;
Matches 591;  Conservative 0;  Mismatches 55;  Indels 0;  Gaps 0;

Qy    62 AGTCTGTTCCTGACACAGCCCGCCCTCAGTGTCTGGGGCCCCAGGGCCAGAAGGTCACCATCT 121
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Db    68 AGTCTGTTGACGCAGCCGCCCTCCAGTGTCTGCGGCCCCAGGACAGAAGGTCACCGTCT 127

Qy   122 CGTGCACTGGGAGCACCTCCAACAACTCCAACATTGGAGTTATGATCTACATTGGTACCAGCAGCTCC 181
         ||||||||||| |||||||||||||||||| ||||||||||||||||| |||||||||||||||||||
Db   128 CCTGCACTGGAAGCAACTCCAACATTGAGAAGAATGATGTTTCCTGGTACCAGCAGGGAC 187

Qy   182 CAGGAACGAGCGCCCCCAAACTCCTCATCTATGACATTAACAGGCGACCCTCAGGAATTTCTG 241
         ||||| || ||||||||| ||||||||||||||||| || || |||||| ||||||| ||||
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Qy   242 ACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGGCTCCCTGGCCATCACTGGGCTCCAGA 301
         ||||||||||||||||||||| |||||||||| ||||||| ||||||| |||||||||| |
Db   248 ACCGATTCTCTGGCTCCAAGTCTCGGCACGTCAGCCACCCTGGCCATCGCTGGGCTCCAGG 307

Qy   302 CTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCGAGCCTGAATGCTCAGGTAT 361
         ||||||||||||||||||||||||||||||| ||| ||| ||||| |||| |||||| | |
Db   308 CTGAGGATGAGGCTGATTATTACTGCCAGTCCCATGACACCACACTCTGAGTGGTCCGATCT 367

Qy   362 TCGGGAGGAGGGACCCCGCTGACCGTGCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTC 421
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Db   368 TCGGCGGGGGGACCCAGCTGACCGTGCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTC 427

Qy   422 TGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAAGGCCACACTGGTGTGTCTCATAA 481
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Db   428 TGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAAGGCCACACTGGTGTGTCTCATAA 487
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          GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April 5, 2003, 19:13:54 ; Search time 1341.86 Seconds
                                     (without alignments)
                                     8508.978 Million cell updates/sec

Title:          US-09-758-173-1
Perfect score:  705
Sequence:       1 ATGAGGGTCCCCGGTCAGCT.........CCCCTACAGAATGTTCATGA 705

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:  32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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           26:  em_gss_pro:*
           27:  em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		558.8	79.3	952	14	BQ711447	BQ711447 AGENCOURT
2		555.6	78.8	931	14	BQ709526	BQ709526 AGENCOURT
3		555.2	78.8	931	14	BQ711683	BQ711683 AGENCOURT
4		552	78.3	796	12	BG757730	BG757730 602714835
5		552	78.3	969	14	BQ707953	BQ707953 AGENCOURT
6		551.2	78.2	921	14	BQ708246	BQ708246 AGENCOURT
7		548.8	77.8	920	14	BQ712280	BQ712280 AGENCOURT
8		547.2	77.6	925	14	BQ710672	BQ710672 AGENCOURT
9	c	546	77.4	832	12	BG746204	BG746204 602723726
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11		545.6	77.4	754	13	BI907909	BI907909 603069019
12		545.2	77.3	924	12	BG756256	BG756256 602713568
13		545	77.3	1086	14	BM924274	BM924274 AGENCOURT
14		544.4	77.2	917	14	BQ711587	BQ711587 AGENCOURT
15		542.4	76.9	949	14	BQ709509	BQ709509 AGENCOURT
16		541.6	76.8	1018	14	BM914338	BM914338 AGENCOURT
17		540.8	76.7	947	14	BQ709579	BQ709579 AGENCOURT
18		540.4	76.7	789	13	BI765865	BI765865 603046058
19		537	76.2	742	13	BI906298	BI906298 603063246
20		533.6	75.7	874	13	BG755301	BG755301 602714044
21		531	75.3	837	13	BG754193	BG754193 602709741
22		530.2	75.2	731	10	AV649126	AV649126 AV649126
23		529	75.0	803	12	BG758687	BG758687 602712935
24		528	74.9	862	12	BF338816	BF338816 602036250
25		527.4	74.8	842	12	BG686249	BG686249 602638157
26		525.6	74.6	788	13	BM007725	BM007725 603617172
27		525	74.5	1010	14	BM914307	BM914307 AGENCOURT
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29		520.2	73.8	871	12	BF398521	BF398521 602439614
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31		516.6	73.3	883	13	BI760703	BI760703 603044891
32	c	515.2	73.1	926	13	BI911261	BI911261 603062819
33		513.8	72.9	868	12	BG745881	BG745881 602724051
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35		512.6	72.7	864	12	BG756128	BG756128 602713428
36		508.4	72.1	782	13	BM007626	BM007626 603617044
37		508.2	72.1	801	13	BG754011	BG754011 602709539
38		508	72.1	829	12	BG745481	BG745481 602724051
39	c	501.8	71.2	688	12	BQ576097	BQ576097 UI-H-E21-
40		499.8	70.9	722	14	BQ757059	BQ757059 602710483
41		499	70.8	872	12	BI517885	BI517885 603041960
42		498.8	70.8	880	13	BF975632	BF975632 602246092
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ALIGNMENTS

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DEFINITION  AGENCOURT_8353624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279618
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ACCESSION   BQ711447
VERSION     BQ711447.1  GI:21850346
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 952)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469 row: h  column: 19
            High quality sequence stop: 584.
FEATURES             Location/Qualifiers
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SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 931)
AUTHORS   NIH-MGC http://mgc.ncci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474 row: 1 column: 21
            High quality sequence stop: 653.
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT   227 a   284 c   245 g   174 t   1 others
ORIGIN

Query Match   78.8%;   Score 555.6; DB 14; Length 931;
Best Local Similarity 89.3%;   Pred. No. 3.1e-133;
Matches 623; Conservative   0; Mismatches 69; Indels 6; Gaps 2;

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Qy   71 TGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGAGACAGCGGCCAGGATCACCTGTGGGG 130
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Db   94 TGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGAGACAGCGGCCAACATTACCTGTGTG 153

Qy   131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGCGGGCCCCTA 190
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Db   154 GAAACAATATTGGAAGTAAAAGTGTGCACTGGTACCAGCAGAGGCCAGGCCAGGCCCCTG 213

Qy   191 TACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250
          ||| ||| || |||||||| || ||||| ||| ||| || ||||| || |||||||||
Db   214 TGCTGGTCGTCAATGATGACAGCGACCGGCCCCGCAGGGATCCCTGAGCGATTCTCTGGCT 273

Qy   251 CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGAGGCCCGGGGATGAGGCTG 310
          |||||||||||| ||| || || |||||||||||||||||||||||| || ||||||||
Db   274 CCAACTCTGGAAACACGGCCACCCTGACCATCGACCGACCGGGGATGAGGCTG 333

Qy   311 ACTATTACTGTCAGGTGTGGGACACGGCTAGTGATCATC---CGGTCTTCGGAGGAGGGA 367
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Db   334 ACTATTACTGTCAGGTGTGGGATACTAGTATTGATCATCATGGTGTTTTCGGCGGAGGGA 393

Qy   368 CCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCCTGTTCCCGCCCT 427
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Qy   428 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 487
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RESULT 2
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DEFINITION AGENCOURT_8443486 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281636
            5', mRNA sequence.
ACCESSION   BQ709526
VERSION   BQ709526.1 GI:21848425
KEYWORDS   EST.

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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT   241 a   282 c   254 g   173 t   2 others
ORIGIN

Query Match   79.3%;   Score 558.8; DB 14; Length 952;
Best Local Similarity 91.9%;   Pred. No. 4.6e-134;
Matches 590; Conservative   0; Mismatches 52; Indels 0; Gaps 0;

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Qy   122 CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC 181
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Qy   182 GGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 241
          ||| |||||||| ||||| || ||||| || |||||||||||||||||||||||||||||
Db   143 AGGCCCCTGTGGTGGTCATGTTTATGATAGGGACCGGCCCTCAGGGATCCCTGAGCGAT 202

Qy   242 TCTCTGGCTCCAAATCAGGGAACACGCCACCCTGACCATCAACAGCAGGGGTCGAGGCCGGGG 301
          |||||||||||||||||| |||||||||||||||||||||| || || ||| |||||||||
Db   203 TCTCTGGCTCCAACTCTGGGAATACGGCCACCCTGACCATCAGCAGGGTCGAGGCCGGGG 262

Qy   302 ATGAGGCTGACTATTACTGTCAGGTGTGGGACACGGCTAGTGATCATCCGGTCTTCGGAG 361
          ||||||||||||||||||||||||||||||| || | |||| | | |||| |||||||
Db   263 ATGAGGCCGACTATTACTGTCACGTGTGGGACAATACTATTGATCACGTGGTATTCGGCG 322

Qy   362 GAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCC 421
          |||||||||| |||||||||||||||||||||||||||| |||||| || ||||||||
Db   323 GAGGGACCAAGCTGACCGTCCTCGGTCAGCCCAAGGCTGCCCCCTCCCTCGGTCACTCGTTCC 382

Qy   422 CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   383 CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 442

Qy   482 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 541
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Db   443 TCTACCCGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 502

Qy   542 TGGAGACCACCACACCCTCCAAACAAGCAACAACAAGCACGGCGGCCAGCGAGCTACCTGA 601
          |||||||||||||||||||||||| || ||||| |||||||| ||||| ||||| |||
Db   503 TGGAGACCACCACACCCTCCAAACAAGCAACAACAAGCACGGCGGCCAGCGAGCTATCCTGA 562

Qy   602 GCCTGAGCGGTGGAAGTCCCACAGAGAGCTACAGCGTGCCACAGTCACGCATGAAG 661
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Db   563 GCCTGAGCAGTGGAAGTCCCACAGAGAGCTACAGCGTGCCACAGTCACGCATGAAG 622

Qy   662 GGAGCACCGTGGAGAAGACAGTGGCCCTACAGAATGTTCAT 703
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Qy  488  CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA  547
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Db  514  CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA  573

Qy  548  CCACCACCCCTCCAAACAAAGCAACAACAACAGTACGGGCCAGCAGCTACCTGAGCCTGA  607
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Qy  608  CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAGGGAGCA  667
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Db  634  CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAGGGAGCA  693

Qy  668  CCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA  705
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Qy  131  GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCCGGCCCCCTA  190
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Db  156  GAAATAAGATTGGAAGTAAAAGTGTGCACTGGTTCCAGCAGAAGCCCAGCCAGGCCCCTG  215

Qy  191  TACTGTGTCATCTATGATAGTGACCGGCCCTCAGGGATTCCTCAGGATTCCTCGGGGCT  250
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Db  216  TCCTGTCGTCTCTGATGATCGGACCGGCCCTCAGGGATCCCTGAGGGATCCCTGGGGCT  275

Qy  251  CCAAATCAGGGAACACCGGCCACCCTGACCATCAACGGGGTCGAGCCGCGGGATGAGGCTG  310
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Qy  311  ACTATTACTGTCAGTGTGGGACAGGCTAGTGATCATCC---GGTCTTCGGAGGAGGGA  367
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Db  336  ACTATTACTGTCAGTGTGGGATTTCAGTAGTAGTATTCCTGTTATTATCCTGTGGTATTCGGCGGAGGGA  395

Qy  368  CCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGTCTCCGCCCT  427
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Qy  428  CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC  487
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Db  456  CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC  515

Qy  488  CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA  547
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Db  516  CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA  575

Qy  548  CCACCACCCCTCCAAACAAAGCAACAACAACAGTACGCGGCCAGCAGCTACCTGAGCCTGA  607
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Db  576  CCACCACCCCTCCAAACAAAGCAACAACAACAGTACGCGGCCAGCAGCTATCTGAGCCTGA  635

Qy  608  CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAGGGGAGCA  667
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Qy  668  CCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  703
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Db  696  CCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  731
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RESULT 4
BG757730
LOCUS   BG757730   796 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602714835F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854921 5',
            mRNA sequence.
ACCESSION   BG757730
VERSION   BG757730.1 GI:14068383
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 796)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D.; Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1703 row: f   column: 10
            High quality sequence stop: 795.
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"

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ACCESSION   BQ707953
VERSION     BQ707953.1  GI:21846852
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 969)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/,
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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            High quality sequence stop: 541.
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT    226 a    309 c    251 g    174 t      9 others
ORIGIN
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Query Match        78.3%;  Score 552;  DB 14;  Length 969;
Best Local Similarity  89.1%;  Pred. No. 2.6e-132;
Matches  620;  Conservative  0;  Mismatches 70;  Indels  70;  Gaps  6;   2;

Qy      11  CCGCTCAGCTCCTGGGGCTCCTGCTCTCTGGCTCCCAGGTGCACGATGTGCCTATGAAC   70
            ||| ||  || || ||  ||||||||||||| |                 | || ||
Db      28  CCGTTCCTCCTCCGCCTCCTCTCTCACTG---CACAGGCTCTGTGACCTCCTATGTCC    84

Qy      71  TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGTGGGG  130
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Db      85  TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGTATTTCCTGTGGGG  144

Qy     131  GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGCGGGCCCCTA  190
            || |||  |  | || | ||| ||| |||||||||||||||||||||||| | ||||||
Db     145  GAAACACCACTGCAAGTAAAAGTGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCCTG  204

Qy     191  TACTGGTCATCTATGATGATAGTAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTGGCT  250
            | |||||| || |||||||| |  |  ||||||||    ||||||||||||||||||||||
Db     205  TGCTGGTCGTCGTCATGATGATAACGACCGGCCCCCCGGGATCCCTGAGCGATTCTGGCT  264

Qy     251  CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGGGGCCGGGATGAGGCTG   310
            ||||  | |||||||||| ||||||||||||||   ||||||  ||||||||||||| |
Db     265  CCAATTCTGGGAACACCGGCCACCCTGACCATCAGTAGGGTCGAAGCCGGGATGAGGCCG  324

Qy     311  ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATC--ATCCGGTCTTCGGAGGAGGGA   367
            ||||||||||||||||||||||| | |  | |||||     |  |  | | | | || |
Db     325  ACTATTACTGTCAGGTGTGGGATGATGATAGTAGTGATCAGAATGTGTATTCGGCGGAGGGA  384

Qy     368  CCGGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTGCACTCTGTTCCCGCCCT   427
            ||   ||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     385  CCAAGCTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCTGCACTCTGTTCCCGCCCT  444
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                     /clone_lib="NIH_MGC 48"
                     /tissue_type="Primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT    177 a    244 c    231 g    143 t      1 others
ORIGIN
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Query Match        78.3%;  Score 552;  DB 12;  Length 796;
Best Local Similarity  89.2%;  Pred. No. 2.5e-132;
Matches  618;  Conservative  0;  Mismatches 71;  Indels  4;  Gaps  2;

Qy      11  CCGCTCAGCTCCTGGGGCTCCTGCTCTCTGGCTCCCAGGTGCACGATGTGCCTATGAAC   70
            ||| ||  || || ||  |||||||||||||| |                | || |||
Db      39  CCGTTCCTCCTCCGCCTCCTCTCTCACTG---CACAGGCTCTGTGACCTCCTATGTGC    95

Qy      71  TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGTGGGG  130
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db      96  TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATTACCTGTGGGG  155

Qy     131  GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGCGGGCCCCTA  190
            || |  ||  || || | |  ||| |||||||| ||||||||||||||| | ||||||
Db     156  GAAATAACATTGAAAGTAAAACATGTGCACTGGTATCAGCAGAAGCCAGGCCAGGCCCCTG  215

Qy     191  TACTGGTCATCTATGATGATAGTAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTGGCT  250
            | ||||||||| | ||||||| |  ||||||||||||||||||||||| ||  |||||||
Db     216  TGCTGGTCATCAATTATGATAGCGACCGGCCCTCAGGGATCCCTGCGCGGTTCTGGCG    275

Qy     251  CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGGGGCCGGGATGAGGCTG   310
            ||||  | |||||||||||||||||||||||||   |||||||||||||||||||| |
Db     276  CCAACTCTGGGAACACCGCCACCCTGACCATCAGCACACGGGTCGGGGCCGGGATGAGGCCG  335

Qy     311  ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGAGGGACCC  370
            ||||||||||||||||||||||| | |    | |||||| |  || | | | || || ||
Db     336  ACTATTACTGTCAGGTGTGGGATAGTAGTTAGCGATCATCATCGGGTGTTTGGCGGCGGGACCA 395

Qy     371  GGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTGCCCCCCTCCT   430
            | ||||||||||||||||||||||||||||||||||||  ||| ||||
Db     396  AGTTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTGC GTCCCCGCCCTCCT  455

Qy     431  CTGAGGAGCTTCAAGCAACAAGGCCACAACAGGCTGTGTCTCATAAGTGACTTCTACCCGG  490
            |||||||||||||||| |||||||||||     |||||||||||||||||||||||||||||
Db     456  CTGAGGAGCTTCAAGCCAACAAGGCCACA    GTGTCTCATAAGTGACTTCTACCCGG     515

Qy     491  GAGCCGTGACAGTGGCGGCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGAGTGGACCA  550
            |||||||||||||||||||||||||||||||||||||||||||||||  ||||||| |||
Db     516  GAGCCGTGACAGTGGCGGCTGGAAGGCAGATAGCAGCCCCGTCAAGGGGGAGTGGGACCA  575

Qy     551  CCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCTACCTGACGCTGACGC    610
            || |||||||||||||||||||||||||||||||| ||| |||||||||| ||||||
Db     576  CCNAACCCTCCAAACAAAGCAACAACAAGTACGCGG-CAGCAGCTACCTGAGCCTGACGC   634

Qy     611  CTGAGGAGCTTCAAGCCAACAAGGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCG  670
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Db     635  CTGAGGAGCTTCAAGCCAACAAGGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCG  694

Qy     671  TGGAGAAGACAGTGGCCCCTACAGAATGTTCAT   703
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Db     695  TGGAGAAGACAGTGGCCCCTACAGAATGTTCAT   727
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RESULT 5
BQ707953
LOCUS       BQ707953    969 bp    mRNA    linear    EST    16-JUL-2002
DEFINITION  AGENCOURT_8353606 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279593
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5', mRNA sequence.

Qy 428 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 487
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Db 445 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 504

Qy 488 CGGGAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGAGTGGAGA 547
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 505 CGGGAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGAGTGGAGA 564

Qy 548 CCACCACACCCTCCAAACAAAGCAACAACAACAAGTACGGGCCAGCAGTACCTGAGCCTGA 607
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Db 565 CCACCACACCCTCCAAACAAAGCAACAACAACAAGTACGGGCCAGCAGTATCTGAGCCTGA 624

Qy 608 CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAGGGAGCA 667
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Db 625 CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAGGGAGCA 684

Qy 668 CCGTGGAAGAAGACAGTGCCCCCTACAGAATGTTCAT 703
        |||||||||||||||||||||||||||||||||||||
Db 685 CCGTGGAAGAAGACAGTGCCCCCTACAGAATGTTCAT 720

RESULT 6
BQ708246
LOCUS   BQ708246   921 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8495393 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301917
            5', mRNA sequence.
ACCESSION   BQ708246
VERSION   BQ708246.1 GI:21847145
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 921)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2518 row: i column: 22
            High quality sequence stop: 628.
FEATURES   Location/Qualifiers
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            /db_xref="taxon:9606"
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            /clone_lib="NIH_MGC_113"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
BASE COUNT 235 a   273 c   252 g   161 t
ORIGIN

Query Match   78.2%; Score 551.2; DB 14; Length 921;
Best Local Similarity   92.1%; Pred. No. 4.2e-132;
Matches 604; Conservative   0; Mismatches 48; Indels   4; Gaps   2;

Qy 52 GCACGATGTGCCTATGAACTGACTCAGCCACCCTCCGTGTCAGTGTCCCCAGGACAGACG 111
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Db   3 GCACGAGGCTCCTATGTGCTGACTCAGCCACCACCGCCACCCTCCGTGTCAGTGCCCCAGGAGCAGACG 62

Qy 112 GCCAGGATCACCT-GTGGGGAGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCA 170
        ||||| ||| |||| ||||||| || | ||||| || | |||| ||||||||||||||
Db   63 GCCAGCATTACCTGGTGGGGAAACACATTACAGTGTGCACTGGTACCAGCA 122

Qy 171 GAAGCCAGGCCAGGCCCCTATACTGGTCATCTATGATGATAGTGATAGTGACGGCCCTCAGGGAT 230
        |||| |||||||||||||| | ||| ||| ||||||| |||||||||| |||||||||||
Db   123 GAAGTCAGGGCCAGGCCCCTGTCGTCGTCTGTGATGATGATGATGACCCGGCCCTCAGGAAT 182

Qy 231 CCCTGAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGT 290
        |||||||||||||||||||||||| || ||||||||||||||||||||||||| |||||
Db   183 CCCTGAGCGATTCTCTGGCTCCAACTCTGGAACACCGCCACCCTGACCATCAGCAGGGT 242

Qy 291 CGAGGCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCC 350
        ||| |||||||||||||| ||||||||||||||||||||||| | | |||| ||||||
Db   243 CGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATACTACTGATGATCATCC 302

Qy 351 --GGTCTTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGGCTTCAGCCCAAGGCTGCCCCCTC 407
          |||| ||||| ||||||||| | || |||||||||| |||||| |||| |||||||||||||||
Db   303 TGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAAGTCAGGCTCCTAAGTCAGCCCAAGGCTGCCCCCTC 362

Qy 408 GGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTG 467
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 GGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTG 422

Qy 468 TCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCC 527
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 TCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCC 482

Qy 528 CGTCAAGGCGGGAGTGGAGACAACAACAAGCAACAACAAGTACGGGC 587
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Db   483 CGTCAAGGCGGGAGTGGAGACAACAACAAGCAACAACAAGTACGGGC 542

Qy 588 CAGCAGTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCA 647
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Db   543 CAGCAGTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCA 602

Qy 648 GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
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Db   603 GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 658

RESULT 7
BQ712280
LOCUS   BQ712280   920 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8353529 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279636
            5', mRNA sequence.
ACCESSION   BQ712280
VERSION   BQ712280.1 GI:21851179
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 920)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469 row: i column: 13
            High quality sequence stop: 698.
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"

VERSION   BQ710672.1 GI:21849571
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 925)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2516 row: e   column: 10
            High quality sequence stop: 661.
FEATURES   Location/Qualifiers
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                     /clone="IMAGE:6301041"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   214 a   293 c   239 g   170 t   9 others
ORIGIN

Query Match   77.6%; Score 547.2; DB 14; Length 925;
Best Local Similarity 88.6%; Pred. No. 4.6e-131;
Matches 617; Conservative 0; Mismatches 73; Indels 6; Gaps 2;

Qy   11 CCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCCAGGTGCACGATGTGCCTATGAAC   70
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Db   38 CCGTTCTCCTCCTCGGCCTCCTCCTCTCACTG---CACAGGCTCTGTGACCTCCTATGTGC   94

Qy   71 TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGTGGGG 130
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Db   95 TGACTCAGCCACCCTCGGTGTCAGTGCCCCCAGGACAGACAGACGGCCAGGATTCTCTGGGG 154

Qy   131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCACCACGGCGCGGGCCCCTA 190
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Db   155 GAAACAATATTGGAAGTAGAGTGTGCACTGGTACCAGCAGCACTTCAGGCCAGGCCCCTG 214

Qy   191 TACTGGTCATCTATGATGATGATGAGTAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250
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Db   215 TGCTGGTCGTCTATGATGATGATGAGCGACCGGCCCTCGGGGATCCCTGAGCGATTCTCTGGCT 274

Qy   251 CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGGGGATGAGGAGGCG 310
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Db   275 CCAACTCTGGGAACACACGCCACCCTGATCATCAGCAGTGTCGAAGCGGGGATGAGGAGGCCG 334

Qy   311 ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGTGATCATCCG---GGTCTTCGGAGGAGGGA 367
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Db   335 CCTATTACTGTCAGGTGTGGGCATAGTGTGGTGTACTCATCCTGTACTTATTCGGCGGAGGGA 394

Qy   368 CCCGGGTGACCTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGGTCACTCTGTTCCCGCCCT 427
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Db   395 CCAAGCTGACCGGTCCTAAGTCAAGCCCAAGGCTGCCCCCTCCGGTCACTCTGTTCCCGCCCT 454

Qy   428 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCATAAGTGACTTCTACC 487
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RESULT 8
BQ710672
LOCUS   BQ710672   925 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8484950 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301041
            5', mRNA sequence.
ACCESSION   BQ710672

Qy   216 a   281 c   246 g   176 t   1 others
BASE COUNT
ORIGIN

Query Match   77.8%; Score 548.8; DB 14; Length 920;
Best Local Similarity 88.8%; Pred. No. 1.8e-131;
Matches 618; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

Qy   11 CCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCCAGGTGCACGATGTGCCTATGAAC   70
          ||||||| ||||| ||||| || ||||| ||||| |||||| || ||||||||||
Db   37 CCGTTCTCCTCCTCGGCCTCCTCCTCTCACTG---CACAGGCTCTGTGACCTCCTATGTGC   93

Qy   71 TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGTGGGG 130
          ||||||||||||| |||||||| |||||||||||||| || ||||||||||||||||||
Db   94 TGTCAGACCACCCTCGGTGTCAGTGCCCCCAGGACAGACAGACGGCCAGGATTCTCTGGGG 153

Qy   131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCACCACGGCGCGGGCCCCTA 190
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Db   154 GAAACAACACCCTTGGAAGAAAAAGTGTTCACTGGTACCAGCAGCACGCGCCAGGCCCCTC 213

Qy   191 TACTGGTCATCTATGATGATGATGAGTAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250
          |||| ||||||||||||||||||| || |||| ||||||||||||||||||||||||||||||||
Db   214 TGGTGGTCGTCTATGATGATGACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 273

Qy   251 CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGGGGATGAGGAGGCTG 310
          |||||||||||||||||||||||||| ||||||||||||| |||||||||||||||
Db   274 CCAACTCTGGGAACACACGGCCACCCTGACCATCAGCAGTGTCGAGGCGGGGATGAGGAGGCTG 310

Qy   311 ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGTGATCATCC---GGTCTTCGGAGGAGGGA 367
          ||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||
Db   334 ACTATTACTGTCAGGTGTGGGATACTAGTGTTGATACGGTTCTGTGGTTTTCGGTGGAGGGA 393

Qy   368 CCCGGGTGACCTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGGTCACTCTGTTCCCGCCCT 427
          ||||||| |||||||| |||||||||||||||| ||||||||||||||||||||||||||
Db   394 CCAAGCTGACCGGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCCGGTCACTCTGTTCCCGCCCCT 453

Qy   428 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCATAAGTGACTTCTACC 487
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Db   454 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 513

Qy   488 CGGGAGCCCGTGACAGTGCCTGGAAGGCAGATAGCAGCGCCCGTCAAGGCGGGAGTGAGA 547
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Db   514 CGGGAGCCCGTGACAGTGCCTGGAAGGCAGATAGCAGCGCCCGTCAAGGCGGGAGTGAGA 573

Qy   548 CCACCACCCTCCAAACAAGCACAACAAGTACGGCGGCCAGCAGCTACCTGAGCCTGA 607
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 CCACCACCCTCCAAACAAGCACAACAAGTACGGCGGCCAGCAGCTATCTGAGCCTGA 633

Qy   608 CGCCTGAGCAGTGAAGTCCCACAGAAGTCACAGCTGCCAGGTCACGGGGAAGGAGGCA 667
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   634 CGCCTGAGCAGTGGAAGTCCCACAGAAGTCACAGCTGCCAGGTCACGGGGATGAAGGAGGCA 693

Qy   668 CCGTTGGGAGAGACAGTGGCCCCTTACAGAATGTTCAT 703
          |||| |||||||| |||||||||||||||||||||||
Db   694 CCGTTGGGAGAAAACAGTGGCCCCCTTACAGAATGTTCAT 729

Db   455 CCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGTGTGTCTCATAAGTGACTTCTACC 514
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Qy   488 CGGGAGCCGTGCAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA 547

Db   515 CGGGAGCCGTGCAGTGGCCTGGAAGGCAGAGATAGCAGCCCCCGTCAAGGCGGGAGTGGAGA 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   548 CCACCACACCCTCCAAACAAGCAACACAAGTAACCGGCCGCAGCGCTACCTGAGCCTGA 607

Db   575 CCACCACACCCTCCAAACAAGCAACACAAGTAACCGGCCGCAGCGCTACCTGAGCCTGA 634
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Qy   608 CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTGCACCGCATGAAGGGAGCA 667

Db   635 CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTGCACCGCATGAAAGGAGCA 694
          ||||||||||||||||||||||||||||||||||||||||||||||| |||| |||||||
Qy   668 CCGTGGAGAAGACAGTGGCCCCTCCTACAGAATGGTCAT 703
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Db   695 CCGCTGAGCAGTGGAAGACAGTGGCCCCTACCTACAGAATGGTCAT 730

RESULT 9
BG746204/c
LOCUS   BG746204   832 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602732726T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4849878 3',
            mRNA sequence.
ACCESSION   BG746204
VERSION   BG746204.1 GI:14056857
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 832)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1690 row: d column: 07
            High quality sequence stop: 827.
FEATURES   Location/Qualifiers
     source   1..832
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   152 a   232 c   263 g   185 t
ORIGIN

Query Match   77.4%; Score 546; DB 12; Length 832;
Best Local Similarity 92.4%; Pred. No. 9.1e-131;
Matches 597; Conservative 0; Mismatches 45; Indels 4; Gaps 2;

Qy   62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGAC-GGCCAGGATC 120
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Db   739 CCAATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGCGGCCAGGATT 680

Qy   121 ACCTGTGGGGGAGCAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180

Db   679 ACCTGTGGGGGTCCCAACATTGGAACATTACAGTGTGCACTGTGCTACCAGCAGAAGTGAGGC 620
          ||||||||||| ||| ||||
Qy   181 CGGGCCCTATACTGGTCATCTATGATGATGATGAGTAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240

Db   619 CAGGCCCCTGTGGTCGTCTCATGATGATGATAGCGACCGGCCCCTCAGGGATCCCTGAGCGA 560
          ||||||||||||||||||||||||
Qy   241 TTTCTGGCTCCAAATCAGGAACACACCCGCACCTGACCATCAACGGGGTCGAGGGCCGGG 300

Db   559 TTTCTGGCTCCAACTCTGGAACACACGCCCACCTGACCATCAGCAGCAGGGTCGAAGCCGGGG 500
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Qy   301 GATGAGGCTGACTATTACTGTCAGGTGGGACAGGGCTAGTGATCATCCGGT---CTTC 357

Db   499 GATGAGGCCGACTATTACTGTCAGGTGTCGATGGTGGTAGTGATCATCCTGTGCAATTC 440
          |||||||||||||||| |
Qy   358 GGAGGAGGGACCCCGGTGACCGTCCTAGGTCAGCCCCAAGGGTGCCCCCTGCTCACTCTG 417

Db   439 GGCGGAGGGGACCAAACTGACCGTCTTAGGTCAGCCCCAAGGGCTGCCCCCTGCCCCCGTCACTCTG 380
          ||| |||| |||| | |||||||

Qy   418 TTCCGCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGTGTGTCTCATAAGT 477
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Db   379 TTCCGCCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGT 320

Qy   478 GACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCG 537
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Db   319 GACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCG 260

Qy   538 GGAGTGGAGACCACCACACCCTCCAAACAAGCAACACAACAAGTACGCGGCCAGCAGCTAC 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   259 GGAGTGGAGACCACCACCACCCTCCAAACAAAGCAACACAACAAGTACGCGGCCAGCAGCTAT 200

Qy   598 CTGAGCCTGACGCGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCAT 657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199 CTGAGCCTGACGCGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTACAGCTGCCAGTGCACGCAT 140

Qy   658 GAAGGGAGCACCGTGGAGAGAGACAGTGGCCCCTACAGAATGTTCAT 703
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Db   139 GAAGGGAGCACCGTGGAGAGAGACAGTGGCCCCTACAGAATGTTCAT 94

RESULT 10
BQ084067
LOCUS   BQ084067   908 bp   mRNA   linear   EST 16-AUG-2002
DEFINITION AGENCOURT_8616484 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302471
            5', mRNA sequence.
ACCESSION   BQ084067
VERSION   BQ084067.1 GI:22276075
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 908)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2519 row: p column: 24
            High quality sequence stop: 687.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6302471"
                     /clone_lib="NIH_MGC_113"

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          /lab_host="DH10B (phage-resistant)"
          /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
          EcoRI; cDNA made by oligo-dT priming. Directionally cloned
          into EcoRI/XhoI sites using the following 5' adaptor:
          GGCACGAG(G). Library constructed by Ling Hong in the
          laboratory of Gerald M. Rubin (University of California,
          Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
          Superscript II RT (Life Technologies). Note: this is a
          NIH MGC Library."
BASE COUNT       205 a      277 c      231 g      167 t       28 others
ORIGIN

Query Match             77.4%;  Score 545.8;  DB 14;  Length 908;
  Best Local Similarity   91.5%;  Pred. No. 1e-130;
  Matches  590;  Conservative    0;  Mismatches   52;  Indels    3;  Gaps    1;

Qy         62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGAGACCGGCCAGGATCA 121
              ||||| || ||||| |||||||||||||||||||| |||||||||||| | |||||||| |
Db         72 CCCATGTTCTGACCAGTCACCCCTCGGGTGTCAGTGGCCCCAGGACAGACACGGCCAGGATAA 131

Qy        122 CCTGTGGGGGAGACAACAGCACTAGAAATGAATATGTCACTGTTGCACGCAGAAGCCAGCGC 181
              ||||||||||| |  || | ||| |||||| ||||| |  ||| |||| |||||||||||| |
Db        132 CCTGTGGGGGAAGCAGCATTGGAAGTCAAAGTGTGCACTGTGCACCAGCAGAAGCCAGGGCC 191

Qy        182 GGGCCCTATACTGGTCATCTATGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 241
              ||||||| |||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        192 AGGCCCCTGTGTTGGTCGTCTATAATGATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGAT 251

Qy        242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGAGGCCGGGG 301
              |||||||||||  |||||| |||||||||||||| |||||||||||||||||||||||||
Db        252 TCTCTGGCTCCAACTCTCGGGGACACGGCCACCCTGTCATCAGCAGGGTCGAAGCCGACG 311

Qy        302 ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATC---CGGTTCTCG 358
              ||||||||||||||| || ||||||||||||  ||| ||||||||||||   |||| |||
Db        312 ATGAGGCCGACTATTACTGTCAGGTGTGGGATATCGATAATGGTCATCTAGTAGTGGTATTCG 371

Qy        359 GAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGTCACTCGT 418
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Db        372 GCGGAGGGACCCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGT 431

Qy        419 TCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATAAGTG 478
              ||||| |||||||||||||||||||||||||||||||||| |||||||||||||||
Db        432 TCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATAAGTG 491

Qy        479 ACTTCTACCCGGGAGCCGTGACAGTGGCCTGCTGGAAGGCAGATAGCAGCCGCGGTACC 538
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Db        492 ACTTCTACCCGGGAGCCGTGACAGTGGCGGAGGCAGATAGCAGCCGCGCGTCAAGGCGG 551

Qy        539 GAGTGGAGACCACCACCACCCCTCAAACAAAGCAACAACACAGGTACGCGGCCAGCTACC 598
              |||||||||||||||||||||||||  |||||  ||||  |||||||||||||||| |||
Db        552 GAGTGGAGACCACCACCACCCCTCCAACAAAGACAACAACAAATACGGCCGCCAGCTATC 611

Qy        599 TGAGCCTGACGCCTGAGCAGTGAAGTCCCACAGAGTCACAGCTGCACGCATG 658
              ||||||||| |||||||||||||||||||||||||||||||||| |||||||
Db        612 TGAGCCTGACGCCTGAGCAGTGAAGTCCCACAGAGTCACAGCTGCTCACGCATG 671

Qy        659 AAGGGAGCACCGTGGAGAAGAAAGACAGTGGCCCCTACACAGAATGTTCAT 703
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RESULT 11
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LOCUS       BI907909                754 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  6030609019F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217796 5',
            mRNA sequence.
ACCESSION   BI907909
VERSION     BI907909.1  GI:16170804
KEYWORDS    EST.
SOURCE   .  human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1547 row: f column: 05
            High quality sequence stop: 749.

FEATURES             Location/Qualifiers
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                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated adult donors. Library is oligo-dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 027. Note:
                     this is a NIH MGC Library."

BASE COUNT       167 a      239 c      210 g      138 t
ORIGIN

Query Match             77.4%;  Score 545.6;  DB 13;  Length 754;
  Best Local Similarity   89.4%;  Pred. No. 1.1e-130;
  Matches  622;  Conservative    0;  Mismatches   69;  Indels    5;  Gaps    3;

Qy         10 CCCGCTCAGCTCCTGGGCTCCTGCTCCTGTCCCTGTGCTCCAGGTGCACGATGTGCCTATGAA 69
              |||| || ||||| || |||||| ||||| |   |||| ||      || | |||| |||||
Db         38 CCCGTTCTCCTCCTCCGCCTCCTCCTCACTG---CACAGCCCTGTAACCTCCTATGTG 94

Qy         70 CTGACTCAGCCACCCGTCCGGTGTCAGTGTCCCAGGACAGCAGCAGGCCAGGATCACCTGTGGG 129
              |||||||||||||||  |||||||| |||    || | ||||||||||| | || | |||||||
Db         95 CTGACTCAGCCACCCTCGGTGTCAGGCGGCCACCGGCCACCATTTCCTGTGTGG 154

Qy        130 GGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGCCAGCGCCCCT 189
              |||||||||||| || | | | ||||| ||||||||||||||| ||||||||||| ||||
Db        155 GGAGACAACAGTCGAACTAAAACTGTCCACTGGTACCAGCAGACAGCCAGGCCAGGCCCCT 214

Qy        190 ATACTGGTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGC 249
              |  ||||||| |||||||||||||||||||||||||||||||||| |||||||||||
Db        215 GTATTGGTCGTCTATGATGATGACCGGCCCTCAGGGATCCCTGACGGATTCTCTGGC 274

Qy        250 TCCAAATCAGGGAACACGCCACCCTGACCATCAACGGGTCGAGGCCGGGATGAGGCT 309
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Qy        310 GACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTTCTCGGCGGAGGGACC 369
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Db        335 GACTATTATTGTCAGGTGTGGGATAGTGATAGTGATCATTGGGTGTTCGGCGGAGGGACC 394

Qy        370 CGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGTCACTCGTTCCCGCCCTCC 429
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Db        395 AGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCCACCCCTCC 454

Qy        430 TCTGAGGAGCTTCAAGCCAACAAGGCCACAAGGCCACACTCGGTGTCTCATAAGTGACTTCTACCCG 489
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Db        455 TCTGAGGAGCTTCAAGCCAACAAGGCCACACTCGGTGTGTCTCATAAGTGACTTCTACCCG 514

Qy        490 GGAGCCGTGACAGTGCCTGGCTGGAAG-GCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGAC 548
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Db   515 GGAGCCGTGACAGTGGCCTGGAAGAGACGAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGAC 574

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Db   575 CACCACACCCTCCAAACAACAAGCAACAACAAGTACGCGGCCAGCTACCTGAGCCTGAC 634

Qy   609 GCCTGAGCGAGTGGAAGTCCCACAGAGCTACA-GCTTGCCAGGTCACGCATGAAGGGAGCA 667
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Db   635 GCCTGAGCGAGTGGAAGTCCCACAAAAGCTACAGGTGTCTCCAGTCACGCATGAAGGGAGCA 694

Qy   668 CCGTGGAAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
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Db   695 CCGTGGAAGAAGACAGTGGCCCCTACAGAATGTTCAT 730

RESULT 12
BG756256
LOCUS   BG756256   924 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602713568F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853801 5',
            mRNA sequence.
ACCESSION   BG756256
VERSION   BG756256.1 GI:14066909
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 924)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1700 row: g column: 18
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                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT   226 a   272 c   257 g   169 t
ORIGIN

Query Match   77.3%; Score 545.2; DB 12; Length 924;
Best Local Similarity 92.7%; Pred. No. 1.5e-130;
Matches 595; Conservative 0; Mismatches 43; Indels 4; Gaps 2;

Qy   62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCA 121
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Qy   122 CCTGTGGGGGAGCAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC 181
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Qy   242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGAGGCGCGGGG 301
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Qy   302 ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
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Db   254 ATGAGGCCGACTATTACTGTCAGGTGTGGGATAGAAGTAGTG---ATGTAGTATTCGGCG 310

Qy   362 GAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC 421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311 GAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC 370

Qy   422 CGCCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371 CGCCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 430

Qy   482 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 490

Qy   542 TGGAGACCACCACACCCTCCAAACAACAAGCAACAACAAGTACGCGGCCAGCTACCTGA 601
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491 TGGAGACCACCACACCCTCCAAACAACAAGCAACAACAAGTACGCGGCCAGCTATCTGA 550

Qy   602 GCCTGAGCGAGTGGAAGTCCCAGAGCTACAGCTGCCAGGTCACGCATGAAG 661
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   551 GCCTGAGCGAGTGGAAGTCCCAGAGCTACAGCTGCCAGGTCACGCATGAAG 610

Qy   662 GGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
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Db   611 GGAGCACCGTGGAGAAGACAGTGG--CCTACAGAATGTTCAT 651

RESULT 13
BM924274
LOCUS   BM924274   1086 bp   mRNA   linear   EST 12-MAR-2002
DEFINITION AGENCOURT_6630576 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760519
            5', mRNA sequence.
ACCESSION   BM924274
VERSION   BM924274.1 GI:19374641
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1086)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12807 row: k column: 16
            High quality sequence stop: 710.
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Organ: pooled colon, kidney, stomach; Vector:

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KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 917)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/,
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: f  column: 22
            High quality sequence stop: 552.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT       223 a    286 c    242 g    166 t
ORIGIN
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Query Match           77.2%;  Score 544.4;  DB 14;  Length 917;
Best Local Similarity 88.5%;  Pred. No. 2.4e-130;
Matches    614;  Conservative    0;  Mismatches   76;  Indels   4;  Gaps   2;

Qy     11 CCGCTCAGCTCCTGGGCTCCTCGCTCTCGGCTCCCAGGTGCACGATGTGCCTATGAAC  70
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Db     38 CCGTTCTCCTCTCGGCCCTCCTCTCTCACTG---CACAGGCGCTGTGACCTCCTATGTGT  94

Qy     71 TGACTCAGCCACCCTCGGTGTGCAGTGTCCCAGGACAGACGGCCAGGATCACCTGTGGGG 130
          |||||||||||||||||||||||||||||| |||||||| |||||||||||||||||||||
Db     95 TGACTCAGCCACCCTCGGTTTCAGTGGCCCCAGGACAGACGGCCAGGATTACCTGTGGGG 154

Qy    131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCGTACCAGCAGAAGCGCGGGCCCTA 190
          |||||||||| ||||  |||||| || ||||||| |||||||||||||| ||| |||||| |
Db    155 GGAACAACATTGACAGTAGTAAAAATGTAAACTGGTACCAGCAGAAGCCCAGCCCCCTG 214

Qy    191 TACTGGTCATCTATGATGATGACGGCCCTGAGCGATTCTCTGGCT 250
          |||||||| ||| |||||| |||||| |||||||||||||||||
Db    215 TATTGGCCGTCTCACGATGATAACGCCCGGCCCTCAGGGATCCCTGAGCGATTCGCTGGCT 274

Qy    251 CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTG 310
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Db    275 CCACTTCTGGTGATACGGCCACCCTGACCATCAGTGTGGTCAACGGGGTCGAGGGGGATGAGGCCG 334

Qy    311 ACTATTACTGTGCAGGGACAGGCTAGTGATCATCCGGTCTTCGGAGGAGGGACCC 370
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Db    335 ACTACTACTGTGCAGGTGTGGGATACTAGTACTGGTCAACGGGGTTCGCGGCGGAGGGACCA 394

Qy    371 GGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCCCGCCCTCCT 430
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Db    395 GGGTGACCGTCCCGGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCCCGCCCTCCT 454

Qy    431 CTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCCGG 490
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Db    455 CTGAGGAACTTCAAGCCAACAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCCGG 514
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BASE COUNT      255 a    355 c    270 g    199 t
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Best Local Similarity 88.6%;  Pred. No. 1.8e-130;
Matches    614;  Conservative    0;  Mismatches   75;  Indels   4;  Gaps   2;

Qy     11 CCGCTCAGCTCCTGGGCTCCTCGCTCTCGGCTCCCAGGTGCACGATGTGCCTATGAAC  70
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Db     50 CCGTTCTCCTCTCGGCCCTCCTCTCTCACTG---CACAGGCGCTGTGACCTCCTATGTGC 106

Qy     71 TGACTCAGCCACCCTCGGTGTGCAGTGTCCCAGGACAGACGGCCAGGATCACCTGTGGGG 130
          |||||||||||||||||||||||||||||| |||||||| |||||||||||||||||||||
Db    107 TGACTCAGCCACCCTCGGTTTCAGTGGCCCCAGGAGAGACGGCCAGGATTACCTGT-GGG 165

Qy    131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCGTACCAGCAGAAGCCGCGGGCCCTA 190
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Db    226 TATTGGCCGTCTCACGATGATAACGCCCGGCCCTCAGGGATCCCTGAGCGATTCGCTGGCT 285

Qy    251 CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTG 310
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Db    286 CCAAGTCTGAAAACACGGCCACTCTGACCATCAGCAGGGTCGAGGCGCGGGGATGAGGCCG 345

Qy    311 ACTATTACTGTGCAGGGACAGGCTAGTGATCATCCGGTCTTCGGAGGAGGGACCC 370
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Db    346 ACTATTACTGTGCAGGTGTGGGACCCTTATAGTGATCATTGGGTGTTCGGCGGAGGGACCA 405

Qy    371 GGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCCCGCCCTCCT 430
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    406 AGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCCCACCCTCCT 465

Qy    431 CTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCCGG 490
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Db    466 CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCCGG 525

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Qy    551 CCACACCCTCCAAACAACAAGCAACAACAAGTACCGGCCAGCTACCTGACGC 610
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Db    586 CCACACCCTCCAAACAACAAGCAACAACAAGTACCGGCCAGCTACCTGACGC 645

Qy    611 CTGAGCAGTGGAAGTCCCACAGAAGTACAGCTGCCAGGTCACGCATGAAGGAGGCACCG 670
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Db    646 CTGAGCAGTGGAAGTCCCACAAAAAGCTACAGCTGCCAGGTCACGCATGAAGGAGGCACCG 705

Qy    671 TGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
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RESULT 14
BQ711587
LOCUS       BQ711587        917 bp    mRNA       linear    EST 16-JUL-2002
DEFINITION  AGENCOURT_8475231 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301461
            5', mRNA sequence.
ACCESSION   BQ711587
VERSION     BQ711587.1  GI:21850486
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Left column panel:

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            pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
            source anonymous pool of 3 colons, age 26 yo male, 49 yo
            female, 71 yo male colon; 46 yo male kidney, and pool of 2
            stomachs, 62 yo male and 70 yo female. Library is
            oligo-dT primed and directionally cloned (EcoRV site is
            destroyed upon cloning). Average insert size 1.4 kb,
            insert size range 1-3 kb. Library is normalized and
            enriched for full-length clones and was constructed by C.
            Gruber (Invitrogen). Research Genetics tracking code
            023. Note: this is a NIH_MGC Library."
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Qy    491 GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA 550
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Qy    551 CCACACCCTCCAAACAAGCAACAACAACAAGCAGCGGGCCAGCAGCTACCTGAGCCTGACGC 610
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Qy    611 CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCA-CC 669
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Db    635 CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCC 694

Qy    670 GTGGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
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RESULT 15
BQ709509
LOCUS        BQ709509                 949 bp    mRNA     linear     EST 16-JUL-2002
DEFINITION   AGENCOURT 8418138 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281593
             5', mRNA sequence.
ACCESSION    BQ709509
VERSION      BQ709509.1  GI:21848408
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 949)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2474 row: k column: 02
             High quality sequence stop: 635.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Jing Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      221 a    301 c     247 g      179 t      1 others
ORIGIN
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Query Match         76.9%;   Score 542.4;  DB 14;  Length 949;
Best Local Similarity 88.2%;   Pred. No. 8e-130;
Matches 614;   Conservative    0;  Mismatches   76;  Indels    6;  Gaps    2;

Qy    11 CCGGCTCAGCTCCTCTGGGCTCCTCTGGCTTCCTGGGCTCCTCCCAGGTGCACGATGTGCCTATGAAC 70
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Qy    71 TGACTCAGCCACCCTCCGGTGTCAGTGTCCCCAGGACGAGCAGACGGCCAGGATCACCTGTGGGG 130
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Db     83 TGACCCAGCCACCCTCGGTGTCCGTGCCCCAGGACAGCAGCCACCGTGGAA 142
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Qy    131 GAGACAACAGTAGAAATGAATATGTCCACTGGTTCCACGCAGCAGAAGCCAGCGGCGGGCCCCTA 190
          |  ||| | |||| || ||| || ||||||| ||||| ||| |||||||||||| ||| ||||
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Qy    191 TACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT 250
          | ||||||| |||||| ||| ||  ||||||  |||||||||||||||||||||||||
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Qy    251 CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGGTCGAGGGATGAGGCTG 310
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Db    263 CCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGGGTCGAGGGATGAGGCCG 322

Qy    311 ACTATTACTGTCAGGTGTGGAACAGGGGCTAGTGATCATGTGATCATCC---GGTCTTCGGAGGAGGGA 367
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Qy    368 CCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCCTCCGGTGTCACTCTGTTCCCGCCCT 427
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Db    383 CCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCCTCGGTGTCACTCTGTTCCCGCCCT 442

Qy    428 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 487
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Db    443 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 502

Qy    488 CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA 547
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    563 CCACCACCCTCCAAACAAGCAACAACAACAACAAGTACGCGGGCCAGCAGCTATCTGAGCCTGA 622

Qy    608 CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCA 667
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Qy    668 CCGTGGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
          ||||||||||||||||||||||||||||||||||||
Db    683 CCGTGGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 718
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Search completed: April   6, 2003, 06:20:13
Job time : 1346.86 secs

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          GenCore version 5.1.3
    Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April  5, 2003, 18:12:24 ; Search time 193.478 Seconds
                               (without alignments)
                        8205.894 Million cell updates/sec

Title:         US-09-758-173-1
Perfect score: 705
Sequence:      1 ATGGAGGGTCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 705

Scoring table: IDENTITY NUC
               Gapop 10_0 , Gapext 1.0

Searched:      2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters:  4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	705	100.0	705	18	AAT62509	Primatised anti-hu
2	705	100.0	705	19	AAV35484	Macaque primatized
3	705	100.0	705	24	AAS17242	DNA sequence of a
4	585.2	83.0	702	18	AAT62867	Ant-CD4 monkey-hum
5	582.6	82.6	926	20	AAZ24427	Human bladder tumo
6	555.6	78.8	836	23	AAS83482	DNA encoding novel
7	540.2	76.6	711	19	AAV35488	Macaque primatized
8	540.2	76.6	711	24	AAS17246	DNA sequence of a
9	538.6	76.4	711	18	AAT62512	Primatised anti-hu
10	527.6	74.8	1027	24	ABQ54438	Human ovarian anti
11	524	74.3	841	23	AAS83486	DNA encoding novel
12 c	520.8	73.9	904	24	AAK28671	Human cDNA encodin
13	520.4	73.8	869	22	AAS22717	Human cDNA encodin
14	516	73.2	791	23	AAS87271	DNA encoding novel
15	515	73.0	1825	22	AAS22777	Human cDNA encodin
16	514.4	73.0	859	22	AAS22481	Human cDNA encodin
17	512.8	72.7	960	21	AAC78188	Human cancer assoc
18	512	72.6	872	9	AAN81655	VDJC regions of hu
19	511	72.5	654	22	AAS13364	Human cDNA encodin
20	509.2	72.2	930	22	AAS22541	Human cDNA encodin
21	506	71.8	793	23	AAS83481	DNA encoding novel
22	504	71.5	807	23	AAS83484	DNA encoding novel
23	495.2	70.2	863	24	ABK28650	Human cDNA encodin
24 c	480	68.1	849	23	AAH98186	Human EST-derived
25	474.2	67.3	884	11	AAQ03609	Sequence encoding
26	473.6	67.2	810	23	AAS87270	DNA encoding novel
27	473	67.1	935	22	AAC66525	Human immune syste
28	472	67.0	768	20	AAX06953	Monoclonal antibod
29 c	472	67.0	768	20	AAX06954	Monoclonal antibod
30	465.6	66.0	826	22	AAI58109	Human polynucleoti
31	462.8	65.6	915	24	ABN97248	Gene #3746 used to
32	462.8	65.6	915	24	ABK64815	Human benign prost
33	462.8	65.6	915	24	ABL65478	Lung cancer relate
34	462.2	65.6	654	14	AAQ49835	Anti-HIV-1 recombi
35	462	65.5	762	22	AAC84209	Plasmid Glambda-1B
36	462	65.5	915	22	AAC84207	Plasmid Glambda-1A
37	461.8	65.5	5679	23	AAS77073	DNA encoding novel
38	457	64.8	902	14	AAQ35100	Antibody D lambda
39	456	64.7	895	22	AAC66530	Human immune syste
40	455.6	64.6	763	23	AAS83480	DNA encoding novel
41	455.4	64.6	891	22	AAC66528	Human immune syste
42	455.2	64.6	708	22	AAH47902	Human type antihum
43	453.6	64.3	783	23	AAS83483	DNA encoding novel
44	452	64.1	876	23	AAS83478	DNA encoding novel
45	451.6	64.1	651	19	AAV11293	Antibody HB4C5 lig

ALIGNMENTS

```
RESULT 1
AAT62509
ID   AAT62509 standard; DNA; 705 BP.
XX
AC   AAT62509;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
```

DR WPI; 1997-108638/10.
DR P-PSDB; AAW01817.
XX
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
XX
PS Claim 7; Fig 8A; 81pp; English.
XX
CC 2 DNA sequences (AAT62509 and AAT62510) respectively code for
CC primatised forms (AAW01817 and AAW01818) of the light and heavy chains
CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC 7C10. Cloned 7C10 light and heavy variable genes are inserted into
CC an expression vector (pref. NEOSPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of primatised
CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC antibodies have been produced (see also AAW01819-22). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
SQ Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match 100.0%; Score 705; DB 18; Length 705;
Best Local Similarity 100.0%; Pred. No. 4e-167;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGGCTGTGCTCTGGGCTCCCAGGTGACGATGT 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGGCTGTGCTCTGGGCTCCCAGGTGACGATGT 60

Qy 61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATC 120
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATC 120

Qy 121 ACCTGTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ACCTGTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180

Qy 181 CGGGCCCCTATACTGGTCATCTATGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CGGGCCCCTATACTGGTCATCTATGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240

Qy 241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGG 300
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGG 300

Qy 301 GATGAGGTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATGGGCTAGTGATCATCCGGTCTTCGGA 360
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GATGAGGTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATGGGCTAGTGATCATCCGGTCTTCGGA 360

Qy 361 GGAGGGACACCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGGTCACTCGTTC 420
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GGAGGGACACCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCGGTCACTCGTTC 420

Qy 421 CCGCCCCTCCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC 480
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 CCGCCCCTCCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC 480

Qy 481 TTCTACCCGGAGCCGTGACAGTGCCTGGAAGGCAGATAGCCAGCCCCGTCAAGGCGGGA 540
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 TTCTACCCGGAGCCGTGACAGTGCCTGGAAGGCAGATAGCCAGCCCCGTCAAGGCGGGA 540

Qy 541 GTGGAGACCACCACCACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTACCTG 600
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GTGGAGACCACCACCACCCTCCAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTACCTG 600

Qy 601 AGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660

Qy 661 GGGGAACACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
|||||||||||||||||||||||||||||||||||||||||||||||
Db 661 GGGGAGCCGCCTGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705

RESULT 2
AAV35484
ID AAV35484 standard; DNA; 705 BP.
XX
AC AAV35484;
XX
DT 29-SEP-1998 (first entry)
XX
DE Macaque primatized 7C10 light chain DNA.
XX
KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW T cell proliferation; ss.
XX
OS Macaca fascicularis.
XX
FH Key Location/Qualifiers
FT CDS 1..705
FT /*tag= a
FT /product= 7C10 light chain
XX
PN WO9819706-A1.
XX
PD 14-MAY-1998.
XX
PF 29-OCT-1997; 97WO-US19906.
XX
PR 08-NOV-1996; 96US-0746361.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N;
XX
DR WPI; 1998-286601/25.
DR P-PSDB; AAW63760.
XX
PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours
XX
PS Example 7; Fig 3a; 87pp; English.
XX
CC This sequence encodes a primatized form of the antibody 7C10 light chain
CC from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressant for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotype reagents. MAb's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
SQ Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match 100.0%; Score 705; DB 19; Length 705;
Best Local Similarity 100.0%; Pred. No. 4e-167;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGGCTGTGCTCTGGGCTCCCAGGTGACGATGT 60

XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11538.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 3a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present nucleic
CC   acid sequence encodes the light chain of 7C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match   100.0%; Score 705; DB 24; Length 705;
Best Local Similarity   100.0%; Pred. No. 4e-167;
Matches 705; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGT 60

Qy   61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATC 120

Qy   121 ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180

Qy   181 CGGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240

Qy   241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCCGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCCGG 300

Qy   301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA 360

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATC 120

Qy   121 ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180

Db   181 CGGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGA 240

Qy   241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCCGG 300

Db   301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA 360

Qy   361 GGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCTCGCCCTCACTCTGTTC 420

Db   361 GGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCTCGCCCTCACTCTGTTC 420

Qy   421 CCGCCCCTCCTCGAGGAGTTCAAGCCACAACAAGGCCACACTGGTGTGTCTCATAAGTGAC 480

Db   421 CCGCCCCTCCTCGAGGAGTTCAAGCCACAACAAGGCCACACTGGTGTGTCTCATAAGTGAC 480

Qy   481 TTCTACCCGGAGGCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAGGGCGGGA 540

Db   481 TTCTACCCGGAGGCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAGGGCGGGA 540

Qy   541 GTGGAGACCACCACACCCTCCAAACAAAGCAACAACAGCACGGGCCCAGCAGCTACCTG 600

Db   541 GTGGAGACCACCACACCCTCCAAACAAAGCAACAACAGCACGGGCCCAGCAGCTACCTG 600

Qy   601 AGCCTGACGCCTGAGCAGTGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660

Db   601 AGCCTGACGCCTGAGCAGTGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660

Qy   661 GGGAGCACCGTGGAGAGACAGTGCCCCCTACAGAATGTTCATGA 705

Db   661 GGGAGCACCGTGGAGAGACAGTGCCCCCTACAGAATGTTCATGA 705

RESULT 3
AAS17242
ID   AAS17242 standard; DNA; 705 BP.
XX
AC   AAS17242;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the light chain of 7C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7.1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..705
FT   /tag= a
FT   /product= "Light chain of 7C10 antibody"

```
Qy   361  GGAGGGACCCGGGTGACCGTCCTAGTCAGCCAGGCTGCCCCCTCGGTCACTCTGTTC  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GGAGGGACCCGGGTGACCGTCCTAGTCAGCCAGGCTGCCCCCTCGGTCACTCTGTTC  420

Qy   421  CCGCCCTCCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCATAAGTGAC  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CCGCCCTCCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCATAAGTGAC  480

Qy   481  TTCTACCCGGGAGCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAGGCGGA  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TTCTACCCGGGAGCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAGGCGGGA  540

Qy   541  GTGGAGACCACCACCCTCCAAACAACAAGCAACAACAAGTACGCGGCCAGCAGCTACCTG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GTGGAGACCACCACCACCCTCCAAACAACAAGCAACAACAAGTACGCGGCCAGCAGCTACCTG  600

Qy   601  AGCCTGACGCCTGAGCAGTGGAAGTCCCAGAGCTACAGCTGCCAGTGCACGCATGAA  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AGCCTGACGCCTGAGCAGTGGAAGTCCCAGAGCTACAGCTGCCAGTGCACGCATGAA  660

Qy   661  GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA  705
          |||||||||||||||||||||||||||||||||||||||||||||
Db   661  GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA  705
```

RESULT 4
AAT62867
ID   AAT62867 standard; DNA; 702 BP.
XX
AC   AAT62867;
XX
DT   18-OCT-1997 (first entry)
XX
DE   Ant-CD4 monkey-human chimeric antibody CE9.1 DNA.
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9.1; ss.
XX
OS   Chimaeric Macaca cynomolgus;
OS   Chimaeric Homo sapiens.
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996; 96WO-US14324.
XX
PR   06-SEP-1995; 95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   P-PSDB; AAW14924.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Example 1; Page 79-80; 155pp; English.
XX
CC   A DNA sequence (AAT62867) codes for lambda variable and constant
CC   domains (AAW14924) of anti-human CD4 monkey/human chimeric antibody
CC   CE9.1. This antibody contains the antigen binding domains (see
CC   also AAW14922-23) of a cynomolgus monkey anti-CD4 monoclonal
CC   antibody, a human heavy chain constant region of gamma 1 isotype
CC   and Gm1a, Gm1z allotype, and a human lambda light constant region
CC   of the Oz minus, mcg minus genotype and Ke minus allotype. The
CC   immunoglobulin genes were cloned into mammalian expression vector

---

CC   TCAE 6, and chimeric antibody was produced in CHO cells. CE9.1
CC   binds to domain 1 of human, but not macaque, CD4, a region involved
CC   in the interaction with MHC Class II molecules on antigen-
CC   presenting cells. It shows potent immunomodulatory activity with
CC   low immunogenicity in humans, and can be used to treat autoimmune
XX   diseases such as rheumatoid arthritis.
SQ   Sequence 702 BP; 151 A; 217 C; 207 G; 127 T; 0 other;

Query Match   83.0%; Score 585.2; DB 18; Length 702;
Best Local Similarity   89.6%; Pred. No. 4.1e-137;
Matches 629; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
Qy     4  AGGGTCCCCGCCTCAGCTCCTGGGGCTCCTGCTCCTGCTCCTGGTCACGATGTGCC  63
          || ||| |||||||||||||| |||||||||||| ||| |||||||||||||||||
Db     1  ATGGCCTGGGCTCTGCTGCTCCTCACCCTCCTCACTGTGCACTTTACAGACTCTGCGGCCTCC  60

Qy    64  TATGAACTGACTCAGCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCACC  123
          |||||||||||||||||| |||||||| |||||||||||||||||||||||||||||
Db    61  TATGAGTTGAGTCAGCCTCGCTCAGTGTCCGTGTCCCAGGACAGACGGCCGGGTTCACC  120

Qy   124  TGTGGGGGAGACAACACAGTAGAAATGAATATGTCCACTGTACCAGCAGAAGCCAGCGCGGG  183
          |||||||| |||||| ||||||||||| |||||||||||||||||||||||||||||
Db   121  TGTGGGGGAGACAACACTTGGAAGAAAAGTGTACAGTGTACCAGCAGAAGAAGCCACCCCAG  180

Qy   184  GCCCCTATACTGGTCATCTATGATGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGATTC  243
          |||||| ||||||| |||||| ||||| |||||||||||||||||||||||||||||
Db   181  GCCCCCTGTCTGGTGGTCATCTATGTGACACGGAACGGCCCTCAGGGATCCCTGCGCGGATTC  240

Qy   244  TCTGGCTCCAAATCAGGGAACACACCGCCACCCTGACCATCAACGGGTCGAGGCGGGGGAT  303
          |||||||||||| ||||||||||||||| ||||| ||||||||||||||||||||||
Db   241  TCTGCTCCAACTCAGGGAACACACCGCCACCCTGACCATCAGCGGGGTCGAGGCCGGGGGAT  300

Qy   304  GAGGCTGACTATTACTGTCAGGTGTGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA  363
          |||||||||||||||||||||||||| ||| ||||||||||| ||||||||||||||
Db   301  GAGGCTGACTATTACTGTCAGGTGTGGGACAGTACTCTGATCATTGGGTCTTCGGCGGA  360

Qy   364  GGGACCCGGGTGACCGTCCTAGTCAGCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG  423
          |||||||||||||||||||||||| |||||||||||||||||| |||||||||||||
Db   361  GGGACCCGGGTGACCGTCCTAGTCAGCCAACAAGGCTGCCCCCTCGGTCACTCTGTTCCCG  420

Qy   424  CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC  483
          |||||||||||||||||||||| |||||||||||||||||||||||||||| |||||
Db   421  CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC  480

Qy   484  TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG  543
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   481  TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG  540

Qy   544  GAGACCACCACCACCCTCCAAACAAGCAACAAGTACGCGGCCAGCAGCTACCTGAGC  603
          |||||||||||||||||| ||||| |||||||||||||||||||||||||||||||
Db   541  GAGACCACCACCACCCTCCAAACAAGCAACAAGTACGCGGCCAGCAGCTACCTGAGC  600

Qy   604  CTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAGGG  663
          ||||||||||||||||||||||| |||||||||||||||||| ||||||||||||||
Db   601  CTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAGGG  660

Qy   664  AGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA  705
          |||||||||||||||||||||||||||||||||||||||||
Db   661  AGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA  702
```

RESULT 5
AAZ24427
ID   AAZ24427 standard; cDNA; 926 BP.
XX
AC   AAZ24427;
XX
DT   14-FEB-2000 (first entry)
XX
DE   Human bladder tumour cDNA library derived EST 39.
XX
KW   Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;

```
KW    treatment; gene therapy; EST; ss.
XX
OS    Homo sapiens.
XX
PN    DE1981861-A1.
XX
PD    28-OCT-1999.
XX
PF    21-APR-1998;    98DE-1018619.
XX
PR    21-APR-1998;    98DE-1018619.
XX
PA    (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI    Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR    WPI; 1999-612028/53.
XX
PT    New nucleic acid sequences expressed in bladder tumor tissue, and
PT    derived polypeptides, for treatment of bladder tumor and identification
PT    of therapeutic agents -
XX
PS    Claim 3; Page 90; 132pp; German.
XX
CC    This invention describes novel polypeptide fragments (I) and the
CC    polynucleotides (II) that encode them that are highly expressed in a
CC    human bladder tumour and which have cytostatic activity. (II) are used
CC    for recombinant expression of (I) and to isolate complete genes. (I) are
CC    used to identify agents suitable for treatment of bladder cancer, to
CC    directly treat this form of cancer (including expression from gene
CC    therapy vectors) or are used in a preparation for cancer treatment. (I)
CC    is also used for the generation of specific antibodies. (II) are
CC    identified by assembling ESTs (expressed sequence tags) from a
CC    particular tissue type before comparison of expression patterns. This
CC    allows a significantly longer fragment of the gene to be revealed, and
CC    therefore reduces the number of failures associated with the fact that
CC    ESTs from different libraries may represent different parts of the same
CC    unknown gene, distorting the estimated frequency of occurrence in a
CC    particular tissue. AAZ43260-Z43309 represent expressed sequence tag (EST)
CC    fragments isolated from a human bladder tumour cDNA library which encode
CC    the proteins represented in AAY66143-Y66198.
XX
SQ    Sequence 926 BP; 249 A; 275 C; 240 G; 162 T; 0 other;

Query Match     82.6%;   Score 582.6;   DB 20;   240 G; 162 T; 0 other;
Best Local Similarity   91.1%;   Pred. NO. 2e-136;;   Length 926;
Matches  631;   Conservative  0;   Mismatches  59;   Indels  3;   Gaps  1;

Qy    11  CCGCTCAGCTCGTCTGGGGCTTCCTGCTTCTGGCTCCCAGTGCACGATGCGCCTATGAAC  70
          ||||| ||||||||  ||| | ||||||  |||||     |  |||||  |||  ||||||||
Db    47  CCGTTCTCCTCCTCGGCCTCCTTCCTCTCTCACTG--CACAGGCTCTTGTGACCTCCTATGTGC  103

Qy    71  TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACAGCCCAGGATCACCTGTGGGG  130
          |||||||||||||||||||||| ||||||||||||||||||||||  |||||||||||||||
Db   104  TGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACAGCCCAGGATTACCTGTGGGG  163

Qy   131  GAGACAACAGTAGAAATGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGCGGGCCCCTA  190
          || |||| || |  | |   | |    ||||||||||||||||  ||||||   )  ||||||||
Db   164  GAAACAACATTGAAGTAAAGTGTGCACTGGTACCAGCAGAAGCCAGCGCCAGGCCCCTG  223

Qy   191  TACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT  250
          ||||||| |||| |||||||||||   |||||||||||||||||||||||||||||||||
Db   224  TGCTGGTCGTCTCATGATGATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCCTCTGGCT  283

Qy   251  CCAAATCAGGAACACCGCCACCCTGACCATCAAGGGGGTCGAGCGCCGGGATGAGGCTG  310
          |||| ||| ||||||| ||||||||||||||| |||| |||||||||||||||||||| |
Db   284  CCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAGCGCCGGGATGAGGCCG  343

Qy   311  ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGAGGGACCC  370
          ||||||||| |||||||||||||  | | |||||| |||| ||||  ||||||||||||| ||
Db   344  ACTATTACTGTCAGGTGTGGGATAGTAGTGATCATTGGGTGTTCGGCGGAGGGACCA  403

Qy   371  GGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCCCGCCCCTCCT  430
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Db   404  AGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCCCGCCCCTCCT  463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   431  CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG  490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   464  CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG  523

Qy   491  GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA  550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   524  GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA  583

Qy   551  CCACACCTTCCAAACAACAACAAGTACGGCCGCCAGCAGCTACCTGAGCCTGACGC  610
          ||||||| ||||||||||||  |||||||||||||||||||| | ||||||||||||
Db   584  CCACACCCTCCAAACAACAAGTACGGCCGCCAGCAGCTATCTGAGCCTGACGC  643

Qy   611  CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACCGTGAAGGAGCACCG  670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   644  CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACCGTGAAGGAGCACCG  703

Qy   671  TGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  703
          |||||||||||||||||||||||||||||||||
Db   704  TGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  736

RESULT 6
AAS83482
ID    AAS83482 standard; cDNA; 836 BP.
XX
AC    AAS83482;
XX
DT    13-FEB-2002  (first entry)
XX
DE    DNA encoding novel human diagnostic protein #19286.
XX
KW    Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW    food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS    Homo sapiens.
XX
PN    WO200175067-A2.
XX
PD    11-OCT-2001.
XX
PF    30-MAR-2001; 2001WO-US08631.
XX
PR    31-MAR-2000; 2000US-0540217.
PR    23-AUG-2000; 2000US-0649167.
XX
PA    (HYSE-) HYSEQ INC.
XX
PI    Drmanac RT, Liu C, Tang YT;
XX
DR    WPI; 2001-639362/73.
DR    P-PSDB; ABG19295.
XX
PT    New isolated polynucleotide and encoded polypeptides, useful in
PT    diagnostics, forensics, gene mapping, identification of mutations
PT    responsible for genetic disorders or other traits and to assess
PT    biodiversity -
XX
PS    Claim 1; SEQ ID No 19286; 103pp; English.
XX
CC    The invention relates to isolated polynucleotide (I) and
CC    polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC    polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC    and gene mapping, and in recombinant production of (II). The
CC    polynucleotides are also used in diagnostics as expressed sequence tags
CC    for identifying expressed genes. (I) is useful in gene therapy techniques
CC    to restore normal activity of (II) or to treat disease states involving
CC    (II). (II) is useful for generating antibodies against it, detecting or
CC    quantitating a polypeptide in tissue, as molecular weight markers and as
CC    a food supplement. (II) and its binding partners are useful in medical
CC    imaging of sites expressing (II). (I) and (II) are useful for treating
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CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 836 BP; 185 A; 262 C; 232 G; 157 T; 0 other;

Query Match   78.8%;   Score 555.6;   DB 23;   Length 836;
Best Local Similarity   91.6%;   Pred. No. 1.1e-129;
Matches   588;   Conservative   0;   Mismatches   54;   Indels   0;   Gaps   0;

Qy   62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACACAGCGGCCAGGATCA 121
           |||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Db   101 CCTTTGCTGCTGCGTCAGCCACCCTCAGTGTCAGTGGCCCCAGGAGACGGCGCAGGATTA 160

Qy   122 CCTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAGCCAGCGC 181
           ||||||||||| ||||||||| |||||||||||||||||||||||||||||||| ||||
Db   161 CCTGTGGGGCAGACAACAACATTGGAAGAAGAAGTGTTCACTGGTACCAACAGAGGCCAGGCC 220

Qy   182 GGGCCCCTATACTGGTCATCTATGATGATGATAGTGACCGGCCCTCAGGGATCCTGAGCGAT 241
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   221 AGGCCCCTGTGTGGTCATCTATTATGATGACGGCGGCCCTCAGAAATCCCTCAGCGAT 280

Qy   242 TCTCTGGCTCCAAATCAGGAGACACCGCCACCCTGACCATCAACGGGTCGAGGCGGGGG 301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 TCTCTGGCTCCAACTCTGGGACACGGCCACCCTGACCATCAGCGCGGGGTCGAGGCGGGGG 340

Qy   302 ATGAGGCTGACTATTACTGTCAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGACG 361
           ||||| |||||| ||||||||||| || | || ||||||||||||||||||||||
Db   341 ATGAGGCGACTATTACTGTCAGTGTGGGATGACGATAAATAGTCATGTGGTCTTCGGCG 400

Qy   362 GAGGGACCACCGGGGTGACCGTCCTAGGTCAGCCGAAGGCTGCCCCCTCCGTCACTCTGTCC 421
           ||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||
Db   401 GAGGGACCAAGCTGACCGTCCTGTCAGCCCAAGGCTGCCCCCTCCGTCACTCTGTTCC 460

Qy   422 CGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCATAAGTGACT 481
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   461 CGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCATAAGTGACT 520

Qy   482 TCTACCCGGGAGCCCGTGACAGTGGCCTGGAAGGCAGCAGATAGCAGCCCCGTCAAGGCGGAG 541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 TCTACCCGGGAGCCCGTGACAGTGGCCTGGAAGGCAGCAGATAGCAGCCCCGTCAAGGCGGGAG 580

Qy   542 TGGAGACCACCACCCTCCAAACAACCCTCCAAACAACAAGTACGCGGCCAGCAGTACCTGA 601
           ||||||||||||||||||| ||||||||||||||||||||||||||||||| |||||
Db   581 TGGAGACCACCACCCTCCAAACAACAAGCAACAAGTACGCGGCCAGCAGCTATCTGA 640

Qy   602 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGTACAGCTGCCAGTCACGCATGAAG 661
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   641 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAG 700

Qy   662 GGAGCACCGTGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
           ||||||||||||||||||||||||||||||||||||||||
Db   701 GGAGCACCGTGAGAAACAGTGGCCCCTACAGAATGTTCAT 742

RESULT 7
AAV35488
ID   AAV35488 standard; DNA; 711 BP.
XX
AC   AAV35488;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 16C10 light chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;

KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..711
FT   /*tag= a
FT   /product= 16C10 light chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,   Brams P,   Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63764.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5a; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 16C10 light chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match   76.6%;   Score 540.2;   DB 19;   Length 711;
Best Local Similarity   86.1%;   Pred. No. 7.8e-126;
Matches   612;   Conservative   0;   Mismatches   93;   Indels   6;   Gaps   1;

Qy   1 ATGAGGGTCCCCGCTCCAGCTCCAGCCACCCTCGGGTCCTCGGGTGTCAGTGTCCCAGGTGCACGATGT 60
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAGGGTCCCCGCTCCAGCTCCAGCTCCAGCTCCTGCTCCTGGTGCTCGGGTGTCAGTGTCACGATGT 60

Qy   61 GCCTATGAACTGACTCAGCCACCCTCCGGTGTCAGTGTCCCAGGACACAGCGGCCAGGATC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTCGGGGCCCCAGGGGCAGAGGTCACCATC 120

Qy   121 ACCTGTGGGG--------AGACAACAGTAGAAATGAATATGTCCACTGTTACCAGCAGAAG 174
           |||||||||| |||||||||| || ||||| ||||| ||||||||||||||
Db   121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATTACACATTGGACCAGCAGCTC 180

Qy   175 CCAGGCGCGGGCCCCTATACTGGTCATCTATGATGATGATAGTGACCGGCCCCTCAGGGATCCCT 234
           |||||| ||||||||||||||||||||||||||||| ||| || || ||| |||| || ||

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DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11645.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 5a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present nucleic
CC   acid sequence encodes the light chain of 16C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match             76.6%;  Score 540.2;  DB 24;  Length 711;
Best Local Similarity   86.1%;  Pred. No. 7.8e-126;
Matches    612;  Conservative    0;  Mismatches   93;  Indels    6;  Gaps    1;

Qy    1 ATGAGGGTCCCCGCTCCCTCAGCTCCTGGGCTCCTCTGCTCTGGGCTCCCAGTGCACGATGT   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGAGGGTCCCCGCTCCCTCAGCTCCTGGGCTCCTCTGCTCTGGGCTCCCAGTGCACGATGT   60

Qy   61 GCCTATGAACTGACTCAGCCACCCTCCGTGTGCAGTGTCCCAGGACAGACAGGCCAGGATC  120
                  | |||| |||  ||| |||||| |||  | |||| ||||||| |||  ||| |||
Db   61 GAGTCTGTGCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC  120

Qy  121 ACCTGTGGGG------AGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAG  174
        | ||| |||       |||||||||||  | | |||| ||  |||||||||||||||
Db  121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC  180

Qy  175 CCAGCGGGCGGCCCCTATACTGGTCATCTATGATGATGCACGGCCCTCAGGGATCCCT  234
        |||| | ||| ||||| |||| ||||||||||| ||  |  |||| ||||| ||| |||
Db  181 CCAGGAACGGCGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT  240

Qy  235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAG  294
        || |||||||||||||||||| || ||  ||| |||||||  || |||| | ||| |  ||
Db  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGCCATCACTGGGCTCCAG  300

Qy  295 GCCGGGATGAGCGTGACTATTACTGCCAGGTGTGGGAGACAGGGTAGTGATCATCCGGTC  354
        || ||||||||| ||| |||||||| ||| ||| |||  |||   |||  |  |||  ||
Db  301 ACTGAGGATGAGCGTGATTATTACTGCCAGTGTCCAGCAGCAGCAGCTGAATGCTCAGGTA  360

Qy  355 TTCGGAGGAGGGACCCCGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT  414
        ||||||||||||||| |||||||||||| |||||||||||||||||||||||||||||||
Db  361 TTCGGAGGAGGGACCCCGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT  420

Qy  415 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  474
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  480

Qy  475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG  534
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG  540

Qy  535 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACACCTACGCGGCCAGCAGC  594
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Db  181 CCAGGAACGGCGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT  240

Qy  235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAG  294
Db  241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCGGCCATCACTGGGCTCCAG  300

Qy  295 GCCGGGATGAGCGTGACTATTACTGCCAGGTGTGGGAGACAGGGTAGTGATCATCCGGTC  354
Db  301 ACTGAGGATGAGCGTGATTATTACTGCCAGTGTCCAGCAGCAGCAGCTGAATGCTCAGGTA  360

Qy  355 TTCGGAGGAGGGACCCCGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT  414
Db  361 TTCGGAGGAGGGACCCCGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT  420

Qy  415 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  474
Db  421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA  480

Qy  475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG  534
Db  481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG  540

Qy  535 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACACCTACGCGGCCAGCAGC  594
Db  541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACACCTACGCGGCCAGCAGC  600

Qy  595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCGTGCCAGGTCACG  654
Db  601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCGTGCCAGGTCACG  660

Qy  655 CATGAAGGGAGCACGTGAGAAGACAGTTGGCCCCTACAGAATGTTCATGA  705
Db  661 CATGAAGGGAGCACGTGGAGAAGACAGTTGGCCCCTACAGAATGTTCATGA  711
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RESULT 8
AAS17246
ID   AAS17246  standard; DNA; 711 BP.
XX
AC   AAS17246;
XX
DT   12-MAR-2002  (first entry)
XX
DE   DNA sequence of a primatised form of the light chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..711
FT                  /tag= a
FT                  /product= "Light chain of 16C10 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Hanna N,  Brams P;
XX
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Qy   61 GCCTATGAACTGACTCAGCCACCCTCGGTCGTCAGTGTGTCCCAGGACAGACGGCCAGGATC 120
        |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   61 GAGTCTGTCCTGACACAGCCGCCGCCCAGTGTCTGGGGCCCCAGGGGCAGAAGTCACCATC 120

Qy 121 ACCTGTGGGG-----AGACACAGTAGAAATGAATATGTCCACTGACCAGCAGAAG 174
        || |||||||| ||| || |||||| || || | ||| ||||||||||
Db 121 TCGTGCACTGGGAGCACCTCCAACATTGGAGTTATGATCTACTACAGCAGCAGCTC 180

Qy 175 CCAGCGCGGGCGCCCTATACTGGTCCATCTATGATGAGTAGTGACCGGCCCTCAGGGATCCT 234
        |||| || | |||| || ||| || | |||| ||| ||||| ||||||||||||
Db 181 CCAGGAACGGCCCCCAAACTCCTCATCTCATGACATTAACAAGCGACCACCCTCAGGAATTTCT 240

Qy 235 GAGCGGATTCTGCTCCAAATCAGGGAACACCGCCACCATCAACCCCTGACCATCAACGGGTCCAG 294
        ||| || || ||||| | || || |||| | ||| ||||| | | ||| |||||||||||||
Db 241 GACCGATTCTCTCGGCTCCAAGTCTGGTACCCGGCCTCCCTGGCCATCACTGGGCTGGGCTCCAG 300

Qy 295 GCCGGGATGAGGCTGACTATTACTGTCAGGTGTGGACAGGGCTAGTGATCATCCGGTC 354
        ||| ||| ||||| | || ||| || |||| || ||||||| || || || |||||
Db 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCAGCCTGAATGCTCAGGTA 360

Qy 355 TTCGGAGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCCGGTCACT 414
        |||||||||||| | ||||| |||||| |||| |||||||||||| |||| |||||||
Db 361 TTCGGAGAGGGACCCGGGTCACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420

Qy 415 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 474
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480

Qy 475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 534
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 AGTGACTACTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540

Qy 535 GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGCAGC 594
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGCAGC 600

Qy 595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 654
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 660

Qy 655 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711

RESULT 10
ABQ54438
ID   ABQ54438 standard; cDNA; 1027 BP.
XX
AC   ABQ54438;
XX
DT   22-AUG-2002 (first entry)
XX
DE   Human ovarian antigen HCNSF57 cDNA, SEQ ID NO:318.
XX
KW   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW   ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW   infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW   PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW   inflammatory condition; immune disorder; blood disorder;
KW   cardiovascular disorder; respiratory disorder; neurological disorder;
KW   gastrointestinal disorder; urinary system disorder; drug screening;
KW   gene therapy; chromosome mapping; forensic analysis;
KW   antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW   antiinflammatory; gynaecological; reproductive; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200200677-A1.
XX
PD   03-JAN-2002.
XX

Db 541 GCGGGAGTGGAGACCACCACACCCTCCAAACAACAAGTACGCGGCCAGC 600
        |||||||||||||||||||||||||||||||||||||||||||||||||
Qy 595 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 654
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 660

Qy 655 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711

RESULT 9
AAT62512
ID   AAT62512 standard; DNA; 711 BP.
XX
AC   AAT62512;
XX
DT   25-MAY-1997 (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 light chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996; 96WO-US10053.
XX
PR   07-JUN-1995; 95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01821.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 11; Fig 10A; 81pp; English.
XX
CC   2 DNA sequences (AAT62512 and AAT62513) respectively code for
CC   primatised forms (AAW01821 and AAW01822) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   16C10. Cloned 16C10 light and heavy variable genes are inserted
CC   into an expression vector (pref. NEOSPLA) which contains human light
CC   and heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 711 BP; 161 A; 226 C; 193 G; 131 T; 0 other;

Query Match   76.4%; Score 538.6; DB 18; Length 711;
  Best Local Similarity   85.9%; Pred. No. 2e-125;
  Matches 611; Conservative   0; Mismatches 94; Indels   6; Gaps   1;

Qy   1 ATGAAGGGTCCCCGTCCAGCTCCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCCAGGTGTCAGCCATGT 60
        |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAGGGGTCCCCGCTCCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGTCAGCCATGT 60

```
Db    432  ATGAGGCTGACTATTACTGTCAGGCGTGGACAGCARCACTG------KGGTATTCGGCG   485
                                                                        
Qy    362  GAGGGACCCGGTGACCGTCCTAGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC   421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486  GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC  545

Qy    422  CGCCCCTCCTTCGGAGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT  481
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546  CGCCCCTCCTTCGGAGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT  605

Qy    482  TCTACCCGGGAGCCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606  TCTACCCGGGAGCCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  665

Qy    542  TGGAGACCACCACCACCCTCCAAACAAAGCAACACAACAAGCAACACAGTACGGGCCAGCAGCTACCTGA  601
           |||||||||||||||||||||||||||||||||||||:||||||||||||||:||||||
Db    666  TGGAGACCACCACCACCCTCCAAACAAAGCAACACAACAAGCAACACAGTACGGGCCAGCAGCTAYCTGA  725

Qy    602  GCCTGAGCCTGAGCAGTGGAAGTCCCAGAAGCTACAGCTGCCAGGTCACGCATGAAG  661
           ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db    726  GCCTGAGCCTGAGCAGTGGAAGTCCCACARAAGCTACAGCTACAGCTGCCAGGTCACGCATGAAG  785

Qy    662  GGAGCACCGTGGAGAGACAGTGCCCCTACAGAATGTTCAT  703
           |||||||||||||||||||||||||||||||||||||||
Db    786  GGAGCACCGTGGAGAGACAGTGGGCCCCTACAGAATGTTCAT  827
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RESULT 11
AAS83486
ID   AAS83486 standard; cDNA; 841 BP.
XX
AC   AAS83486;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #19290.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG19299.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 19290; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
```

```
PF    07-JUN-2001; 2001WO-US18569.
XX
PR    07-JUN-2000; 2000US-209467P.
XX
PA    (HUMA-) HUMAN GENOME SCI INC.
XX
PI    Birse CE, Rosen CA;
XX
DR    WPI; 2002-147878/19.
DR    P-PSDB; ABP41361.
XX
PT    Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT    useful in the prevention, treatment and diagnosis of cancer (e.g.
PT    ovarian cancer), immune disorders, cardiovascular disorders and
PT    neurological diseases -
XX
PS    Claim 1; SEQ ID No 318; 2922pp; English.
XX
CC    The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC    ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC    encompasses polypeptides 90% identical and polynucleotides 95% identical
CC    to the sequences of the invention. The invention additionally relates to
CC    recombinant vectors and host cells comprising human ovarian antigen
CC    polynucleotides, antibodies against human ovarian antigens, and the use
CC    of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC    treating, prognosing or preventing various ovary and/or breast-related
CC    disorders. Such conditions include ovarian cancer and breast cancer, and
CC    metastatic tumours of ovarian or breast origin, reproductive system
CC    disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC    polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC    disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC    shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC    vaginitis), immune disorders (e.g., congenital and acquired
CC    immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC    blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC    respiratory disorders, neurological disorders, gastrointestinal disorders
CC    and urinary system disorders. Ovarian antigen polypeptides and
CC    polynucleotides may also be used in screening for compounds which
CC    modulate ovarian antigen expression or activity. The polynucleotides may
CC    further be used for gene therapy, chromosome mapping, in the
CC    identification of individuals and in forensic analysis, and the
CC    polypeptides may be used as food additives or to prepare antibodies
CC    useful in disease diagnosis, drug targeting and phenotyping. The present
CC    sequence represents cDNA encoding a human ovarian antigen of the
CC    invention.
CC    Note:The sequence data for this patent did not form part of the printed
CC    specification, but was obtained in electronic format directly from WIPO
CC    at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ    Sequence 1027 BP; 253 A; 306 C; 264 G; 192 T; 12 other;
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Query Match     74.8%;  Score 527.6; DB 24;  Length 1027;
Best Local Similarity  89.7%;  Pred. No. 1.2e-122;
Matches  576;  Conservative  3;  Mismatches  57;  Indels  6;  Gaps  1;

Qy     62  CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACACGGCCAGGATCA  121
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||| ||
Db    192  CCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACACAGCAGCCAGCATCA  251

Qy    122  CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC  181
           ||||| | |||||||||||||||||||  |||||||||||||||||||||||||||||
Db    252  CCTGCTCTGGAGATAAATTGGGGGATAAAATATGCTTGCTGGTATCAGCAGAAGCCAGGCC  311

Qy    182  GGGCCCCTATACTGGTCATCTATGATGATAGTAGTGACCGGCCCTCAGGGATCCCTGAGGGAT  241
           |||||||||||||||||||||||||| |  ||||||||||||||||||||||||||||
Db    312  AGTCCCCTGTGCTGGTCATCTATCATCAAGATAACAASCGGCCCTCAGGGATCCCTGAGCGAT  371

Qy    242  TCTCTGGCTCCAAATCAGGAACACACCGACCATCAACGGGGTCGAGGGCCGGGG  301
           ||||| |||||||||||||||||||||||||||||||||||||||||||| ||
Db    372  TCTCTGGCTCCAACTCTGGGACACAGCACCACTCTGACCATCAGCGGACCCAGGCTATGG  431

Qy    302  ATGAGGCTGACTATTACTGTCAGGCGTGGGACAGGGCTAGTGATCATCCGGCTCTTCGGAG  361
           ||||||||||||||||||||||||||| |||  | || |  |
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CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have application in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note:The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 841 BP; 191 A; 273 C; 224 G; 153 T; 0 other;

Query Match             74.3%;  Score 524;  DB 23;  Length 841;
Best Local Similarity   89.7%;  Pred. No. 9.3e-122;
Matches  576;  Conservative    0;  Mismatches  60;  Indels   6;  Gaps    1;

Qy     62 CCTATGAACTGACTCAGCCACCCTCCGGTCAGTGTCCCCAGGACAGACGGCCAGGATCA 121
          ||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db     82 CCTATGAGCTGACTCAGCCACCCTCCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCA 141

Qy    122 CCTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC 181
          ||| ||||| | |||| |  |||| | |||||||||||||||||||||||||||||||
Db    142 CCTGCTCTGGAGATACATTGGGGAGTATAAATATGCTTGCTGGTATCAGCAGAAGCCAGGCC 201

Qy    182 GGGCCCCTATACTGGTCATCTATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 241
          ||  |||| | || | ||| | ||  |||||||||||||||||||||||||||||||
Db    202 ACTCCCCTGTCTGGTCATCTTCAAGATAGCAAGCGGCCCTCAGGGATCCCTGACGAT 261

Qy    242 TCTCTGGCTCCAAATCAGGGAAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGG 301
          ||||||| ||| |||||||||||| |||| |||||||||||||||||||||| ||||
Db    262 TCTCTGGCTCCAACTCTGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGG 321

Qy    302 ATGAGGCTGACTATTACTGTCAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
          |||||||||||||||||||||||||||  |||| |  ||  |||||||||||||||
Db    322 ATGAGGCTGACTATTACTGTCAGGGTGGGACAGCAGCACTG------CGGTATTCGGCG 375

Qy    362 GAGGGACCCGGTGACCGTCCTAGGTCAGCCAAGGTGCCCCCTCGGTCACTCTGTTCC 421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376 GAGGGACCAAGCTGACCGTCCTAGGTCAGCCAAGGTGCCCCCTCGGTCACTCTGTTCC 435

Qy    422 CGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGGTGTGTCTCATAAGTGACT 481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 CGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGGTGTGTCTCATAAGTGACT 495

Qy    482 TCTACCCGGGAGCCGTGACAGTGGCCTGAAAGGCCAGATAGCAGCCCCGTCAAGGGCGGAG 541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 TCTACCCGGGAGCCGTGACAGTGGCCTGAAAGGCGAAGGCAGCAGCCCCGTCAAGGGCGGGAG 555

Qy    542 TGGAGACCACCACCCTCCAAACACAAGCAACAACAGTACGGGCCAGCAGCTACCTGA 601
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 TGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGGGCCAGCAGCTATCTGA 615

Qy    602 GCCTGAGCGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCGTGCCAGGTCACGCATGAAG 661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    616 GCCTGAGCGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCGTGCCAGGTCACGCATGAAG 675

Qy    662 GGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 703
          |||||||||||||||||||||||||||||||||||||||||
Db    676 GGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 717

RESULT 12
ABK28671
ID   ABK28671 standard; cDNA; 904 BP.
XX
AC   ABK28671;
XX
DT   09-APR-2002  (first entry)
XX
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DE   Human cDNA encoding secreted potein SECP38.
XX
KW   Human; ss; gene; SECP; antinflammatory; cytostatic; cardiant;
KW   immunosuppressive; antiviral; anti-HIV; antiarthritic; antirheumatic;
KW   muscular active general; anticonvulsant; nootropic; neuroprotective;
KW   antiallergic; hypotensive; cardiovascular disorder; atherosclerosis;
KW   hypertension; myocardial infarction; autoimmune disorder;
KW   inflammatory disorder; AIDS; acquired immunodeficiency syndrome;
KW   allergy; rheumatoid arthritis; cell proliferative disorder; cancer;
KW   developmental disorder; Duchenne muscular dystrophy;
KW   neurological disorder; epilepsy; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200198353-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US19862.
XX
PR   20-JUN-2000; 2000US-212890P.
PR   23-JUN-2000; 2000US-213466P.
PR   27-JUN-2000; 2000US-214601P.
PR   31-JUL-2000; 2000US-222372P.
PR   08-SEP-2000; 2000US-231435P.
PR   15-SEP-2000; 2000US-232889P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Hillman JL,  Tang YT,  Yue H,  Elliott VS,  Tribouley CM,  Lee EA;
PI   Ramkumar J,  Lal P,  Xu Y,  Warren BA,  Hafalia AJA,  Baughn MR;
PI   Azimzai Y,  Batra S,  Burford N,  Yao MG,  Nguyen DB,  Lu DAM;
PI   Walia NK,  Gandhi AR,  Au-Young J,  Patterson C;
XX
DR   WPI; 2002-090431/12.
DR   P-PSDB; AAU82012.
XX
PT   Forty four human secreted proteins (referred to as SECP-1 to SECP-44),
PT   useful in the diagnosis, treatment and prevention of cardiovascular
PT   (e.g. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and
PT   cell proliferative disorders -
XX
PS   Claim 5; Page 190; 195pp; English.
XX
CC   The invention relates to forty four human secreted proteins (referred to
CC   as SECP-1 to SECP-44) and the nucleic acids encoding them. Also
CC   included are a host cell transformed with the nucleic acid, a
CC   transgenic animal comprising the nucleic acid, an anti-SECP
CC   antibody, use of the SECP proteins in isolating agonists and antagonists
CC   of SECP activity and a method of isolating compounds which alter the
CC   expression of the SECP nucleic acid. The SECP polynucleotides and
CC   polypeptides are useful in the diagnosis, treatment and prevention of
CC   cardiovascular (e.g. atherosclerosis, hypertension, myocardial
CC   infarction), autoimmune/inflammatory (e.g. acquired immunodeficiency
CC   syndrome (AIDS), allergies, rheumatoid arthritis), cell proliferative
CC   (e.g. cancer), developmental (e.g. Duchenne and Becker muscular
CC   dystrophy), and neurological (e.g. epilepsy, Alzheimer's disease)
CC   disorders. Numerous other examples of each disorder are given in the
CC   specification. The present sequence is a cDNA encoding a SECP protein.
XX
SQ   Sequence 904 BP; 225 A; 281 C; 231 G; 167 T; 0 other;

Query Match             73.9%;  Score 520.8;  DB 24;  Length 904;
Best Local Similarity   84.0%;  Pred. No. 6e-121;
Matches  588;  Conservative    0;  Mismatches 112;  Indels   0;  Gaps    0;

Qy      4 AGGGTCCCCGCTCAGCTCCCGGGGGCTCCGCGTCCTCGGCTCCAGTCCGCACGATGTGCC 63
          ||||||||||||||||||||| || |||||||||||||||||||||||||||
Db     54 ATGGGCTTGGACCCCTGTCCTGCTCCCCCCTCCACTTTCTGCACAGTCTCTGAGGCCTCC 113

Qy     64 TATGAACTGACTCAGCCACCCTCCGGTGTGCAGTGTCAGTGCCAGGATCACC 123
          ||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db    114 TATGAGCTGACAGCAGCCACCCCCTGGTGTGTCCCCAGGACAAACGGCCCAGGATCACC 173
```

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XX
DR   WPI; 2001-451939/48.
DR   P-PSDB; AAU14412.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Claim 1; Page 695; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human
CC   proteins or their active domains. The polypeptides, polynucleotides and
CC   antibodies raised against the polypeptides are used in a method of
CC   treatment of a mammal and prevention of disorders caused by the aberrant
CC   protein expression or activity.  The polypeptides can be used as
CC   molecular weight markers, food supplements, and in antibody production.
CC   The polypeptides are used to identify compounds which bind to the
CC   polypeptides. Polynucleotides of the invention are used as probes and
CC   primers, for sequencing, for chromosome or gene mapping, in the
CC   production of recombinant proteins, and in generating anti-sense DNA or
CC   RNA and in gene therapy.  Polypeptides of the invention can be used to
CC   target drugs to a tumour, in assays to determine biological activity, to
CC   raise antibodies/elicit an immune response, to determine quantitative
CC   protein levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   graft-versus-host disease, eczema, haemophilia, thrombosis,
CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence encodes a protein of the invention.
XX
SQ   Sequence 869 BP; 164 A; 219 C; 272 G; 214 T; 0 other;

Query Match        73.8%;   Score 520.4;  DB 22;  Length 869;
Best Local Similarity  89.3%;   Pred. No. 7.4e-121;
Matches 573;  Conservative   0;  Mismatches  66;  Indels   3;  Gaps   1;

Qy   62 CCTATGAACTGACTCAGCCACCCTCGGTCAGTGTCCCAGGACAGACGGCCAGGATCA 121
        ||||| || ||||||||||||||| |||| |||||||||||||||| ||  ||||| |
Db  789 CCTATGAGTTGACTCAGCCACCCTCAGTGTCCGTGTCCCAGGACACAGCCAGCATCA 730

Qy  122 CTGTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC 181
        | || |||| ||| |||| ||| |||| |||||| | |||| |||| |||||| || | |
Db  729 CCTGCTCTGGAGATAACCTGGCAATAAATATGTTGCCTGGTATCAACAGGAGGCAGGGCC 670

Qy  182 GGGCCCCTATACTGTCATCTATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 241
         || ||||| | |||||| || || |||| | |||||||||| || ||||||||||||
Db  669 AGTCCCCTGTGTTGGTCATTTATCAAGATGACAAGCCGGCCCTCAGAGATCCCTGAGCGAT 610

Qy  242 TCTCTGGCTCCAAATCAGGGAACCACCCTGACCATCAACGGGGTCGAGGCCGGGGG 301
        |||||||||||| ||| ||||| ||| | |||||||||  | | |  ||   || |
Db  609 TCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCACGCGGGACCCAGGCTATGG 550

Qy  302 ATGAGGCTGACTATTACTGTCAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
        ||||||||||| ||||||||||| | ||||||   |  |||||  |  |  |  |||| |
Db  549 ATGAGGCTGATTATTACTGTCAGGCGTGGGACAG---CAGCACTGCTGTGATGTTCGGCG 493

Qy  362 GAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCGTTCC 421
        |||||||| | ||||||||||||||||||||||||||||||| |||||||||||||||
Db  492 GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCGGTCACTCGTTCC 433

Qy  422 CGCCCTCCCTGAGGAGCTTCAAGCCAACAAGGCCACAAGGCCACCACTCGGTGTCTCATAAGTGACT 481
        |||||||||||||||||||||||||||||||||||| |||| ||||||||||||| |||||||||||
Db  432 CGCCCTCCCTGAGGAGCTTCAAGCCAACAAGGCCACCACTCGGTGTGTCTCATAAGTGACT 373

Qy  482 TCTACCCGGAGCCGTGACAGTGGCCTGAAGGCAGCGATAGCAGCCCCGTCAAGGCGGGAG 541
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  372 TCTACCCGGAGCCGTGACAGTGGCCTGAAGGCAGCGATAGCAGCCCCGTCAAGGCGGGAG 313
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Qy  124 TGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGCGG 183
        |||  |    ||   ||  |||  ||| || | |||||||||||||||||| ||  ||||
Db  174 TGCTCTGGAGATGCATTGCCAAAAAAATATGCTTATTGGTACCAGCAGAAGTCAGGCCAG 233

Qy  184 GCCCCTATACTGTCATCTATGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGATTC 243
        |||||| | | ||||| |||||||| |  |  | ||||||| |||||||||||| | ||||
Db  234 GCCCCTGTGTGGTCATCTATGAGGACAACAAACGACCCTCCGGGATCCCTGAGAGATTC 293

Qy  244 TCTGGCTCCAAATCAGGGAACCACCGGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
        |||||||||| |||||||||  ||| | | ||| |||| |||||| |  ||   |   |||
Db  294 TTTGGCTCCAGCTCAGGGACAATGGCCACCTTGACTATCAGTGGGGCCCAGGTGGAGGAT 353

Qy  304 GAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA 363
        |||||||||| | ||||| | || |||||||||   | || ||  |  |  |  ||| |||
Db  354 GAGGCTGACTACTACTGTTTACTCAACAGACAGCAGCAGTGGTAATGATAGGGTGTTCGGCGGA 413

Qy  364 GGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCCCG 423
        |||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  414 GGGACCAAGCTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCCTCGGTCACTCGTTCCCA 473

Qy  424 CCCTCCCTGAGGAGCTTCAAGCCAACAAGGCCACAAGGCCACCACTGGTGTCTCATAAGTGACTTC 483
        ||||||||||||||||||||||||||||||||||| |||| ||||||||||| ||||||||||||||
Db  474 CCCTCCCTGAGGAGCTTCAAGCCAACAAGGCCACCACTGGTGTGTCTCATAAGTGACTTC 533

Qy  484 TACCCGGAGCCGTGACAGTGGCCTGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG 543
        ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  534 TACCCGGAGCCGTGACAGTGGCCTGAAGGCAGCAGATAGCAGCCCCGTCAAGGCGGGAGTG 593

Qy  544 GAGAGCCACCACCCCTCCAAACAAAGCAACAACAGTACGCGGCCAGCAGCTACCTGAGC 603
        ||||||||||||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db  594 GAGAGCCACCACCACCCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGC 653

Qy  604 CTGAGCGCCTGAGCAGTGGAAGTCCCACAGAAAGCTACAGCTGCCAGTCACGCATGAAGGG 663
        ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  654 CTGAGCGCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCTGCCAGTCACGCATGAAGGG 713

Qy  664 AGCACCGTGGAAGAACAGTGGCCCCTACAGAATGTTCAT 703
        |||||||||||||||||||||||||||||||||||||||
Db  714 AGCACCGTGGAAGAACAGTGGCCCCTACAGAATGTTCAT 753

RESULT 13
AAS22717/c
ID   AAS22717 standard; cDNA; 869 BP.
XX
AC   AAS22717;
XX
DT   24-OCT-2001   (first entry)
XX
DE   Human cDNA encoding a novel human protein #283.
XX
KW   Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02623.
XX
PR   25-JAN-2000; 2000US-0491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
```

SQ   Sequence 791 BP; 183 A; 252 C; 208 G; 148 T; 0 other;

     Query Match   73.2%; Score 516; DB 23; Length 791;
     Best Local Similarity   88.9%; Pred. No. 9.2e-120;
     Matches 571; Conservative   0; Mismatches   65; Indels   6; Gaps   1;

Qy   62 CCTATGAACTGACTCAGCCACCCTCCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCA 121
           ||||||| ||||||||||||||||| ||||| ||||||||||||||||| |||||| ||
Db   68 CCTATGAGTTGACTCAGCCACCCTCAGTGTCCGTGTCCCAGGACAGACAGCCAGCATCA 127

Qy   122 CCTGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGCGC 181
           |||| || |||| | | |||| |||||| || |||| | |||||||||||||| ||||
Db   128 CCTGCTTTGGAGATAAATTGGGTGATAAATATTCTTCGTGGTATCAGCAGAAGCCGGGCC 187

Qy   182 GGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCCTCAGGGATCCCTGAGCGAT 241
           ||| ||||||||||||| | ||| | |||| |||||||||||||||||||||||||||| |
Db   188 AGTCCCCTCTACTGGTCCTGTATCAAGATACCAACCGGCCCCTCAGGGATCCCTGAGCGAT 247

Qy   242 TCTCTGGCTCCAAATCAGGGAACACCGCCCCTGACCATCACGGGGTCGAGGCCCGGGG 301
           ||||||||||||| || |||||||| || ||| |||||| || | |||| |||||| |
Db   248 TCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGAGACCCAGGCTATGG 307

Qy   302 ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
           |||||||||||||||||||||||| |||||||| | | || ||||||||||| |
Db   308 ATGAGGGTGACTATTACTGTCAGGCGTGGGAC------AGTAACACTGTGGTCTTCGGCG 361

Qy   362 GAGGGACCCAGGCTGACCGTCCTAGTCAGCCCAAGGCTGCCCCCTCCGGTCACTCTGTTCC 421
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   362 GAGGGACCAAGCTGACCGTCCTAGTCAGCCCAAGGCTGCCCCCTCCGGTCACTCTGTTCC 421

Qy   422 CGCCCTCCTCTGAGGAGCTTCAAGCCAACAGAGGCCACACTGGTGTGTCATAAGTGACT 481
           ||||||||||||||||||||||||||||||| ||| | | ||||||||||||||||
Db   422 CGCCCTCCTCTGAGGAGCTTCAAGCCAACAGCAACAAGCCACACTGGTGTGTCATAAGTGACT 481

Qy   482 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 541

Qy   542 TGGAGACCACCACACCCTCCAAACAAAGCAACAAGTACGCGGCCAGCTACCTGA 601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542 TGGAGACCACCACACCCTCCAAACAAAGCAACAAGTACGCGGCCAGCTACCTGA 601

Qy   602 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAG 661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   602 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAG 661

Qy   662 GGAGCACCGTGGAGAAGAGACAGTGGCCCCTACAGAATGTTCAT 703
           ||||||||||||||||||||||||||||||||||||||||||||
Db   662 GGAGCACCGTGGAGAAGAGACAGTGGCCCCTACAGAATGTTCAT 703

RESULT 15
AAS22777
ID   AAS22777 standard; cDNA; 1825 BP.
XX
AC   AAS22777;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human cDNA encoding a novel human protein #343.
XX
KW   Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX

Qy   542 TGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCGGCCAGCCAGCTACCTGA 601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   312 TGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCGGCCAGCCAGCTACCTGA 253

Qy   602 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAG 661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   252 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGTCACGCATGAAG 193

Qy   662 GGAGCACCGTGGAGAAGAGACAGTGGCCCCTACAGAATGTTCAT 703
           |||||||||||||||||||||||||||||||||||||||||||||
Db   192 GGAGCACCGTGGAGAAGAGACAGTGGCCCCTACAGAATGTTCAT 151

RESULT 14
AAS87271
ID   AAS87271 standard; cDNA; 791 BP.
XX
AC   AAS87271;
XX
DT   13-FEB-2002 (first entry)
XX
DE   DNA encoding novel human diagnostic protein #23075.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG23084.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity
PT   -
XX
PS   Claim 1; SEQ ID No 23075; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX

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PD    02-AUG-2001.
XX
PF    25-JAN-2001; 2001WO-US02623.
XX
PR    25-JAN-2000; 2000US-0491404.
XX
PA    (HYSB-) HYSEQ INC.
XX
PI    Tang YT, Liu C, Drmanac RT;
XX
DR    WPI; 2001-451939/48.
DR    P-PSDB; AAU14472.
XX
PT    Isolated polypeptides useful for treating anti-inflammatory diseases,
PT    nervous system disorders, and for regenerating bone and cartilage -
XX
PS    Claim 1; Page 721-722; 894pp; English.
XX
CC    The invention relates to polynucleotides encoding novel human
CC    proteins or their active domains. The polypeptides, polynucleotides and
CC    antibodies raised against the polypeptides are used in a method of
CC    treatment of a mammal and prevention of disorders caused by the aberrant
CC    protein expression or activity.  The polypeptides can be used as
CC    molecular weight markers, food supplements, and in antibody production.
CC    The polypeptides are used to identify compounds which bind to the
CC    polypeptides. Polynucleotides of the invention are used as probes and
CC    primers, for sequencing, for chromosome or gene mapping, in the
CC    production of recombinant proteins, and in generating anti-sense DNA or
CC    RNA and in gene therapy.  Polypeptides of the invention can be used to
CC    target drugs to a tumour, in assays to determine biological activity, to
CC    raise antibodies/elicit an immune response, to determine quantitative
CC    protein levels, as tissue markers, and to isolate receptors or ligands.
CC    Polypeptides of the invention may also be useful in treating platelet
CC    disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC    ligament and/or nerve tissue, wound healing, treating burns, promoting
CC    the proliferation, differentiation and survival of stem cells, as a
CC    contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC    Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC    sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC    fungal infection or from autoimmunity, cancer, allergy, asthma,
CC    graft-versus-host disease, eczema, haemophilia, thrombosis,
CC    anti-inflammatory diseases, nervous system disorders, and infection.
CC    The present sequence encodes a protein of the invention.
XX
SQ    Sequence 1825 BP; 361 A; 509 C; 560 G; 395 T; 0 other;

Query Match     73.0%;  Score 515;  DB 22;  Length 1825;
Best Local Similarity   87.4%;  Pred. No. 2e-119;
Matches  576;  Conservative   0;  Mismatches   80;  Indels    3;  Gaps    1;

Qy  45 CCCAGGTGCACGATGTGCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGG 104
        ||||||||||| |||||||||||||||||||||||||||||| |||||| ||||||||||
Db  73 CACAGGGGCCCGTGGCCTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGG 132

Qy 105 ACAGACGGCCAGGATCACCTGTGGGGAGCAACAGTAGAAATGAATATGTCCACTGGTA 164
        ||||| ||||| |||||||| ||||||||||| |  |||||  |||| || ||||||||
Db 133 ACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGATAAAATTGCTTGCTGGTA 192

Qy 165 CCAGCAGAAGCCAGCGCGGAGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTC 224
        ||||  |||| |||||   ||||||| |||| |||  || ||| ||||||||||| |||||
Db 193 TCAGCTGAAGCCAGGCGGCCAGTCCCCTTTAGTGGTCATCCATCAAGATACCAAGCGGCCCTC 252

Qy 225 AGGGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAA 284
        ||||||||| |||||||||||||||||  ||||||||| ||| || ||||| ||||||
Db 253 AGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAG 312

Qy 285 CGGGGTCGAGGCCGGGATGAGGCCGACTATTACTGTCAGGTTGGGACAGGGCTAGTGA 344
        ||||| ||||| |||||| |||||| | |||||||||| |||  || |||||||| |
Db 313 CGGGACCCAGGCCTATGATGAGGCTGACTATTACTGTCAGCCGTGGGACAG--CAGCTC 369

Qy 345 TCATCCGGTCTTCGGAGGAGGGACCCCGGGTGACCGTCCTAGGTGACCTCTAGGTCGCCCC 404
        |||||||  ||  || ||||||||| || || |||||||| ||||| ||| |||  ||||
Db 370 TTATGTGGCGTTCGGCGGAGGGACCAAGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCC 429
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Qy 405 CTCGGTCACTCTGTTCCCGCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGT 464
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 430 CTCGGTCACTCTGTTCCCGCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGT 489

Qy 465 GTGTCTCATAAGTGACTTCTACCCGGAGCCGTGACAGTGGCCTGGACAGGCAGATAGCAG 524
        ||||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||||
Db 490 GTGTCTCATAAGTGACTTCTACCCGGAGTCGTGACAGTGGCCTGGACAGTGGCAGATAGCAG 549

Qy 525 CCCCGTCAAGGCGGGAGTGGAGACCACACACCCTCCAAACAAAGCAACAACAAGTACGC 584
        ||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||||
Db 550 CCCCGTCAAGGCGGGAGTGGAGACCACACACCCTCCAAACAAAGCAACAACAAGTACGC 609

Qy 585 GGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGAAGTACAGCTG 644
        ||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db 610 GGTCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCAGAAGTACAGCTG 669

Qy 645 CCAGGTCACCCATGAAGGAGCACCGTGGAGAAGACACGTGGCCCCTACAGAATGTTCAT 703
        ||||||||||||||||||||||||||||||||||||| ||||||||||||||| || |
Db 670 CCAGGTCACCCATGAAGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATATTTAT 728

Search completed: April  5, 2003, 20:19:14
Job time : 196.478 secs
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OM nucleic - nucleic search, using sw model

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Run on: April 5, 2003, 19:13:05 ; Search time 2212.18 Seconds
(without alignments)
9274.790 Million cell updates/sec

Title: US-09-758-173-1
Perfect score: 705
Sequence: 1 ATGAGGGTCCCGCTCAGCT.........CCCCTACAGAATGTTCATGA 705

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	705	100.0	705	6	AR108862	AR108862 Sequence
2	585.2	83.0	702	6	AR135374	AR135374 Sequence
3	574.4	81.5	820	9	AB064177	AB064177 Homo sapi
4	571.2	81.0	901	9	BC028090	BC028090 Homo sapi
5	569.8	80.8	803	9	HSIGVL022	X57812 Human rearr
6	561.8	79.7	747	9	HSIGVL031	X57821 Human rearr
7	542.8	77.0	648	9	HSA309319	AJ309319 Homo sapi
8	540.2	76.6	711	6	AR108866	AR108866 Sequence
9	538	76.3	790	9	AB064230	AB064230 Homo sapi
10	534.4	75.8	826	9	AB064174	AB064174 Homo sapi
11	529.6	75.1	824	9	AB064176	AB064176 Homo sapi
12	526.4	74.7	813	9	AB064167	AB064167 Homo sapi
13	525.2	74.5	895	9	BC022823	BC022823 Homo sapi
14	524	74.3	725	9	HSIGVL002	X57802 Human rearr
15	522.4	74.1	890	9	BC032452	BC032452 Homo sapi
16	522	74.0	788	9	AB064168	AB064168 Homo sapi
17	520.8	73.9	904	6	AX402510	AX402510 Sequence
18	517	73.3	1154	9	BC007782	BC007782 Homo sapi
19	516.8	73.3	821	9	AB064179	AB064179 Homo sapi
20	516	73.2	791	9	HSIGVL028	X57818 Human rearr
21	514.4	73.0	839	9	HSIGVL026	X57816 Human rearr
22	512	72.6	798	9	AB064184	AB064184 Homo sapi
23	512	72.6	872	6	E01593	E01593 cDNA encodi
24	512	72.6	872	6	HUMIGLAM2	M18645 Human Ig re
25	511	72.5	654	6	AX232564	AX232564 Sequence
26	510.4	72.4	789	9	AB064210	AB064210 Homo sapi
27	510.4	72.4	795	9	AB064209	AB064209 Homo sapi
28	508.8	72.2	737	9	HSIGVL023	X57813 Human rearr
29	508.8	72.2	795	9	AB064213	AB064213 Homo sapi
30	507.2	71.9	794	9	AB064185	AB064185 Homo sapi
31	507.2	71.9	794	9	AB064214	AB064214 Homo sapi
32	507.2	71.9	807	9	AB064165	AB064165 Homo sapi
33	506	71.8	780	9	HSIGVL011	X57810 Human rearr
34	504	71.5	806	9	HSIGVL005	X57805 Human rearr
35	501.2	71.1	811	9	AB064173	AB064173 Homo sapi
36	499	70.8	788	9	AB064211	AB064211 Homo sapi
37	497.6	70.6	796	9	AB064182	AB064182 Homo sapi
38	496	70.4	790	9	AB064233	AB064233 Homo sapi
39	495.8	70.3	801	9	AB064183	AB064183 Homo sapi
40	495.2	70.2	863	6	AX402489	AX402489 Sequence
41	491.2	69.7	791	9	AB064181	AB064181 Homo sapi
42	490	69.5	886	6	AX400073	AX400073 Sequence
43	488	69.2	793	9	AB064180	AB064180 Homo sapi
44	486.4	69.0	788	9	AB064212	AB064212 Homo sapi
45	481.6	68.3	790	9	AB064169	AB064169 Homo sapi

ALIGNMENTS

RESULT 1
AR108862
LOCUS   AR108862   705 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6113898.
ACCESSION   AR108862
VERSION   AR108862.1 GI:12825138
KEYWORDS
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 705)
AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE   Human B7.1-specific primatized antibodies and transfectomas
            expressing said antibodies
JOURNAL   Patent: US 6113898-A 1 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

Right panel

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FEATURES             Location/Qualifiers
     source          1..702
                     /organism="unknown"
BASE COUNT    151 a   217 c   207 g   127 t
ORIGIN

Query Match          83.0%;   Score 585.2;  DB 6;  Length 702;
Best Local Similarity 89.6%;  Pred. No. 6.6e-133;
Matches 629;  Conservative 0; Mismatches 73;  Indels 73;  Gaps 0;

Qy    4 AGGGTCCCGCTCAGCTCCTGGGGCTCCTGGCTCCTGCTCCCAGGTGCACGATGTGCC   63
          ||||||||||||||| ||||||||    |||||||||||||||||||||||
Db    1 ATGGCCTGGGCTCTGCTGCTCCTCGGCGTCCTTCTCCTCACTTACAGACTCTGCGGCCTCC  60

Qy   64 TATGAACTGACTCAGCCACCCTCGGTGTCCAGTGCCCAGGACAGACGGCCAGGATCACC  123
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Db   61 TATGAGTTGAGTCAGCCTGCGTCCAGTGTCCCGTGCCCAGGACAGACGCCGGTTCACC  120

Qy  124 ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGCGGG  183
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Db  121 TGTGGGGGAGACAACGTTGGAAGGAAAAGTGTACAGTGGTACCAGCAGAAGCCACCAGCAG  180

Qy  184 GCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCTGAGCGATTC  243
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Db  181 GCCCCTGTCGTGGTCATCTATGATGACAGCGAACGGCCCTCAGGGATCCCTGCGCGATTC  240

Qy  244 TCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCAGGTCGAGGCCGGGGAT  303
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Db  241 TCTGGCTCCAACTCAGGGAACACCGCCACCCTGACCATCAGCGGGGTCGAGGCCGGGGAT  300

Qy  304 GAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA  353
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Db  301 GAGGCTGACTATTACTGTCAGGTGTGGGACAGTGCTGATCATTGGGTCTTCGGTTCGGA  360

Qy  364 GGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCCCG  423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG  420

Qy  424 CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC  483
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Db  421 CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC  480

Qy  484 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG  543
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG  540

Qy  544 GAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTG  603
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Db  541 GAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTG  600

Qy  604 CTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGG  663
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Db  601 CTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGG  660

Qy  664 AGCACCGTGGAGAAGACAGTGCCCCTCACAGAATGTTCATGA  705
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Db  661 AGCACCGTGGAGAAGACAGTGCCCCTCACAGAATGTTCATGA  702
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Left panel

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BASE COUNT    162 a   214 c   207 g   122 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3e-162;
Matches 705;  Conservative 0; Mismatches 0; Indels 0;  Gaps 0;

Qy    1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGGCTCCTGCTCCCAGGTGCACGATGT  60
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Db    1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGGCTCCTGCTCCCAGGTGCACGATGT  60

Qy   61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCCAGTGCCCAGGACAGACGGCCAGGATC  120
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Qy  121 ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGCG  180
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Qy  181 CGGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCTGAGCGA  240
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Qy  241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGA  300
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Qy  301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGA  360
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Qy  361 GGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCGTCTGTTC  420
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Qy  421 CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC  480
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Db  421 CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC  480

Qy  481 TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGA  540
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Db  481 TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGA  540

Qy  541 GTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTG  600
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Db  541 GTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTG  600

Qy  601 AGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA  660
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Db  601 AGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA  660

Qy  661 GGGAGCACCGTGGAGAGACAGTGCCCCTCACAGAATGTTCATGA  705
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RESULT 2
AR135374
LOCUS   AR135374   702 bp   DNA   linear   PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6136310.
ACCESSION   AR135374
VERSION   AR135374.1 GI:14476046
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 702)
AUTHORS   Hanna,N., Newman,R.Anthony, and Reff,M.Elliot.
TITLE   Recombinant anti-CD4 antibodies for human therapy
JOURNAL   Patent: US 6136310-A 5 24-OCT-2000;

RESULT 3
AB064177
LOCUS   AB064177   820 bp   mRNA   linear   PRI 02-JUL-2002
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L37.
ACCESSION   AB064177
VERSION   AB064177.1 GI:21669560
KEYWORDS   .
SOURCE   Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L37.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,

TITLE   Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
         Miura,K. and Kurosawa,Y.
         Construction and characterization of antibody libraries: isolation
         of therapeutic human antibodies and application to functional
         genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 820)
AUTHORS Kurosawa,Y.
TITLE   Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
         Comprehensive Medical Science, Fujita Health University;
         Kutsukake-cho, Toyoake 470-192, Japan
         (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT Please visit our web site
         URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES   Location/Qualifiers
     source   1..820
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                  /db_xref="taxon:9606"
                  /clone="L37"
                  /clone_lib="AIMS4"
                  /note="mixture of tissues:tonsils, umbilical cords,
                  peripheral blood and bone marrow"
     gene   1..820
                  /gene="IGL"
     CDS   1..>820
                  /gene="IGL"
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                  /db_xref="GI:21669561"
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                  GGNNIGSKSVHWYQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVBAG
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                  SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQ
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     sig_peptide 1..66
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                  /note="PelB signal peptide"

BASE COUNT   183 a   240 c   238 g   159 t
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Query Match   81.5%;   Score 574.4; DB 9;   Length 820;
Best Local Similarity   93.6%;   Pred. No. 2.9e-130;
Matches 599; Conservative   0; Mismatches 41;   Indels   0;   Gaps   0;

Qy   62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCA 121
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Db   68 CCTATGTGCTGACTCAGCCACCCTCCAGTGTCAGTGCCCAGGAAAGACGGCCAGGATTA 127

Qy 122 CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC 181
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Qy 182 GGGGCCCTATACTGGTCATCATGATGATGAGACGGGCCCTCAGGGATCCCTGAGGCGAT 241
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Db 188 AGGGCCCCGTGCTGGTCATCTATTATGATAGCGACCGGCCCTCAGGGATCCCTGAGGCGAT 247

Qy 242 TCTCTGGCTCCAAATCAGGGAACACCGGACCATCAACGGGGTCGAGGCCGGGG 301
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Db 248 TCTCTGGCTCCAACTCTGGGAACACGGGACCACCTGACCATCAGCAGGGTCGAAGCCGGGG 307

Qy 302 ATGAGGCTGACATTACTGTCAGGTGTGGGACAGGCCTAGTGATCATCCGGTCTTCCGGAG 361
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Qy 362 GAGGGACCCGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCGTTCC 421
         |||||| || | ||||||||||||||||| |||||||||||||||||||||||||||
Db 368 GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCCAAGCTGCCCCCTCGGTCACTCGTGTTCC 427

Qy 422 CGCCTCCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 481
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Db 428 CGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 487

Qy 482 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 541
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 488 TCTACCCGGGAGCCGTGACAGTGGCTTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 547

Qy 542 TGGAGACCACCACCCTCCAAACAACAAGCAACAACAAGTACGCGCCGCCAGCAGCTACCTGA 601
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Db 548 TGGAGACCACCACCCTCCAAACAACAAGCAACAACAAGTACGCGCCGCCAGCAGCTATCTGA 607

Qy 602 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGTACAGCTGCCAGTCACGCATGAAG 661
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Db 608 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGTACAGCTGCCAGTCACGCATGAAG 667

Qy 662 GGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC 701
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Db 668 GGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC 707

RESULT 4
BC028090
LOCUS   BC028090   901 bp   mRNA   linear   PRI 01-MAY-2002
DEFINITION Homo sapiens, clone MGC:40381 IMAGE:4184029, mRNA, complete cds.
ACCESSION   BC028090
VERSION   BC028090.1 GI:20380867
KEYWORDS   MGC.
SOURCE   Homo sapiens
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 901)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (08-APR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,
            Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
            Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
            Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
            Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 62 Row: k Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Similarity but not
            identity to protein.
FEATURES   Location/Qualifiers
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                     /note="Vector: pCMV-SPORT6"
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                     /codon_start=1

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BASE COUNT    221 a    283 c    237 g    160 t
ORIGIN

Query Match                81.0%;  Score 571.2; DB 9;  Length 901;
Best Local Similarity      90.8%;  Pred. No. 1.8e-129;
Matches 632; Conservative   0; Mismatches  58; Indels   6; Gaps    2;

Qy    11 CCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGCCTATGAAC  70
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Db    50 CCGTTCTCCTCCGGCCTCCTCTCACTG---CACAGGCTCTGTGACCTCCTATGTGC   106

Qy    71 TGACTCAGGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCACCTGTGGGG  130
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Db   107 TGACTCAGGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCAGGATTACCTGTGGGG  166

Qy   131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGCAGCCGGGGCCCCTA   190
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Db   167 GAAACAACATTGGAAGTAAAAGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCCTG   226

Qy   191 TACTGGTCATCTATGATGAGTAGT  250
         ||| |||| |||||||||| |||||||||||||||||||||||
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Qy   251 CCAAATCAGGGACACCGGCACCCTGACCATCAACGGGGTCGAGGCCCGGGATGAGGCTG   310
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Db   287 CCAACTCTGGGAACACGCGCACCCTGACCATCAGCAGGGTCGACGCGCGGGATGAGGCCG   346

Qy   311 ACTATTACTGTCAGTGTGGGACAGGGCTAGTGATCATCC---GGTCTTCGGAGGAGGGA  367
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Db   347 ACTATTACTGTCAGCTGTGGGATTAGTGAGTAGTGATCATCCCGGTCTTCGGCGGAGGGA  406

Qy   368 CCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCGCCCCT  427
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Qy   488 CGGAGCCGGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA  547
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Db   527 CGGGAGCCGGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA  586

Qy   548 CCACCACCCCTCCAAAACAACAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGA  607
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Qy   608 CGCCTGAGCAGTGGAAGTCCCACAGAAGCTCACGGTCACCAGTCACGCATGAAGGGAGCA  667
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Qy   668 CCGTGGAGAAGACAGTGGCCCCTACAGAAATGTTCAT   703
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Db   707 CCGTGGAGAAGACAGTGGCCCCTACAGAAATGTTCAT   742

RESULT 5
HSIGVL022
LOCUS       HSIGVL022              803 bp    mRNA       linear    PRI 04-NOV-1994
DEFINITION  Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION   X57812
VERSION     X57812.1  GI:33723
KEYWORDS  , Ig lambda light chain; immunoglobulin.
SOURCE      Homo sapiens
ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 803)
AUTHORS     Klobeck,H.G.
TITLE       Direct Submission
JOURNAL     Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
            Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
            Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE   2 (bases 347 to 393)
AUTHORS     Combriato,G. and Klobeck,H.G.
TITLE       V lambda and J lambda-C lambda gene segments of the human
            immunoglobulin lambda light chain locus are separated by 14 kb and
            rearrange by a deletion mechanism
JOURNAL     Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE     91257162
PUBMED      1904362
COMMENT     for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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                     /note="variable region; V(lambda)III"
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BASE COUNT    177 a    254 c    226 g    146 t
ORIGIN

Query Match                80.8%;  Score 569.8; DB 9;  Length 803;
Best Local Similarity      92.8%;  Pred. No. 3.9e-129;
Matches 596; Conservative   0; Mismatches  46; Indels   0; Gaps    0;

Qy    62 CCTATGAACTGACTCAGGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCA  121
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Db    68 CCTATGTGCTGACTCAGGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCAGGATTA  127

Qy   122 CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGCAGCCGGGGC  181
         |||||||||| ||||| |  || | | ||| ||||||||||||||||||||||  |||
Db   128 CCTGTGGGGGAAACAACATTGGAAGTAAAAGTGCACTGGTACCAGCAGAAGCCAGGCC  187

Qy   182 GGGCCCCTATACTGGTCATCTATGATGATGAGTAGTGATCATGATGAGTAGTGATCATC  241
         ||||||||| ||||||| || ||||||| || ||||||||||  ||||||| |||||
Db   188 AGGCCCCTGTGCTGGTCGTCTATGATGAGTAGTGATAGGCCACGGTCACCGGTCCCTGAGGAT  247
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Qy   242  TCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGG  301
          |||||||| |||  ||||||||||||||||||||||||||| ||||||||  ||||||||
Db   248  TCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGAACATCAGTCAGGGGTCGAAGCCGGGG  307

Qy   302  ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGCTAGTGATCATCCGGTCTTCGGAG  361
          |||||| ||||  |||||||||||||||||||||  |||||||||||||||||||||||||
Db   308  ATGAGGCCGCCTATTACTGTCAGGTGTGGGATAGTAGTAGTGATCATCGGTGGTATTCGGCG  367

Qy   362  GAGGGACCCGGGTGACCGTCCTAGGTGCAGCCAAGGCTGCCCCCTCGGTCACTCTGTTCC  421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368  GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC  427

Qy   422  CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT  481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428  CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT  487

Qy   482  TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488  TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  547

Qy   542  TGGAGACCACCACACCCTCCAAACAAGCAACAACAAGCAACAACAAGTACGCGGCAGCGAT  601
          |||||||||||||||||||||||        |||||||||||||||||||||||||||||
Db   548  TGGAGACCACCACACCCTCCAAACAGGCAACAACAAGTACGCGGCCAGCAGCTATCTGA  607

Qy   602  GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAG  661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   608  GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAG  667

Qy   662  GGAGCACCGTGGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  703
          ||||||||||||||||||||||||||||||||||||||||||
Db   668  GGAGCACCGTGGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  709
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```
RESULT 6
HSIGVL031
LOCUS      HSIGVL031        747 bp    mRNA    linear    PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION  X57821
VERSION    X57821.1   GI:33741
KEYWORDS   Ig lambda light chain; immunoglobulin.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 747)
AUTHORS    Klobeck,H.G.
TITLE      Direct Submission
JOURNAL    Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
           Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
           Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE  2  (bases 340 to 386)
AUTHORS    Combriato,G. and Klobeck,H.G.
TITLE      V lambda and J lambda-C lambda gene segments of the human
           immunoglobulin lambda light chain locus are separated by 14 kb and
           rearrange by a deletion mechanism
JOURNAL    Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE    91257162
PUBMED     1904362
COMMENT    for overlapping sequences see: X51754-55; J00252-54; M15641-42.
FEATURES            Location/Qualifiers
    source          1..747
                    /organism="Homo sapiens"
                    /isolate="individual ML"
                    /db_xref="taxon:9606"
                    /chromosome="22"
                    /clone="cML70"
                    /cell_type="B-cell"
                    /tissue_type="spleen"
                    /clone_lib="phage library cML"
    gene            1..747
                    /gene="immunoglobulin lambda light chain"
    mRNA            1..747
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    CDS             6..704
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                    /codon_start=1
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                    /db_xref="GI:33742"
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                    NIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEA
                    DYYCQVWDSSSDVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFY
                    PGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE
                    GSTVEKTVAPTECS"
    sig_peptide     6..62
                    /gene="immunoglobulin lambda light chain"
    misc_feature    63..384
                    /gene="variable region; V(lambda)III"
    misc_feature    347..384
                    /gene="J-segment"
    misc_feature    385..704
                    /gene="constant region"

BASE COUNT   171 a   230 c   211 g   135 t
ORIGIN
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Query Match         79.7%;  Score 561.8;  DB 9;  Length 747;
Best Local Similarity 93.1%;  Pred. No. 3.6e-127;
Matches  598;  Conservative  0;  Mismatches  41;  Indels  3;  Gaps  1;

Qy    62  CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGACACGGCCAGGATCA  121
          ||||| | ||||||||||||||||||||||||||||||||| | |||||||| ||||
Db    64  CCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGAAAGACCAGTATTA  123

Qy   122  CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCACTGGTACCAGCAGAAGCCAGCGC  181
          ||||||||||||| || || ||  ||  ||||||| |||||||||||||||||||| |||
Db   124  CCTGTGGGGGAAATAACATTGGAAGTAAAAGTGTGCACTGGTACCAGCAGAAGCCAGGCC  183

Qy   182  GGGCCCTATACTGTCTCATCTATGATGATAGTGATAGCGACCCCTGACCTCAGGATGCGAT  241
          |||||||  ||||||| ||| ||||||||||||||||||||||||||||| |||||||||
Db   184  AGGCCCTTGTCTGTCTCATCTATGATGATAGTGATAGGCACCCGGACCTCAGGATGCGAT  243

Qy   242  TCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGG  301
          |||||||||||||  ||| ||||| |||||||||| |||||| ||  |||||||||||||
Db   244  TCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGAACATCAGTCAGGGGTCGAAGCCGGGG  303

Qy   302  ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGCTAGTGATCATCCGGTCTTCGGAG  361
          |||||| | |||||||||||||||||||||  ||| |||||||||||  |||||||||||
Db   304  ATGAGGCCGCCTATTACTGTCAGGTGTGGGATAG---TAGTAGTGATGGTATTCGGCG  360

Qy   362  GAGGGACCCGGGTGACCGTCCTAGGTGCAGCCAAGGCTGCCCCCTCGGTCACTCTGTTCC  421
          |||||||| |  |||||||||||||||||||| |||||||||||||||||||||||||||
Db   361  GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC  420

Qy   422  CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT  481
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT  480

Qy   482  TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  541
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  540

Qy   542  TGGAGACCACCACACCCTCCAAACAGCAACAACAAGCAACAACAAGTACGCGGCAGCTACCTGA  601
          ||||||||||||||||||||||||| |||||||| ||||||||||||||||| ||||||||
Db   541  TGGAGACCACCACACCCTCCAAACAGCAACAACAAGTACGCGGCCAGCAGCTATCTGA  600

Qy   602  GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAG  661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAGCTACAGCTGCCAGGTCACGCATGAAG  660

Qy   662  GGAGCACCGTGGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  703
          |||||||||||||||||||||||||||||||||||||||||||
Db   661  GGAGCACCGTGGGAGAAGACAGTGGCCCCTACAGAATGTTCAT  702
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RESULT 7

```
HSA309319
LOCUS       HSA309319               648 bp    mRNA    linear   PRI 16-NOV-2001
DEFINITION  Homo sapiens partial mRNA for anti-peptide/MHC complex
            HLA-A1/MAGE-A1 monoclonal antibody light chain.
ACCESSION   AJ309319
VERSION     AJ309319.1  GI:11974103
KEYWORDS    constant region; immunoglobulin light chain; monoclonal antibody;
            variable region.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chames,P., Rojas,G., Dieckmann,D., Rem,L., Schuler,G. and
            Hoogenboom,H.R.
  TITLE     TCR-like Human anti MHC-peptide antibodies: peptide
            fine-specificity is possible over a wide range of affinity
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 648)
  AUTHORS   Chames,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-2001) Chames P., Pathology, Azm, P. Debyelaan 25,
            6202AZ Maastricht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1..648
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /rearranged
     CDS             <1..648
                     /function="immune response"
                     /codon_start=1
                     /product="anti-peptide/MHC complex HLA-A1/MAGE-A1
                     monoclonal antibody light chain"
                     /protein_id="CAC85285.1"
                     /db_xref="GI:11974104"
                     /translation="AQSVLTQPPSVSVAPGKTRITCGGDNIGRKSVHWYQQRPGQAP
                     LLIVDDGDRPSGIPDRFSGGSNSESAATLTISMVAPADEADYFCQVWDSTTDQWVFGG
                     GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA
                     GVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS"
     V_region        <1..327
                     /product="immunoglobulin light chain variable region"
     C_region        328..>648
                     /product="immunoglobulin light chain constant region"
BASE COUNT   152 a    199 c    182 g    115 t
ORIGIN
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Query Match   77.0%; Score 542.8; DB 9; Length 648;
Best Local Similarity   90.3%; Pred. No. 1.6e-122;
Matches 580; Conservative   0; Mismatches 62; Indels   0; Gaps 0;

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Qy      64 TATGAACTGACTCAGCCACCCTCGGTCTCAGTGTCCCAGGACAGACGGCCAGGATCACC 123
           |||  |||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       7 TCTGTGTCGACTCAGCCACCCTCGGTCTCAGTGTCCCAGGACACCAGGATTACC  66

Qy     124 TGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGTACCAGCAAGCCAGCGCGG 183
           || |||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      67 TGTGGGGGAGACAACATTGGACGTAAAAGTGTCCATTGGTATCAGCAGAGGCCAGGCCAG 126

Qy     184 GCCCCTATACTGGTCATCTATGATGATGGACCGGCCCTGAGCGATTC 243
           ||||| |||||||||||||||||||||| |||||||||||||||||||
Db     127 GCCCCTCCTCCTCGTCGTCCTCGTCTATGATGATGGCGCACCGGATCCCTGACCGATTC 186

Qy     244 TCTGGCTCCAAATCAGGGAACACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
           |||||||||||||||||||||||||||||||||||||||||||| ||||  |||||||
Db     187 TCTGGCTCCAATTCTGAGACGCGCGCCACCAGTATGGTCGCACCCGCAGAT 246

Qy     304 GAGGCTGACTATTACTTGTCAGGTGTGGGACAGGCTAGTGACTATCCGGTCTTCGGAGGA 363
           |||||||| |||||||||||||||||| |||||  ||||||| ||||||
Db     247 GAGGCCGACTATTCTGTCAGGTGTGGGATGATTAGGATCAGTGGGTGTTCGGCGGA 306
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RESULT 8

```
AR108866
LOCUS       AR108866                711 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6113898.
ACCESSION   AR108866
VERSION     AR108866.1  GI:12825142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE     Human B7.1-specific primatized antibodies and transfectomas
            expressing said antibodies
  JOURNAL   Patent: US 6113898-A 9 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1..711
                     /organism="unknown"
BASE COUNT   160 a    226 c    193 g    132 t
ORIGIN
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Query Match   76.6%; Score 540.2; DB 6; Length 711;
Best Local Similarity   86.1%; Pred. No. 7e-122;
Matches 612; Conservative   0; Mismatches 93; Indels   6; Gaps 1;

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Qy       1 ATGAGGGTCCCGCTCAGCTCTCGGGGCTCCTGCTGCTCTGCTCTCCAGTGCACGATGT  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGAGGGTCCCCGCTCAGCTCTCGGGGCTCCTGCTGCTCTGCTCTCCAGTGCACGATGT  60

Qy      61 GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCAGTGACGCGGCCAGGATC 120
           |||||||| ||||  |||||||||||||||||||||||||||||||||||||||||||
Db      61 GAGTCGTGTCCGACACAGCCGCCCTCGGTGTCTGGGGCCCCAGGGCCAGGAGGTCACCATC 120

Qy     121 ACCTGTGGGG------AGACAACAGTAGAAATGAATATGTCCACGCAGAAG 174
           ||||||||||      ||||||||||||| ||||||||| ||||||||||
Db     121 TCGTGCACTGGGAGCCAGTCCGTCAGCTATGGAGGGTTATGATGATCATGGTACCAGCAGCTC 180

Qy     175 CCAGCGCGGGCCCCTATACTGGTCATCTATGATGATGGACCGGCCCTGAGCGATTC 234
           |||||| ||||||||||||||||||||||  ||||| |||||||||||||||||
Db     181 CCAGGAACCGCCCCCAAACTCCTCATCTATGACCATTACAAGCGACCCTCAGGAATTTCT 240

Qy     235 GAGGGATTCTCTGGCTCCAAATCAGGGAACACACCGCCACCCTGACCATCAACGGGGTCGAG 294
           |||||||||||||||||||||||||||| ||||| |||||||||||||||| |||||
Db     241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGGCCGCCTCCCATCACTGGGCTCCAG 300

Qy     295 GCCGGGGATGAGGCTGACTATTACTTGTCAGGTGTGGGACAGGCTAGTGACTATCCGGTC 354
           |||||||||||||||| || |||||| ||||||||||||||| |||| |||||||||||
Db     301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCAGCCTGAATGCTCAGGTA 360
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                    FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT
                    HEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGS"

sig_peptide     1. .66
                    /gene="IGL"
                    /note="pelB signal peptide"
BASE COUNT    183 a    238 c    223 g    146 t
ORIGIN

Query Match        76.3%;      Score 538;  DB 9;   Length 790;
Best Local Similarity   91.9%;   Pred. No. 2.4e-121;
Matches  581;  Conservative    0;  Mismatches 45;   Indels   6;   Gaps   1;

Qy    70  CTGACTCAGCCACCCTCCGTGTCAGTGTCCCAGGACAGAGACGGCCAGGATCACCTGTGGG 129
          |||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||
Db    76  CTGACTCAGCCACTCTCCAGTGTCAGTGGCCCTGGACACAGACGGCCAGGATTACCTGTGGG 135

Qy   130  GGAGACAACAGTAGAAATGAATATGTCCACTGTGACCAGGACCAGGAAGCCAGCGCGGGGCCCT 189
          ||||| | ||||||||||||||||| |||||||||||||| || |||||||||||||||||
Db   136  GGAAACAACATTGAAGTAAAAATGTGCACTGTTACCAGGATCCCTGAGGGATTCTCTGGC 195

Qy   190  ATACTGGTCATCTATGATGATAGTGACCGGCCCTCTGAGGGATCCCTGAGGGATCTTCTGGC 249
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   196  GTGCTGGTCATCTATAGGGATAGCACCGGCCCTCTGGGATCCCTGAGGGATTCTCTGGC 255

Qy   250  TCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGTCGAGGCGTGGGGATGAGGCT 309
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   256  TCCAACTCGGGGAACACCGCCACCCTGACCATCAGCAGACAGAGCCAAGCCGGGGATGAGGCT 315

Qy   310  GACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGTCTTCGGAGGAGGACC 369
          ||||||||||||||||||||||||||||||||| ||||         |||||||||||
Db   316  GACTATTACTGTCAGGTGTGGGACAGCAGCACTG-----TGGTATTCGGCGGAGGGACC 369

Qy   370  CGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCCCCCTC 429
          || ||||||||||||||||||||||||||||| ||||||||||||
Db   370  AAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCACTCTGTTCCCGCCCTCC 429

Qy   430  TCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCG 489
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   430  TCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCG 489

Qy   490  GGAGCCGGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGAGTGGAGACC 549
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   490  GGAGCCGGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGAGTGGAGACC 549

Qy   550  ACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACG 609
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   550  ACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACG 609

Qy   610  CCTGAGCAGTGGAAGTCCCACAGAAGCTCACAGCTGCCAGGTCACGCATGAGGGAGCACC 669
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   610  CCTGAGCAGTGGAAGTCCCACAGAAGCTCACAGCTGCCAGGTCACGCATGAAGGGAGCACC 669

Qy   670  GTGGAGAAGACAGTGGCCCCTACAGAATGTTC 701
          ||||||||||||||||||||||||||||||||
Db   670  GTGGAGAAGACAGTGGCCCCTACAGAATGTTC 701


RESULT 10
AB064174
LOCUS       AB064174         826 bp    mRNA    linear    PRI 02-JUL-2002
DEFINITION  Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L34.
ACCESSION   AB064174
VERSION     AB064174.1  GI:21669554
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L34.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
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Qy   355  TTCGGAGGAGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 414
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   361  TTCGGAGGAGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 420

Qy   415  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 474
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480

Qy   475  AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 534
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 540

Qy   535  GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC 594
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC 600

Qy   595  TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTCACAGCTGCCAGGTCACG 654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTCACAGCTGCCAGGTCACG 660

Qy   655  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711


RESULT 9
AB064230
LOCUS       AB064230         790 bp    mRNA    linear    PRI 02-JUL-2002
DEFINITION  Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L90.
ACCESSION   AB064230
VERSION     AB064230.1  GI:21669666
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L90.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
TITLE       Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 790)
AUTHORS     Kurosawa,Y.
TITLE       Direct Submission
JOURNAL     Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="L90"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1..790
                     /gene="IGL"
     CDS             1..>790
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                     /codon_start=1
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                     /protein_id="BAC01858.1"
                     /db_xref="GI:21669667"
                     /translation="MKYLLPTAAAGLLLLAAQPAMANFMLTQPLSVSVALGQTARITC
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Qy   482  TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  541
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Db   488  TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG  547

Qy   542  TGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACCGCGGCCAGCAGCTACCTGA   601
              ||||||||||||||||||   |||| ||||||||||||||||||||||||||||||||
Db   548  TGGAGACCACCACCCTCCAGACAAACAACAACAAGTACCGCGGCCAGCAGCTACCTGA   607

Qy   602  GCCTGAGCGGTGGAGTCAGTGGAAGTCCCACAGAAGCTACAGTTCAGGTCACGCATGAAG  661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   608  GCCTGAGCGGTGGAGTCAGTGGAAGTCCCACAGAAGCTACAGTTCAGGTCACGCATGAAG  667

Qy   662  GGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC  701
              ||||||||||||||||||||||||||||||||||||||||
Db   668  GGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC  707
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RESULT 11
AB064176
LOCUS       AB064176                 824 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
            region, partial cds, clone:L36.
ACCESSION   AB064176
VERSION     AB064176.1  GI:21669558
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L36.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 824)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1..824
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="L36"
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                     peripheral blood and bone marrow"
     gene            1..824
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     CDS             1..>824
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                     /db_xref="GI:21669559"
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                     GGDNVGGKSLHWYQVKPGQAPVLVVFDDRDRPSGIPERFSGANSRDTAALTISRVEAG
                     DEADYCQVWDDISRLVIFGGGTRLIVLRQPKAAPSVTLFPPSSEELQANKATLVCLI
                     SDFYPGAVTVAWKADSSPVKAGVETTTPSRQSNNKYAASSYLSLTPEQWKSHRSYSCQ
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     sig_peptide     1..66
                     /gene="IGL"
                     /note="pelB signal peptide"
BASE COUNT      170 a    248 c    242 g    164 t
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  TITLE     Miura,K. and Kurosawa,Y.
            Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 826)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1..826
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="L34"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1..826
                     /gene="IGL"
     CDS             1..>826
                     /gene="IGL"
                     /codon_start=1
                     /product="immunoglobulin lambda light chain VLJ region"
                     /protein_id="BAC01802.1"
                     /db_xref="GI:21669555"
                     /translation="MKYLLPTAAAGLLLLAAQPAMASYVLTQPPSVSVAPGETATITC
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                     DEADYCQVWDDSSRLVIFGGGTRLIVLRQPKAAPSVTLFPPSSEELQANKATLVCLI
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     sig_peptide     1..66
                     /gene="IGL"
                     /note="pelB signal peptide"
BASE COUNT      172 a    244 c    246 g    164 t
ORIGIN

Query Match         75.8%;  Score 534.4;  DB 9;  Length 826;
Best Local Similarity   89.7%;  Pred. No. 1.8e-120;
Matches  574;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy    62  CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGGCCAGGATCA  121
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Db    68  CCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGTCGCCAGGAGAGACGGGCCACAATTA  127

Qy   122  CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC  181
              ||||||||||||||| || || |||| ||||||||||||||| ||||||||||||| ||
Db   128  CCTGTGGGGGAGACGACGTTGGAGGTAAAAGTTTCCACTGGTATCAGCAGAAGCCAGGCC  187

Qy   182  GGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGGACCCTCAGGGATCCCTGAGCGAT  241
              ||||||| ||| ||||| ||| |||| | || ||||| |||||||||||||||||||||
Db   188  AGGCCCCGTGTCCTGGTCTTTGATGACCGCGACCGGCCATCCCTGAGCGAT  247

Qy   242  TCTCTGGCTCCAAATCAGGGAACACCCGACCACCCTGACCATCAACGGGGTCGAGGCCGGGG  301
              |||||| ||||||| ||||||| ||||| |||||| |||| | ||||||| |||||||||
Db   248  TCTCTGGAACCAACCTCAGGGACACCGCAGCCACTGCCTGCTATCAGCAGGGTCGAGGCCGGGG  307

Qy   302  ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCCTAGTGATCATCCGGTCTTCGGAG  361
              ||||||||||||||||||||||||| |  |  | ||| |||| |||| || ||||||||||
Db   308  ATGAGGCGACTATTATTGTCAGGTGGGATGATAGTGTTTCCCGTCTTGTGATATTCGGCG  367

Qy   362  GAGGGACCCGGGTGACCGTGACCGTGTCAGTCCAAGGTGCCCCCTCCCTCACTCTGTTCC  421
              |||||||||||||||||  ||||  |||||||||||||||||||||||| |||||||||
Db   368  GAGGGACCAGGTTGATCGTCCTACGTCAGCCCAAGGCTGCCCCCTCGGCTCACTCTGTTCC  427

Qy   422  CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT  481
              ||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||||
Db   428  CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCCACACTGGTGTGTCCTCATAAGTGACT  487
```

COMMENT   Comprehensive Medical Science, Fujita Health University;
                Kutsukake-cho, Toyoake 470-1192, Japan
                (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
                Please visit our web site
                URL:http://www.fujita-hu.ac.jp/immunity/.

FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="L27"
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                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"

     gene   1..813
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     CDS   1..>813
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                     /codon_start=1
                     /product="immunoglobulin lambda light chain VLJ region"
                     /protein_id="BAC01795.1"
                     /db_xref="GI:21669541"
                     /translation="MKYLLPTAAGLLLLAAQPAMASYVLTQPPSVSVSPGQTARITC
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                     DEADYYCQSADSSGTYVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
                     SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQ
                     VTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGSGSGGSGGG"

     sig_peptide   1..66
                     /gene="IGL"
                     /note="pelB signal peptide"

BASE COUNT   187 a   242 c   227 g   157 t
ORIGIN

Query Match   74.7%;   Score 526.4;   DB 9;   Length 813;
Best Local Similarity   88.9%;   Pred. No. 1.7e-118;
Matches   569; Conservative   0; Mismatches 71;   Indels   0;   Gaps   0;

Qy   62 CCTATGAACTGACTCAGCCACCCTCGGTGTCCCCAGGACAGACGGGCCAGGATCA 121
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Db   68 CCTATGTGCTGACTCAGCCACCCTCGGTGTCCCCAGGACAGACGGGCCAGGATCA 127

Qy   122 CCTGTGGGGGAGACAACAGTAGAAATGATGAATATGTCCACTGGTACCAGCAGGCC 181
           |||||||||||| ||||||||||||||||||||| ||| |||||| |||||||||
Db   128 CCTGCTCTGCGATGCATTGCCAAAGCAATATGCTTATTGGTACCAGCAGCCAGGCC 187

Qy   182 GGGCCCCTATACTGGTCATCTATGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 241
           ||||||| ||||||| ||| |||| || ||||||||||||||||||||||||
Db   188 AGGCCCCCGTGTCCTGGTCGTCTTTGATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 247

Qy   242 TCTCTGGCTCCAAATCAGGAGAACACCGGGGTCGAGGCCGGGG 301
           |||||| ||| ||||||||||||||||||||||||||||||||
Db   248 TCTCTGGAGCCAACTCTAGGGACACGGGGTCGAGGCCGGGG 307

Qy   302 ATGAGGCTGACTATTACTGTCAGTGTGGGACAGGCTAGTGATCATCCGGTCTTCGGAG 361
           |||||||||||||||||||| |||||||||||||| || ||| |||||||||||||||
Db   308 ACGAGGCTGACTATTACTGTCAATCAGCAGACAGCAGCAGTGGTACTTATGTGGTATTCGGCG 367

Qy   362 GAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGGCTGCCCCCTCGGTCACTCTGTTCC 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368 GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC 427

Qy   422 CGCCCTCCTCTGAGGAGCTTCAAGCAACACCACTGGTGTGTCTCATAAGTGACT 481
           ||||| ||||||||||||||||||||||||||||||||| |||||||||||||
Db   428 CGCCCTCCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 487

Qy   482 TCTACCGGGAGCGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCAACAACAAGTCAGGGGAG 541
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Db   488 TCTACCGGGAGCGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCAACAACAAGTCAGGGGAG 547

Qy   542 TGGAGACCACCACCACCCTCCAAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTACCTGA 601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   548 TGGAGACCACCACCACCCTCCAAAACAAAGCAACAACAAGTACGGCGGCCAGCAGCTACCTGA 607

Qy   602 GCCTGACGCGCCTGAGCAGTGGAAGTCCCACAGAAGAGTCACAGTGCCAGGTCACGCATGAAG 661

Query Match   74.5%;   Score 525.2; DB 9;   Length 895;
Best Local Similarity 88.6%;   Pred. No. 3.3e-118;
Matches 569; Conservative   0; Mismatches 73; Indels   0; Gaps   0;

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Qy     62  CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCA   121
           ||||||||||||||||||||||||||||||||| ||||||||||| |||| | ||| |||
Db     96  CCTATGAGCTGACACAGCCACCCTCGGTGTCAGTGTCCCAGGACAGACGGCCAGGATCA   155

Qy    122  CCTGTGGGGGAGCAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAGCCAGCGC   181
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Db    156  CCTGTCTGGGGATGCATTGCCAAAGCAATATGCTTATTGGTACCAGCAGAAGCCAGGCC   215

Qy    182  GGGCCCCTATACTGGTCATCTATGATGAGTGACCGGCCCTCAGGGATCCCTGAGCGGAT   241
           ||| ||||   |||||||||||| ||| |||| ||||||||||||||||||| ||| ||||
Db    216  AGGCCCCTGTGTTGGTGATATATAAAGACAATGAGAGAGCCCTCAGGGATCCCTGAGCGGAT   275

Qy    242  TCTCTGGCTCCAAATCAGGGAACACCGCACCCTGACCATCAACGGGTCGAGGCCGGGG   301
           ||||||||||||||||||||| |||||| |||||||||||||||||||||| ||||||||
Db    276  TCTCTGGCTCCAGCTCAGGGACAACAGTCACGTTGACCATCAGTGAGTCCAGGCAGAAG   335

Qy    302  ATGAGGCTGACTATTACTTGTCAGTGTGGGACAGGCCAGTGATCATCCGGTCTTCGGAG   361
           ||||||||||||||||||||||| |||||||||||||||| | ||||||||||||||||
Db    336  ACAGAGGCTGACTATTACTTGTCAATCAGCAGACAGCAGTGGTACTTATTGGGTGTTCGGCG   395

Qy    362  GAGGGACCCCGGTGACCGTCCTAGGTCAGCCCAAGGTCGCCCCTCGGTCACTCTGTTCC   421
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Db    396  GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC   455

Qy    422  CGCCCTCCTCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT   481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456  CGCCCTCCTCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT   515

Qy    482  TCTACCCGGGAGCCGTGACAGTGGCCTGACAGGCAGATAGCAGCCCGTCAAGGCGGGAG   541
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Db    516  TCTACCCGGGAGCCGTGACAGTGGCCTGACAGGCAGATAGCAGCCCGTCAAGGCGGGAG   575

Qy    542  TGGAGACCACCACCACCCTCCAAACAAAGCAACAACAACAGTACGGGGCAGCAGCAGTACCTGA   601
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Db    576  TGGAGACCACCACCACCCTCCAAACAAAGCAACAACAACAGTACGGGGCCAGCAGCAGTACCTGA   635

Qy    602  GCCTGACGCGCTGGAGCAGTCCAGTCCCACAGAGTGGAAGTGCCCAGTGCACGCCATGAAG   661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636  GCCTGACGCGCTGGAGCAGTCCAGTCCCACAAAAGCTACAGCTGCCCAGTGCACGCCATGAAG   695

Qy    662  GGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT   703
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Db    696  GGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT   737
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RESULT 14
HSIGVL002
LOCUS   HSIGVL002   725 bp   mRNA   linear   PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION   X57802
VERSION   X57802.1 GI:33701
KEYWORDS   Ig lambda light chain; immunoglobulin.
SOURCE   Homo sapiens.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 725)
  AUTHORS   Klobeck,H.G.
  TITLE   Direct Submission
  JOURNAL   Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
            Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
            Muenchen, Schillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE   2 (bases 355 to 401)
  AUTHORS   Combriato,G. and Klobeck,H.G.
  TITLE   V lambda and J lambda-C lambda gene segments of the human
            immunoglobulin lambda light chain locus are separated by 14 kb and
            rearrange by a deletion mechanism
  JOURNAL   Eur. J. Immunol. 21 (6), 1511-1522 (1991)
  MEDLINE   91257162

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Db    608  GCCTGACGCGCTGGAGCAGTCCAGTCCCACAGAGAAGCTACAGCTGCCCAGTGCACGCCATGAAG   667
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Qy    662  GGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTC   701
           |||||||||||||||||||||||||||||||||||||||
Db    668  GGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTC   707
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RESULT 13
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LOCUS   BC022823   895 bp   mRNA   linear   PRI 07-FEB-2002
DEFINITION Homo sapiens, clone MGC:39283 IMAGE:4856249, mRNA, complete cds.
ACCESSION   BC022823
VERSION   BC022823.1 GI:18606083
KEYWORDS   MGC.
SOURCE   Homo sapiens.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 895)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (04-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 42 Row: g Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction, Similarity but not identity
            to protein.
FEATURES   Location/Qualifiers
     source   1..895
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MGC:39283 IMAGE:4856249"
                     /tissue_type="Primary B-Cells from Tonsils"
                     /clone_lib="NIH_MGC_48"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS   38..739
                     /codon_start=1
                     /product="Unknown (protein for MGC:39283)"
                     /protein_id="AAH22823.1"
                     /db_xref="GI:18606084"
                     /translation="MAWIPLLLPLLTLCTGSEASAYELTQPPSVSVSPGQTARITCSGD
                     ALPKQYAYWYQQKPGQAPVLVIYKDNERPSGIPERFSGSSSGTTVTLTISGVQAEDEA
                     DYYCQSADSSGTYWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATIVCLISDF
                     YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTH
                     EGSTVEKTVAPTBCS"
BASE COUNT   230 a   275 c   225 g   165 t
ORIGIN
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PUBMED      1904362
COMMENT     for overlapping sequences see: X51754-55; J00252-54; M15641-42.
FEATURES             Location/Qualifiers
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                     /isolate="individual ML"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /clone="cML23"
                     /cell_type="B-cell"
                     /tissue_type="spleen"
                     /clone_lib="phage library cML"
     gene            1..725
                     /gene="immunoglobulin lambda light chain"
     mRNA            1..725
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                     /note="cDNA"
                     /evidence=experimental
     CDS             24..719
                     /gene="immunoglobulin lambda light chain"
                     /codon_start=1
                     /protein_id="CAA40940.1"
                     /db_xref="GI:33702"
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                     TLGDKYACWYQQKPGHSPVLVIFQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEA
                     DYYCQAWDSSTAVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYP
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                     /gene="immunoglobulin lambda light chain"
     misc_feature    81..399
                     /gene="immunoglobulin lambda light chain"
                     /note="variable region, V(lambda)III"
     misc_feature    362..399
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                     /note="J-segment"
     misc_feature    400..719
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                     /note="constant region"
BASE COUNT    164 a    226 c    199 g    136 t
ORIGIN

Query Match    74.3%;  Score 524;  DB 9;  Length 725;
Best Local Similarity    89.7%;  Pred. No. 6.5e-118;
Matches  576;  Conservative   0;  Mismatches  60;  Indels    6;  Gaps    1;

Qy     62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGGCCAGGATCA 121
          ||||||||||||||||||||||||||| ||||||||||  ||||| |||||||| ||||||
Db     82 CCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCAGCCAGCATCA 141

Qy    122 CCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGCGC 181
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Db    142 CCTGCTCTGGAGATACATTGGGGGATAAATATGTCTGGTATCAGCAGAAGCCAGGCC 201

Qy    182 GGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 241
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Db    202 ACTCCCCTGTGTGCTGGTCATCTTTCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGAT 261

Qy    242 TCTCTGGCTCCAAATCAGGGAACACACCGACCATCAACGGGTCGAGGCCGGGG 301
          || ||||||||||| |  |||| | ||||||||||||| ||||| ||||||||
Db    262 TCTCTGGCTCCAACTCTGGGAACACAGCCACCCTCTGACCATCAGCGGGACCCAGGCTATGG 321

Qy    302 ATGAGGCTGACTATTACTGTCAGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
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Db    322 ATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTG------CGGTATTCGGCG 375

Qy    362 GAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCC 421
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Qy    422 CGCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT 481
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Qy    482 TCTACCCGGGAGCCGTGACAGTGGCTGGCACAGTGGCAGATAGCAGCCCGTCAAGGCGGAG 541
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Qy    542 TGGAGACCACCACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCAGCTACCTGA 601
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Db    556 TGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGA 615

Qy    602 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAAGTCACCCATGAAG 661
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Db    616 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAAGTCACCCATGAAG 675

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RESULT 15
BC032452
LOCUS       BC032452                890 bp    mRNA    linear    PRI 26-JUN-2002
DEFINITION  Homo sapiens, clone MGC:40425 IMAGE:5177123, mRNA, complete cds.
ACCESSION   BC032452
VERSION     BC032452.1  GI:21595391
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L, Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Magrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            series: IRAK Plate: 64 Row: f Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction.
FEATURES             Location/Qualifiers
     source          1..890
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MGC:40425 IMAGE:5177123"
                     /tissue_type="Brain, Lung, Testis, adult, pooled whole"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             26..727
                     /codon_start=1
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/product="Unknown (protein for MGC:40425)"
/protein_id="AAH32452.1"
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ALPKKTAYWYQQKSGQTPVLVIYDDTERPSGIPERFSGSSSGTVATLTLSGAQVEDEA
DYYCYSSDSSGNHWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
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EGSTVEKTVAPTECS"
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BASE COUNT   230 a   277 c   219 g   164 t
ORIGIN

Query Match   74.1%;   Score 522.4; DB 9;   Length 890;
Best Local Similarity 84.1%;   Pred. No. 1.6e-117;
Matches 589; Conservative   0; Mismatches 111;   Indels   0; Gaps   0;

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Qy      4 AGGGTCCCGCCTCAGCTCCTGGGGCTTCCTGCTCTGCTCCCAGGTGCACGATGTGCC     63
          |||||   ||||||||||||||||||||||||||||||   ||||||||| |||||
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Qy     64 TATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACC    123
          |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
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Qy    124 TGTGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGAGAAGCCAGCGCGG    183
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Qy    184 GCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTC    243
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Qy    484 TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTG    543
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Qy    544 GAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGC    603
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Search completed: April 6, 2003, 01:55:54
Job time : 2214.18 secs

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            GenCore version 5.1.3
       Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     April  5, 2003, 18:12:24 ; Search time 392.719 Seconds
                                       (without alignments)
                                       8205.894 Million cell updates/sec

Title:            US-09-758-173-3
Perfect score:    1431
Sequence:         1 ATGAAACACCTGTCGTTCTT.........CCCTGTCTCCGGGTAAATGA 1431

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         218539 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:        4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database   :      N_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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                        SUMMARIES

                         %
Result           Query
No.    Score  Match Length DB   ID           Description
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  1    1431  100.0  1431   18   AAT62510     Primatised anti-hu
  2    1431  100.0  1431   19   AAV35485     Macaque primatized
  3    1431  100.0  1431   24   AAS17243     DNA sequence of a
  4   1315.8  91.9  1431   18   AAT62513     Primatised anti-hu
  5   1315.8  91.9  1431   19   AAV35489     Macaque primatized
  6   1315.8  91.9  1431   24   AAS17247     DNA sequence of a
  7   1246.4  87.1  1634   21   AAZ25012     Human immune syste
  8   1237.2  86.5  1431   17   AAT18059     Monoclonal antibod
  9   1234.8  86.3  1567   22   AAC66522     Human immune syste
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 10   1221.6  85.4  1418   17   AAT26889     Anti-rhesus D reco
 11   1171.4  81.9  1404   18   AAT62868     Human gamma-4 heav
 12   1168.2  81.6  1404   18   AAT62870     Human gamma-4PE he
 13   1166.6  81.5  1404   18   AAT62869     Human gamma-4E hea
 14    1135   79.3  1428   22   AAH74680     Nucleotide sequenc
 15   1125.2  78.6  1428   18   AAT61241     Human anti-RSV mon
 16   1124.2  78.6  1507   21   AAA09695     Human immunoglobul
 17   1122.2  78.5  1437   24   AAK98701     cDNA of the heavy
 18   1117.2  78.1  1437   19   AAV35487     Macaque primatized
 19   1117.2  78.1  1437   24   AAS17245     DNA sequence of a
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 21   1115.4  77.9  1442   22   AAC84208     Plasmid Glambda-1B
 22   1113.4  77.8  1798   21   AAC98220     Human colon cancer
 23   1113.2  77.8  1644   22   AAS22593     Human cDNA encodin
 24   1112.8  77.8  19035  19   AAV61794     Traget Plasmid Man
 25   1112.2  77.7  6281   22   AAC84206     Plasmid Glambda-1A
 26   1110.8  77.6  1428   18   AAT61279     Human anti-RSV mon
 27   1103.6  77.1  1467   14   AAQ35099     Antibody D heavy c
 28    1103   77.1  1599   24   ABK64550     Reshaped CAMPATH-1
 29   1102    77.0  1599   24   ABL62673     Human benign prost
 30   1102    77.0  1599   24   ABL65479     Colon adenocarcino
 31   1102    77.0  1599   24   ABL66294     Lung cancer relate
 32   1102    77.0  1599   24   AAV41429     Lung cancer relate
 33   1100.8  76.9  1427   19   AAV41431     Plasmid Hu19BHcpcd
 34   1100.8  76.9  1427   19   AAV41431     Plasmid Hu19CHcpcd
 35   1098.8  76.8  1449   20   AAX06951     Monoclonal antibod
 36   1098.8  76.8  1449   18   AAX06952     Monoclonal antibod
 37   1097.6  76.7  1427   19   AAV41432     Plasmid Hu19DHcpcd
 38   1096.6  76.6  1612   22   AAS22482     Human cDNA encodin
 39    1096   76.6  7521   22   AAF30315     Bicistronic chimer
 40    1094   76.5  1549   13   AAQ20066     Encodes heavy chai
 41   1093.8  76.4  1458   13   AAQ23571     Reshaped CD4 antib
 42   1093.8  76.4  1458   13   AAQ23581     Reshaped CD4 antib
 43   1092.8  76.4  6284   19   AAV41427     Plasmid Hu19AHcpcd
 44   1092.6  76.4  6557   17   AAT15932     Anti-IgE VH expres
 45   1092.2  76.3  1617   24   AAS62784     cDNA sequence #571
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                                    ALIGNMENTS

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RESULT 1
AAT62510
ID   AAT62510 standard; DNA; 1431 BP.
XX
AC   AAT62510;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 heavy chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
```

```
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01818.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 7; Fig 8B; 81pp; English.
XX
CC   2 DNA sequences (AAT62509 and AAT62510) respectively code for
CC   primatised forms (AAW01817 and AAW01818) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   7C10.  Cloned 7C10 light and heavy variable genes are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells.  Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppresants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

Query Match             100.0%;  Score 1431;  DB 18;  Length 1431;
Best Local Similarity   100.0%;  Pred. No. 1.1e-276;
Matches  1431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 TGCGTTGTCTTCTGGTGGCTCCATCAGCGGTTACTACTACTGGACCTGGATCCGCCAGACC 180
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Qy        181 CCAGGGAGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC 240
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Db        181 CCAGGGAGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC 240

Qy        241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 300

Qy        301 CTGAACTTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAACTTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT 360

Qy        361 CGCCCTGATTGCACAACCATTTGTTATGGCGGTGGGTCGATGGTCTGGGGCCCGGGGAGAC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCCTGATTGCACAACCATTTGTTATGGCGGTGGGTCGATGGTCTGGGGCCCGGGGAGAC 420

Qy        421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480

Qy        481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
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Qy        541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
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Db        541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600

Qy        601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
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Db        601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660

Qy        661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720

Qy        721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
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Db        721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780

Qy        781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
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Qy        901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
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Qy        961 CGGGAGGAGCAGTACAACAGCACGTACCGTGGTGGTCAGCGTCCTCCAACAAAGCCCTCC 1020
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Db        961 CGGGAGGAGCAGTACAACAGCACGTACCGTGGTGGTCAGCGTCCTCCAACAAAGCCCTCC 1020

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy       1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy       1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy       1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy       1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy       1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
```

```
RESULT 2
AAV35485
ID   AAV35485 standard; DNA; 1431 BP.
XX
AC   AAV35485;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7C10 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1431
FT                   /*tag= a
FT                   /product= 7C10 heavy chain
XX
```

PN   WO9819766-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;   97WO-US19906.
XX
PR   08-NOV-1996;   96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63761.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3b; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 7C10 heavy chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

Query Match   100.0%; Score 1431; DB 19; ID No.1.1e-276; Length 1431;
Best Local Similarity   100.0%; Pred. No.1.1e-276;
Matches 1431; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy      1 ATGAAACACCTGTCGTTCTTCCTCCTCCTGGTGCAGCTCCAGATGGTCCTGTCCCAG   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGAAACACCTGTCGTTCTTCCTCCTCCTGGTGCAGCTCCAGATGGTCCTGTCCCAG   60

Qy     61 GTGGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGCAGACCCTGTCCCGCACC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGCAGACCCTGTCCCGCACC  120

Qy    121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGAGTCGGTTCCGCCAGACC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGAGTCGGTTCCGCCAGACC  180

Qy    181 CCAGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGGCACCAACTAC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGGCACCAACTAC  240

Qy    241 AATCCCTCCCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATCCCTCCCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC  300

Qy    301 CTGAACTTGAATTCTGTGACCGACGCGGCACGGCCCGTCTATTACTGTGCGAGAGGGCCCT  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGAACTTGAATTCTGTGACCGACGCGGCACGGCCCGTCTATTACTGTGCGAGAGGGCCCT  360

Qy    361 CGCCCTGATTGCACAACCATTGTTATGGCGGCTGGTGCGATGTCTGGGGCCCGGGAGAC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CGCCCTGATTGCACAACCATTGTTATGGCGGCTGGTGCGATGTCTGGGGCCCGGGAGAC  420

Qy    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480

Qy    481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy    541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy    601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660

Qy    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720

Qy    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780

Qy    781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900

Qy    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy   1081 ATCGAGAAAACCATCTCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCGAGAAAACCATCTCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
```

RESULT 3
AAS17243

```
ID   AAS17243 standard; DNA; 1431 BP.
XX
AC   AAS17243;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the heavy chain of 7C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1431
FT                   /*tag=  a
FT                   /product= "Heavy chain of 7C10 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Hanna N,  Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11539.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 3b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present nucleic
CC   acid sequence encodes the heavy chain of 7C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

Query Match         100.0%;  Score 1431;  DB 24;  Length 1431;
Best Local Similarity   100.0%;  Pred. No. 1.1e-276;
Matches 1431;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAG 60
```

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Db                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCCAG  60

Qy       61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCTGTCCCGCCACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCTGTCCCGCCACC  120

Qy      121 TGCGTTGTCTCTGGTGCTTCCATCAGCCGGTTACTACTCGGTTACTACTGGAACTCGCCAGACC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGCGTTGTCTCTGGTGCTTCCATCAGCCGGTTACTACTCGGTTACTACTGGAACTCGCCAGACC  180

Qy      181 CCAGGGAGGGAGACTGGAGTGGCCATATTATGGTAATGGTGGCACCAACTAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CCAGGGAGGGAGACTGGAGTGGCCATATTATGGTAATGGTGGCACCAACTAC  240

Qy      241 AATCCCTCCCTCAAGAGTCCAGTCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AATCCCTCCCTCAAGAGTCCAGTCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTC  300

Qy      301 CTGAACTTGAATTCTGTGACGACGGACACGGCCGTCTATTACTGTGCGAGGGCCCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTGAACTTGAATTCTGTGACGACGGACACGGCCGTCTATTACTGTGCGAGGGCCCT  360

Qy      361 CGCCCTGATTGCACAACCATTTGTTATGGCGGCTGGGTCGATGTCGGGGCCCGGGAGAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGCCCTGATTGCACAACCATTTGTTATGGCGGCTGGGTCGATGTCGGGGCCCGGGAGAC  420

Qy      421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCTCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCTCC  480

Qy      481 TCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGCTGTCAAGGACTACTTCCCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGCTGTCAAGGACTACTTCCCC  540

Qy      541 GAACCGGTGACGGTGTCGTGAACTCAGGCGCCCCTGACCAGCGGCGTGCACACCTTCCCG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GAACCGGTGACGGTGTCGTGAACTCAGGCGCCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy      601 GCTGTCCTACAGTCCTCAGGACTCTCCTACTCCCTGCAGCGTGGTGACCGTGCCCTGCAGC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTGCAGCGTGGTGACCGTGCCCTGCAGC  660

Qy      661 AGCTTGGGCACCCAGACCTACACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTG  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 AGCTTGGGCACCCAGACCTACACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTG  720

Qy      721 GACAAGAAAGCAGAGCCCAAATCTGTGACAAAACTCACACATGCCACCTGCCCAGCA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GACAAGAAAGCAGAGCCCAAATCTGTGACAAAACTCACACATGCCACCTGCCCAGCA  780

Qy      781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy      841 ATGATCTCCCGGACCCCTGAGGTCACACGTACCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAGCCCT  900

Qy      901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy      961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020

Qy     1021 GACTGGCTGAATGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCCC  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GACTGGCTGAATGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCCCA  1080

Qy     1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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CC        and graft-versus-host disease.
XX
SQ        Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

          Query Match        91.9%;   Score 1315.8;   DB 18;   Length 1431;
          Best Local Similarity   95.0%;   Pred. No. 1.1e-253;
          Matches 1359;   Conservative   0;   Mismatches 72;   Indels   0;   Gaps   0;

Qy       1 ATGAAACACCTGTGGTTCCTCCTCCTCGGTGCAGCTCCCAGATGGGTCCTGTCCCAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGAAACACCTGTGGTTCCTCCTCCTCGGTGCAGCTCCCAGATGGGTCCTGTCCCAG   60

Qy      61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTCCGGACCCTGTCCGCACC  120
           ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      61 GTGGAGCTGCAGCAGTCGGGCCCAGGACTCGGCGAAGCCTCCGGAGACCCGTCCCTCACC  120

Qy     121 TGGCTTGTCTCTGTGGCTCCATCAGCGGTTACTACTACTGGGTACTACTGGGAACAC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     121 TGCCTGTCTCTGTGGGCTCCATCAGCGGTGGTTATGGTGGCTGGGGACCGGCTGGGAACAC  180

Qy     181 CCAGGGAGGGGGCTGGAGTGGGATTGGGGCCATATTTATGGTAAGTAGTAGTGGGAACACCTACTAC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCAGGGAGGGGGCTGGAGTGGGATTGGGGCCATATTTATGGTAAGTAGTAGTGGGAACACCTACTAC  240

Qy     241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTC  300
           |||||||||||||||||||||||||||||||| |||| ||||| |||||||||||||||||
Db     241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTC  300

Qy     301 CTGAACTTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGGCCCT  360
           |||||||||||||||||||||||||||||||||||||||||||| |||| |||||
Db     301 CTGAAGCTGAACTCTATGAAGACCGACGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT  360

Qy     361 CGCCCGATTGCACAACCATTTGTTATGGCGGCTGGGCGGGCCCGGGAGAC  420
           |||||| |||||||||||||||||||| |||||||||||||||||||||
Db     361 CTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCAGTTCTGTGGGGCCCGGGAGTC  420

Qy     421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCCCACCTCC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCCCACCTCC  480

Qy     481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy     541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy     601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCAGC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660

Qy     661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720

Qy     721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780

Qy     781 CCTGAACTCCTCGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCTGAACTCCTCGGGGGGACCGTCAGTCGTTCCTCTTCCCCCCAAAACCCAAGGACACCCT  840

Qy     841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900

Qy     901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy     961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
```

(continued left column, rotated)

```
Db      1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTACACCCTG 1140
Qy      1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
Qy      1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
Qy      1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
Qy      1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGCATGAGGCT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGCATGAGGCT 1380
Qy      1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
```

```
RESULT 4
AAT62513
ID   AAT62513 standard; DNA; 1431 BP.
XX
AC   AAT62513;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01822.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 11; Fig 10B; 81pp; English.
XX
CC   2 DNA sequences (AAT62512 and AAT62513) respectively code for
CC   primatised forms (AAW01821 and AAW01822) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   16C10.  Cloned 16C10 light and heavy variable genes are inserted
CC   into an expression vector (pref. NEOSPLA) which contains human light
CC   and heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells.  Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
```

Db   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCCACCGTCCTGCCACCAG 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC   1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC   1080

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG   1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG   1140

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC   1200

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC   1260

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGTCACC   1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGTCACC   1320

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT   1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT   1380

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431

RESULT 5
AAV35489
ID   AAV35489 standard; DNA; 1431 BP.
XX
AC   AAV35489;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 16C10 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1431
FT   /tag= a
FT   /product= 16C10 heavy chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63765.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B

PT   cells, e.g. graft rejection or tumours

XX
PS   Example 7; Fig 5b; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 16C10 heavy chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressant. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

Query Match   91.9%; Score 1315.8; DB 19; Length 1431;
Best Local Similarity   95.0%; Pred. No. 1.1e-253;
Matches 1359; Conservative   0; Mismatches   72; Indels   0; Gaps   0;

Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCCCCGAGACCCTTCTGCAGCCACC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCCCCGAGACCCTTCTGCAGCCACC 60

Qy   61 GTGAAGCTGCAGCAGTGGGCGCGAGGACTTCTGCAGCCTTCGCAGCACCCTGTCCCGCACC 120
           ||| ||||||||||||| ||||||||||||||||||||| ||||||||||||||||||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy   121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGAGCTGGATCCGGCCAGACC 180
           ||||| |||||||||| || || ||||||||||| || ||||||||||||| |||||||
Db   121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTTATGGGTTATGGGTCTGGATCCGGCCCC 180

Qy   181 CCAGGGAGGGGACTGGAGTGGATTGGCCACATATTATGTAATGGTCGCACCACCAACTAC 240
           ||||||||||||||||||||||||||| ||||||||| |||||||||||||||||||||
Db   181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTCTATAGTAGTAGTAGGGAACACCTACTAC 240

Qy   241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 300
           ||||| |||||||||||||||||||||||| ||||| ||||||||||||||||||||||
Db   241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300

Qy   301 CTGAACTTGAATTCTGTGACCGACGCGGGACACGGCGTCTATTACTGTGCGAGAGGCCCT 360
           ||||| ||||| || ||||| |||||| |||||| ||||| || ||||||||||| ||||
Db   301 CTGAAGCTGACTCTATGACCGACGCGGGACACGGCGTGTATTACTGTGTGAGAGATCGT 360

Qy   361 CGCCCGATTGCACAACCATTTGTTATGGCGGTCGGTGGTGCAATGGTTTGGGGCCCGGGAGAC 420
           | ||||| |||||| |||||||||| |||||| |||||||||||| |||| |||||||
Db   361 CTTTTTCAGTGTGTTGGAATGGTTTCACAAACTGTTCGATGTCTGGGGCCGGGAGTC 420

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCGCACCCTCC 480
           ||||| ||||||||||||||||||||||||||||||||||| ||||||| |||||||||
Db   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660

```
Qy    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACACAGCCCAGCAACCACCAAGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACACAGCCCAGCAACCACCAAGGTG 720

Qy    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780

Qy    781 CCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900

Qy    901 GAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy   1321 GTGGACAAGAGAGGTGGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGGACAAGAGAGGTGGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTCTCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTCTCCGGGTAAATGA 1431
```

RESULT 6
AAS17247
ID   AAS17247 standard; DNA; 1431 BP.
XX
AC   AAS17247;
XX
DT   12-MAR-2002 (first entry)
XX
DE   DNA sequence of a primatised form of the heavy chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.

XX
FH   Key   Location/Qualifiers
FT
FT   CDS   1..1431
FT   /*tag= a
FT   /product= "Heavy chain of 16C10 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11646.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 5b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present nucleic
CC   acid sequence encodes the heavy chain of 16C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

Query Match   91.9%; Score 1315.8; DB 24; Length 1431;
Best Local Similarity   95.0%; Pred. No. 1.1e-253;
Matches 1359; Conservative   0; Mismatches   72; Indels   0; Gaps   0;

```
Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60

Qy     61 GTGAAGTTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTGGAGACCCTGTCCGTGCCGACC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGCAGTTGCAGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC 120

Qy    121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGAGCTGGATCCGGATCCGCCAGACC 180
          |||| || ||||||||||| ||||||||| |||||||||||||||||||||||||||||
Db    121 TGCGCTGTCTCTGGTGGCTCCATCAGCAGCGGTTATGGCTGGTTATGGGCTGGATCCGCCAGCCC 180

Qy    181 CCAGGGAAGGGGCTGGAGTGGATTGGGTGCCATATTTATGGTGACACCAACTAC 240
          |||||||||||||||||||| |||||||| ||||||||||| |||||||||||
Db    181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTTTCATAGTAGTAGTGGAAGCACCTACTAC 240

Qy    241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAGACACGTTCAAGAACCAGTTCTTC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTTCAAGAACCAGTTCTCC 300
```

```
Qy   1381  CTGCACAACCACTACACGCGCAGAAGAGCCCTCCTCCCTGTCTCCGGGTAAATGA  1431
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTGCACAACCACTACACGCGCAGAAGAGCCCTCCTCCCTGTCTCCGGGTAAATGA  1431
```

```
RESULT 7
AAZ50012
ID   AAZ50012 standard; cDNA; 1634 BP.
XX
AC   AAZ50012;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human immune system molecule, ISMO-2 cDNA.
XX
KW   Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW   treatment; prevention; cell proliferation; immune system disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             78..1490
FT                   /tag= a
FT                   /product= "ISMO-2"
FT                   /note= "ISMO-2 shows homology to vertebrate
FT                   immunoglobulin gamma heavy-chain"
FT   sig_peptide     78..134
FT                   /tag= b
FT   mat_peptide     135..1487
FT                   /tag= c
FT                   /product= "Mature ISMO-2 protein"
FT   misc_binding    432..473
FT                   /tag= d
FT                   /bound_moiety= "Hybridisation probe"
XX
PN   WO200000608-A2.
XX
PD   06-JAN-2000.
XX
PF   21-JUN-1999;   99WO-US13995.
XX
PR   30-JUN-1998;   98US-0107223.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
PI   Baughn MR;
XX
DR   WPI; 2000-170916/15.
DR   P-PSDB; AAY44721.
XX
PT   Immune system molecules used in the diagnosis, treatment and prevention
PT   of disorders associated with the immune system and cell proliferation
PT   -
XX
PS   Claim 7; Pages 64-65; 69pp; English.
XX
CC   The present sequence is a cDNA encoding an immune system molecule,
CC   ISMO-2 from an Incyte clone 2849752 isolated from the human breast
CC   tumour cDNA library (BRSTUT13). This sequence is expressed in several
CC   libraries, generally those associated with cancer, cell
CC   proliferation, immune response or trauma.
CC   The present sequence is useful in the diagnosis, treatment and
CC   prevention of disorders associated with the immune system and
CC   cell proliferation.
XX
SQ   Sequence 1634 BP; 369 A; 541 C; 432 G; 292 T; 0 other;
```

```
Query Match             87.1%;  Score 1246.4;  DB 21;  Length 1634;
Best Local Similarity   94.0%;  Pred. No. 7.9e-240;
Matches 1346;  Conservative   0;  Mismatches  66;  Indels  20;  Gaps  4;
```

```
Qy      1  ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGGTCCTGTCCCAG  60
```

```
Qy    301  CTGAACTTGAATTCTGTGACCGACACGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT  360
            |||| |||| |||||||||||||||||||| ||||||||  ||| |||||||||| ||||
Db    301  CTGAAGCTGAACTTCTATGACCCGCCGGACACGGCCGCCGTGTTACTACTGTGTGAGAGATCGT  360

Qy    361  CGCCCTGATTGCACAACCATTTGTTATGGCGGCTGGGTCGATGTCTGGGGGCCCGGGAGAC  420
            ||||| |||||||||||| |||  |||||| ||||||||||||||||||||||||||
Db    361  CTTTTTCAGTTGTTGGAATGGTTTACAACACTGGTTCGATGTCTGGGGGCCCGGGAGTC  420

Qy    421  CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCCTCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCCTCC  480

Qy    481  TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTCCCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy    541  GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600

Qy    601  GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660

Qy    661  AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720

Qy    721  GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAAACTCACACATGCCACCGTGCCCAGCA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAAACTCACACATGCCACCGTGCCCAGCA  780

Qy    781  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy    841  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900

Qy    901  GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960

Qy    961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020

Qy   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080

Qy   1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140

Qy   1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200

Qy   1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260

Qy   1261  AAGACCACGCCTCCCGTGCTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  AAGACCACGCCTCCCGTGCTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320

Qy   1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
```

Db   1139 CATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT 1198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1140 GCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG 1199
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1199 GCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG 1258

Qy   1200 CTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTA 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 CTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTA 1318

Qy   1260 CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC 1319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC 1378

Qy   1320 CGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1379 CGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGG 1438

Qy   1380 TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1439 TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1490

RESULT 8
AAT18059
ID   AAT18059 standard; DNA; 1431 BP.
XX
AC   AAT18059;
XX
DT   16-AUG-1996 (first entry)
XX
DE   Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
XX
KW   Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW   65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1428
FT   /*tag= a
FT   sig_peptide   1..57
FT   /*tag= b
FT   mat_peptide   58..1425
FT   /*tag= c
FT   3'UTR   1426..1431
FT   /*tag= d
XX
PN   JP08038178-A.
XX
PD   13-FEB-1996.
XX
PF   20-FEB-1995; 95JP-0030742.
XX
PR   18-FEB-1994; 94JP-0021628.
XX
PA   (NISN) NISSHINBO IND INC.
PA   (TANA/) TANAKA H.
XX
DR   WPI; 1996-154852/16.
DR   P-PSDB; AAR93553.
XX
PT   Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT   produced by primer amplification, used in the diagnosis of hCMV
PT   infection
XX
PS   Claim 6; Page 16-18; 22pp; Japanese.
XX
CC   The sequences given in AAT18059-60 encode the heavy and light chains
CC   respectively of a monoclonal antibody against a 65 kD antigen of human
CC   cytomegalovirus (hCMV). These sequences were amplified using the
CC   sequences given in AAT18040-58. The monoclonal antibody may be used
CC   in the diagnosis of hCMV.

Db   78 ATGAAACATCTGTGGTTCTTCCTCCTCGTGGCTGGCAGTCCCAGATGGGCTCCTGTCCCAG 137
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 GTGAAGCTGCAGCAGTGGGGCGAGGACTTCTGCAGCCTTCGGACGACCCGTGCCCGCACC 120

Db   138 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 197

Qy   121 TGCGGTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGAGCTGGATCCGCCAGCCCAGACC 180

Db   198 TGCACTGTCTCTGGTGGCTCCATCAGCAGT---TACTACTGGAACTGGATCCGGCTGCCC 254

Qy   181 CCAGGGAGGGGACTGGAGTGGATTGGGTAATTTATGGTAATGTGCGACCACCAAACTAC 240

Db   255 CCAGGGAAGGGACTGGAGTGGATTGGGTATATCTA---TACTAGTGGAGCACCAACTAC 311

Qy   241 AATCCCCTCCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 300

Db   312 AACCCCTCCCTCAAGAGTCGAGTCACCATGTCACGTAGACAGGTCCAAGAACCAGTTCTCC 371

Qy   301 CTGAACTTGTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT 360

Db   372 CTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGACCCCG 431

Qy   361 CGGCCCTGATTGCACAACCATTGTTATGGCGGCTGGGTCGATGTCTGGGGCC--CGGGAGA 419

Db   432 CCCAACGCTACTACTACTA-----------CGGTATGGACTTCTGGGGCCAAGGGAGC 478

Qy   420 CCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 479

Db   479 CCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 538

Qy   480 CTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC 539

Db   539 CTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC 598

Qy   540 CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCC 599

Db   599 CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCC 658

Qy   600 GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG 659

Db   659 GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG 718

Qy   660 CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGT 719

Db   719 CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGT 778

Qy   720 GGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGC 779

Db   779 GGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGC 838

Qy   780 ACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT 839

Db   839 ACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT 898

Qy   840 CATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC 899

Db   899 CATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCC 958

Qy   900 TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC 959

Db   959 TGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC 1018

Qy   960 GCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCA 1019

Db 1019 GCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCA 1078

Qy 1020 GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC 1079

Db 1079 GGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC 1138

Qy 1080 CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT 1139

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Db    955 CCGCGGGAGGAGCAGTACACAGCACGTACCGTGTGGTCAGGTCCTCACCGTCCTGCGAC 1014
          ||||||||||||||||||  | ||||||||||||||||||||  ||  |||||||||||
Qy   1018 CAGGACTGCTGAATGGCAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   1015 CAGGACTGCTGAATGGCAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCCCCAGCC 1074

Qy   1078 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTACACC 1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1075 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTACACC 1134

Qy   1138 CTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1135 CTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1194

Qy   1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAAC 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1195 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAAC 1254

Qy   1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGGGAACTGTCCTCTTCCTCTACAGCAAGTC 1317
          |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db   1255 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGGGAACTGTCCTCTTCCTCTACAGCAAGTC 1314

Qy   1318 ACCGTGGACAAGAGCAGGTGGCAGCGAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1315 ACCGTGGACAAGAGCAGGTGGCAGCGAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1374

Qy   1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTCTCCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1375 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCGTCTCCCGGGTAAATGA 1428
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RESULT 9

AAC66522

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ID   AAC66522 standard; cDNA; 1567 BP.
XX
AC
XX
DT   15-FEB-2001 (first entry)
XX
DE   Human immune system associated protein HISAP-4 coding sequence.
XX
KW   Human; immune system associated protein; HISAP-4; immune disorder;
KW   infection; autoimmune disease; cancer; ss.
XX
OS   Homo sapiens.
XX
XX
PN   US6135941-A.
XX
PD   24-OCT-2000.
XX
PF   27-MAR-1998;    98US-0049672.
XX
PR   27-MAR-1998;    98US-0049672.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Tang YT, Yue H, Lal P,   Corley NC,   Guegler KJ,   Baughn MR;
PI   Hillman JL, Au-Young J;
XX
DR   WPI; 2001-030926/04.
DR   P-PSDB; AAB36206.
XX
PT   New human immune system associated proteins (HISAP) and polynucleotides
PT   encoding the HISAP, useful for diagnosing, treating or preventing
PT   immune or cell proliferative disorders or infections -
XX
PS   Claim 3; Column 79-80; 54pp; English.
XX
CC   The present invention provides the coding and protein sequences for a
CC   number of human immune system associated proteins (HISAP8). These can be
CC   used in the diagnosis and treatment of various autoimmune disorders,
CC   immune or cell proliferative disorders or infections -
CC   infections and cell proliferation diseases. The diseases include AIDS,
CC   adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
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XX
SQ   Sequence 1431 BP; 314 A; 475 C; 379 G; 263 T; 0 other;

Query Match        86.5%;   Score 1237.2; DB 17; Length 1431;
Best Local Similarity  92.9%;  Pred. No. 5.4e-238;
Matches 1332;  Conservative 0;  Mismatches 93;  Indels 9;  Gaps 3;
```

```
Qy     1 ATGAAACACCTGTCGTTCTTCCTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
         ||||| || |||||  ||||||||||||  |||||| ||||||||||||||||||||||||
Db     1 ATGAAGCATCTGTGTTCTTCCTCCTGTGGCGGCTCCCAGATGGGTCCTGTCCCAG 60

Qy    61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTCGGGAGACCCTGTCCGCACC 120
         |||| ||||||| |||  ||||| ||||| ||||| ||||||||||||||||||| |||
Db    61 CTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy   121 TGGGTTGTCTCTGGTGGCTCCATCAGC---GGTTACTACTACTGGAGCTGGATCCGCCAG 177
         || || ||||||||| | ||||  ||| ||| || |||| |||  || ||  |||||||||
Db   121 TGCACTGTCTCTGGTGACTGCAGCAGGAGTAGTTACTCCTGGGGCTGCATCCGCCAG 180

Qy   178 ACCCCAGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGGACCACCAAC 237
         | ||| ||||| ||| |||||||||||||| ||||| ||| | || ||  ||| |||| |||
Db   181 CCCCCGGGAAGGGCCTGAGTGGATTGGGACTATCTA---TTATAGTGGGAGCACCTAC 237

Qy   238 TACAATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTC 297
         ||||| || |||||||||||||||||||||||| |  | |||||| |||||||||||||
Db   238 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGGCCAAGAACCAGTTC 297

Qy   298 TTCCTGAACTTGAATTCTGTGACCGCCGACACGGCCGTCTATTACTGTGCGAGAGGC 357
         | |||||| || | |||||||||||| ||||||| || |||||||||||||||  |
Db   298 TCCCTGAAGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGCGAGAACC 357

Qy   358 CCTCGCCCCTGATTGCACAACCATTGTTATGGCGGGTGGGTCGATGTCTGGGGCCGGGA 417
         | | | |  ||  |||| |||||    ||||||||  | |||||  || ||| ||||||
Db   358 TCGCCGCAGTATTACGA---TCTTTTGACTGGTTCCTTTCCCTCATACTGGGGCCAGGGA 414

Qy   418 GACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 477
         | |||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Db   415 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 474

Qy   478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 537
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   475 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 534

Qy   538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   535 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 594

Qy   598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 657
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   595 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 654

Qy   658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   655 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 714

Qy   718 GTGGACAAGAAAGCAGAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
         |||||||||||| ||  |||||||||||||||||||||||||||||||||||||||||||
Db   715 GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 774

Qy   778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 837
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   775 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 834

Qy   838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 897
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   835 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 894

Qy   898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   895 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 954

Qy   958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTGCTCACCGTCCTGCGAC 1017
         ||||||||||||||||||||||||||||||||||||||||
```

```
CC   Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC   gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC   erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ   Sequence 1567 BP; 346 A; 503 C; 428 G; 289 T; 1 other;

Query Match       86.3%;  Score 1234.8;  DB 22;  Length 1567;
Best Local Similarity   92.9%;  Pred. No. 1.6e-237;
Matches 1332;  Conservative   0;  Mismatches 87;  Indels 15;  Gaps 3;

Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTGTGGAGCTCCCAGATGGGTCCTGTCCCAG   60
         ||||||||||||||||||||||||||||||||||    |||||||||||||||||||||||
Db    78 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG  137

Qy    61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGCAGCCCTGTCCCGCCACC  120
         |||  |||||||||||| ||||| |||||  |||||||| || |||||||||| ||||||
Db   138 GTGCAGCTGCAGCAGTCGGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  197

Qy   121 TGCGGTGTCTCTGGTGGCTCCATC---AGGGGTTACTACTGGAGCTGGATCCGCCAGCC   177
         |||||||||||||||||||| |||     |||||||||||||||||||||| |||||||
Db   198 TGCGGTGTCTCTGGTGGCTCCATCACTAGTGGTGTTACTACTGGAGCTGGATCCGCCAGCC  257

Qy   178 ACCCCAGGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGGAATGTGCGACCACCAC  237
         | ||||||| ||||| |||||||||||||||| ||| ||||||||| |||| |||||||
Db   258 CCCCCAGGGGAAGGGGCTGGAGTGGATTGGGTACTACTGGAGCTGAGGAGTTCCAAGAACCCCCAG  314

Qy   238 TACAAATCCCTCCCTCAAGAGTCGAGTCCACCATTTCAAAAGACACGTCCAAGAACCAGTTC  297
         |||||| ||||||||||| |||| |||| ||||| ||| | | |||||||||||||||||||
Db   315 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTC  374

Qy   298 TTCCTGAACTTGAATTCTGTGACCACGGACACGGCCGTCTATTACTGTGCGAGAGGC  357
         ||  ||||||| |||      ||| | |||| |||||||||||||||||||
Db   375 TCCCTGAAGCTGAGCTCTGTGACTGCCGCAGACACGGCCGTGTATTACTGTGCCAGAG--  432

Qy   358 CCTCGCCCTGATTGCACAACCATTTGTTATGGCGGCTGGGTCGTGGGCCCGGGA  417
         |||
Db   433 ------ATGACGTAGGTTTAAGGGGGGGAACTACGGTATGGACGTCTCGGGGCCAGGGA  485

Qy   418 GACCTGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  477
         ||||||||||||||||| ||||||||| ||||||||| |||| |||||||||||||||||
Db   486 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  545

Qy   478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  537
         |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||||||
Db   546 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  605

Qy   538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  597
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  665

Qy   598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  657
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  725

Qy   658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  717
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  785

Qy   718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA  777
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786 GTGGACAAGAAAGCAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA  845

Qy   778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  837
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  905

Qy   838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  897
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  965

Qy   898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG  957
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 1025

Qy   958 CCGCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
         |||||||||||||||||||||||||||||||| |||||||||| |||||||||||||||||
Db  1026 CCGCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1085

Qy  1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1086 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1145

Qy  1078 CCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTACACC 1137
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1146 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1205

Qy  1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1206 CTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1265

Qy  1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1266 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1325

Qy  1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1326 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1385

Qy  1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1386 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTTTTCTCATGCTCCGTGATGCATGAG 1445

Qy  1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
         |||||||||||||||||||||||||||||||||||||||
Db  1446 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1499
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RESULT 10
AAT26889
ID   AAT26889 standard; cDNA; 1418 BP.
XX
AC   AAT26889;
XX
DT   30-OCT-1996 (first entry)
XX
DE   Anti-rhesus D recombinant antibody D7C2 heavy chain cDNA.
XX
KW   Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
KW   rhesus positive; rhesus negative; haemolysis; heavy chain; gamma 1;
KW   variable region; insect host cell; baculovirus; recombinant production;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..57
FT                   /*tag= a
FT                   /note= "encoded by synthetic linker corresp. to
FT                   mouse VH gene signal sequence"
FT   mat_peptide     58..1416
FT                   /*tag= b
FT                   /product= heavy chain
FT                   /note= "constructed from PCR fragments coding for
FT                   human gammal heavy chain constant region
FT                   and the variable region from anti-rhesus D
FT                   antibody D7C2"
XX
PN   FR2724182-A1.
XX
PD   08-MAR-1996.
XX
PF   02-SEP-1994;                              94FR-0010566.
XX
PR   02-SEP-1994;                              94FR-0010566.
XX
```

PA   (INSP) INST PASTEUR.
PA   (PROT-) PROTEINE PERFORMANCE.
XX
PI   Chaabihi H, Edelman L, Kaczorek M, Margaritte C;
XX
DR   WPI; 1996-162018/17.
DR   P-PSDB; AAR93166.
XX
PT   Recombinant anti-rhesus D monoclonal antibody - expressed by
PT   baculovirus-transformed insect cells and useful for preventing
PT   haemolysis in new-born babies
XX
PS   Claim 1; Page 35-37; 46pp; French.
XX
CC   The human monoclonal antibody D7C2, of isotype IgM, recognises a
CC   30-32 kD polypeptide on the membrane of rhesus positive red blood
CC   cells. The antibody agglutinaces rhesus positive cells but not
CC   rhesus negative cells and is useful diagnostically and also for
CC   preventing haemolysis in new-born rhesus positive babies.
CC   Recombinant IgM-D7C2 can be produced by insect cells which have
CC   been transformed by a baculoviral vector comprising a D7C2
CC   expression cassette. The present sequence encodes a recombinant
CC   IgM-D7C2 heavy chain fused to a mouse VH signal peptide.
XX
SQ   Sequence 1418 BP; 333 A; 458 C; 378 G; 249 T; 0 other;

Query Match   85.4%;   Score 1221.6;   DB 17;   Length 1418;
Best Local Similarity 92.9%;   Pred. No. 7e-235;
Matches 1317;   Conservative   0;   Mismatches   89;   Indels   12;   Gaps   3;

Qy   13 TGGTTCTTCCTCCTCCTGGTTGGCAGCTCCCAGATGGTCCTGTCCCAGGTGAAGCTGCAG 72
            ||||||||| ||| ||| |||||||| ||||| |||||||||||||||||||||||||||
Db   13 TGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCCAGGTCCAACTGCAG 72

Qy   73 CAGTGGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGGCACCTGCCGTTGTCTCT 132
            |||||||| |||||| ||||| |||||||||||||||||||||||| |||||||||||
Db   73 CAGTGGGGGGCCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCACTGCACTGTCTAT 132

Qy   133 GGTGGCTCCATCAGCGGTGTTACTACTACTGGACCTGACCTCGGCCAGGACCCCAGGAGGGA 192
            ||||||||||||||||||| ||| |||||| ||||||||||||||||||||||||||
Db   133 GGTGGCGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCCGCCAGGAAGGGG 189

Qy   193 CTGGAGTGGATTGGCCATATTATTATGGTAATGGTGCGACCACCAACTACAAATCCCTCCCTC 252
            |||||||||||||||||||| || ||||||||||||||||||| |||||||||
Db   190 CTGGAGTGGATTGGGGAAATCAA---TCATAGTGAAGCACCAACTACAACCCGTCCCTC 246

Qy   253 AAGAGTCGAGTCACCATTTCAAAAGACACAGTCCAAGAACCAGTTCTTCCTGAACTTGAAT 312
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   247 AAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAACTGAAC 306

Qy   313 TCTGTGACCGACGCGGACACGGCCCGTCTATTACTGTGCGAGAGGCCCTCGCCCTGATTGC 372
            |||||||||||||||||||||||||| ||| |||||||| ||||||||| |||||
Db   307 TCTGTGACCGACGCGGACACGGCCCGTGTGTATTACTGTGCGAGGG------CCCCAGAGTAT 360

Qy   373 ACAACCATTTGTTATTGGCGCGGCTGGGTCGATGTCTGGGGCCCCGGAGACCTGGTCACCGTC 432
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AAATGGAAGTATCATGGGGACTGGTTCGACCCCTGGGGCCAAGGTACCACTGTCACCGTC 420

Qy   433 TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTCCAAGAGCACC 492
            |||||||| |||||| ||||||||||||||||||||||||||||||||||||| ||||
Db   421 TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 480

Qy   493 TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG 552
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG 540

Qy   553 GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG 612
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG 600

Qy   613 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 672
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 660

Qy   673 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA 732
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA 720

Qy   733 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 792
            |||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||||
Db   721 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 780

Qy   793 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 852
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 840

Qy   853 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 912
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 900

Qy   913 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 972
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 960

Qy   973 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1032
            ||||||||||||||| ||||||||||||||||| |||||||||||||||||||||||||
Db   961 TACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1020

Qy   1033 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1092
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   1021 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1080

Qy   1093 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1152
            ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1081 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1140

Qy   1153 GATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1212
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1141 GATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1200

Qy   1213 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1260

Qy   1273 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1332
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1320

Qy   1333 AGGTGGCAGCAGGGGAACGTGTTCTCCTGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1392
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGGTGGCAGCAGGGGAACGTGTTCTCCTGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1380

Qy   1393 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG 1430
            ||||||||||||||||||||||||||||||||||||||
Db   1381 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG 1418

RESULT 11
AAT62868
ID   AAT62868 standard; DNA; 1404 BP.
XX
AC   AAT62868;
XX
DT   18-OCT-1997   (first entry)
XX
DE   Human gamma-4 heavy chain DNA.
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9 gamma 4; ss.
XX
OS   Homo sapiens.
XX
PN   WO9709351-A1.
XX

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PD   13-MAR-1997.
XX
PF   05-SEP-1996; 96WO-US14324.
XX
PR   06-SEP-1995; 95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   P-PSDB; AAW14925.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Disclosure; Page 82-84; 155pp; English.
XX
CC   DNA sequences (AAT62868-70) respectively code for the heavy chain
CC   regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC   mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC   mutations. They can be used to provide novel monoclonal and
CC   chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC   gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC   combined with the antigen binding domains (see also AAW14922-23) of
CC   macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC   show high affinity to human CD4, have little or no immunogenicity
CC   in humans and show reduced or absence of effector function. They
CC   can be used to treat autoimmune diseases such as rheumatoid
CC   arthritis.
XX
SQ   Sequence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;

Query Match             81.9%;  Score 1171.4;  DB 18;  Length 1404;
Best Local Similarity   90.0%;
Matches 1288;  Conservative    0;  Mismatches 116;  Indels   27;  Gaps  2;
                                   Pred. No. 7.4e-225;
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Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG  60
          |||||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||
Db      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCCCCCAGATGGGTCTTGTCCCAG  60

Qy     61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGCTCCCGCACC 120
          |||  |||||||| || ||||| || |||| || |||||||||||||||| | ||| ||||
Db     61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy    121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTACTGGAGCTGGATCCGCCAGACC 180
          ||| |||||||||||||||||||||||  |||  || ||||| | |||||||||||||| ||
Db    121 TGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTGACTATTATTGGTTCTGGATCCGCCAGTCC 180

Qy    181 CCAGGGAGGGGACTGGAGTGGATTGGGTATATCTATTATAGTGGTAACTGTGAATATGGTGGTGGCCGACCACCAACTAC 240
          ||||||| |||||||||||||||||||||||||||||||||||||| |
Db    181 CCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTATAGTGGTAGCACCAATTAC 240

Qy    241 AATCCCTCCCTCAAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 300
          |||||||||||||| ||| |    |  |||||||||| |||||||||||||||| |||||||
Db    241 AATCCCTCCCTCAAGAGTCTCAATCAGTCTCATTTCAATAGACACGTCCAAGAACCTCTTCTCC 300

Qy    301 CTGAACTGACTTGATTCTGTGACCGACGCGGGACACGGCCGCGTCTATTACTGTGCGAGAGAGCCCT 360
          ||||||||  |   ||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGAACTGAG----GTCTGTGACCGACGCGGGACACGGCCGCGTCTATTACTGTGCGA-------- 352

Qy    361 CGGCCCTGATTGCACAACCATTGTTATGGCGGCTGGGTCGATGTCTGGGGCCCGGGGAGAC 420
                     ||| |   ||||| ||| ||  |      |||||||||||||| ||| ||
Db    353 -------GTAATATATTGAAATATCTTCACTGGTTATTATACTGGGGCCCAGGGAGTC 402

Qy    421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||| ||| |
Db    403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGC 462

Qy    481 TCCAAGAGCACCTCTGGGGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    463 TCCAGGAGCACCTTCCGAGAGCACAGCCGCCCTGGCGTCGCTGCTGCTGGTCAAGGACTACTTCCCC 522

Qy    541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 582

Qy    601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 642

Qy    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
          |||||||||||  |||||||||| ||||||||| ||||||||||||||||||||||||||
Db    643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG 702

Qy    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
          ||||||| ||| ||| ||||||  ||         |    |  ||| |   |||| ||||||
Db    703 GACAAGAGAGTTGAGTCCAAATATGG-------TCCCCATGCCCATCATGCCCAGCA 753

Qy    781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
          |||||  ||||||||||||| |||||||||||| ||||||||||||||||||||||| |||
Db    754 CCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC 813

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGAAGACCCT 900
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||| |
Db    814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCC 873

Qy    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          ||||||  ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 933

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 993

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1080
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||  |  ||
Db    994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC 1053

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG 1113

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
          ||||||||||  ||| || |||||||||||||||||||||||||||||||||||||||||
Db   1114 CCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1173

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1233

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTCACC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC 1293

Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||||||| |||||||||||||||||||||||||||||||
Db   1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1404
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RESULT 12
AAT62870
ID   AAT62870 standard; DNA; 1404 BP.
XX
AC   AAT62870;
XX
DT   18-OCT-1997 (first entry)
XX
DE   Human gamma-4PE heavy chain DNA.
XX
```

KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
XX
OS Homo sapiens.
XX
PN WO9709351-A1.
XX
PD 13-MAR-1997.
XX
PF 05-SEP-1996; 96WO-US14324.
XX
PR 06-SEP-1995; 95US-US23894.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Hanna N, Newman RA, Reff ME;
XX
DR WPI; 1997-201913/18.
DR P-PSDB; AAW14927.
XX
PT Chimeric antibody comprising monkey variable domains and human
PT constant domains - affects CD4-mediated immune functions, esp.
PT useful for treatment of autoimmune disease, e.g. rheumatoid
PT arthritis
XX
PS Disclosure; Page 91-93; 155pp; English.
XX
CC DNA sequences (AAT62868-70) respectively code for the heavy chain
CC regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC mutation. They can be used to provide novel monoclonal and
CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC combined with the antigen binding domains (see also AAW14922-23) of
CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC show high affinity to human CD4, have little or no immunogenicity
CC in humans and show reduced or absence of effector function. The
CC gamma-4E and -4PE mutations confer activity enhanced stability and
CC eliminate depleting activity. The antibodies can be used to treat
CC autoimmune diseases such as rheumatoid arthritis.
XX
SQ Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;

Query Match   81.6%; Score 1168.2; DB 18; Length 1404;
Best Local Similarity   89.9%; Pred. No. 3.2e-224;
Matches 1286; Conservative   0; Mismatches 118; Indels   27; Gaps   2;

Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTTCCTGTCCCAG 60
          ||||||||||||||||||||||||||||| |||||||||||||||||| ||||||||||||
Db   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCTTGTCCCAG 60

Qy   61 GTGAGCTGCAGCAGTGGGGCGAAGGACTTCTCGAGCCTTCGGAGAACCAGGTCCCGCACC 120
          ||| | |||| |||| ||||||| |||| ||| ||| || ||||| |||||||| ||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

Qy   121 TGCGGTTGTCTCTGGCTCCATCAGCGGGTTACTACTAGTGGAACTGGATCCGGCCAGACC 180
          |||| ||||| ||||| ||| |||| ||||||| |||| ||||| |||||||||||||||
Db   121 TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGTGACTATTATTGGTTCTGGATCCGGCCAGTCC 180

Qy   181 CCAGGAGGGACTGGATGATTGGCCATATTATGGTAATAGTGCGACCACCAACTAC 240
          |||||||| | || ||| | ||||| ||| |||| ||| ||||||| ||||| |||
Db   181 CCAGGGAAGGGACTGGAGTGGATGGGCTACATCTATTACAGTGGTGGGGCACCAATTAC 240

Qy   241 AATCCCTCCAAGAGTCACCATTTCAAAAGAACACAGTCCAAGAAACCAGTTCTTC 300
          ||||||||| ||| |||||||| || ||| ||| || |||| |||||||| ||||
Db   241 AATCCCTCCCTCAACAATGACAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTTTCTCC 300

Qy   301 CTGAACTTGAATTCGTGACCGACGGACGACGCGGACACGGCCGTCTATTACTACTGTGCGAGAGGCCCT 360
          |||||||| ||| || |||| ||||||||| ||| |||| ||||||| ||||||||||
Db   301 CTGAAACTGAGCTCTGTGACCGCCGCCGACACGGCCGTCTATTACTGTGCGA 352

Qy   361 CGCCCTGATTGCACAACCATTGTTATGGGGCGGGCCCGGGAGAC 420
          ||||| ||| | || || ||||||
Db   353 GTAATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTC 402

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
          |||||||||||||||||| ||||||||||||||||| |||||||||||||||||||||||
Db   403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGC 462

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   463 TCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 522

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 582

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
          ||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||||||
Db   583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 642

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG 702

Qy   721 GACAAGAAAGCAGAGCCCAAAATCTTGTGACAAAATCTCACACATGCCCACCGTGCCAGCA 780
          |||||||||||||||||| |||||| ||| || -------TCCCCCATGCCCACCGTGCCCAGCA
Db   703 GACAAGAGAGTTGAGTCCAAATATGG------TCCCCCATGCCCACCGTGCCCAGCA 753

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
          ||||||| |||||||||||| ||| |||||||||| ||||| ||||||||||||||||
Db   754 CCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC 813

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGAAGACCCT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCC 873

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          ||||| |||||||||||||||||||| ||||| |||||||||| ||||| |||||||| |
Db   874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 933

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          |||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db   934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 993

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
          ||||||||||| ||||||||||||||||||||||| |||||||||||| | ||||| ||
Db   994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC 1053

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG 1113

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGGC 1200
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1114 CCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1173

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1233

Qy   1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTAACC 1293

Qy   1321 GTGGACAAGAGAGCAGGTGGCAGCAGGGGAACGTCTTCAAGAACCAGTTCTTC 1380
          ||||||||||||| |||||||||| |||||||| |||||||||||||||||||
Db   1294 GTGGACAAGAGAGCAGGTGGCAGGAGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          ||||||||||||||| ||||||||||||||||||||||||||| |||||||
Db   1354 CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1404

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RESULT 13
AAT62869
ID   AAT62869 standard; DNA; 1404 BP.
XX
AC   AAT62869;
XX
DT   18-OCT-1997 (first entry)
XX
DE   Human gamma-4E heavy chain DNA.
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9 gamma-4E; ss.
XX
OS   Homo sapiens.
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996; 96WO-US14324.
XX
PR   06-SEP-1995; 95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   P-PSDB; AAW14926.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Disclosure; Page 86-88; 155pp; English.
XX
CC   DNA sequences (AAT62868-70) respectively code for the heavy chain
CC   regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC   mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC   mutations. They can be used to provide novel monoclonal and
CC   chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC   gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC   combined with the antigen binding domains (see also AAW14922-23) of
CC   macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC   show high affinity to human CD4, have little or no immunogenicity
CC   in humans and show reduced or absence of effector function. The
CC   gamma-4E and -4PE mutations confer activity enhanced stability and
CC   eliminate depleting activity. The antibodies can be used to treat
CC   autoimmune diseases such as rheumatoid arthritis.
XX
SQ   Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;

Query Match             81.5%;  Score 1166.6;  DB 18;  Length 1404;
Best Local Similarity   89.8%;  Pred. No. 6.7e-224;
Matches 1285;  Conservative     0;  Mismatches  119;  Indels   27;  Gaps    2;
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Db  181 CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCAATTAC  240

Qy  241 AATCCCTCCCTCAAGAGTCGAGTCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTC   300
        |||||||||||| ||||| |||||| ||||||| |||| |||||||||||||| ||||||
Db  241 AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC  300

Qy  301 CTGAACTTGAATTCTGTGACCGACGCGGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT  360
        ||||| || ||| ||||||||||| |||||||||||||||||||||||||||||
Db  301 CTGAAACTGAGGTCTGTGACCGACCGGGACACGGCCGTCTATTACTGTGCGA--------  352

Qy  361 CGCCCTGATTGCACAACCATTGTTATGGCGCTGGTCGTGATGTCTGGGGCCGGGGAGAC   420
Db  353 --------GTAATATATTGAAAATATCTTCACTGGTTATTATATACTGGGGCCAGGGAGTC  402

Qy  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCC   480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGGCCATCCGTCTTCCCGTGGCGCCCTGC   462

Qy  481 TCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540
        ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  463 TCCAGGAGCACCTCCGAGAGCACAGCCGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  522

Qy  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   600
        |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG   582

Qy  601 GCTGTCCTACAGTCCTCACTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
Db  583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  642

Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   720
        |||||||||||||||||||||||||||||| ||||||||| |||||||||||||||||||
Db  643 AGCTTGGGCACGCAGACGTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG   702

Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA   780
        ||||||||| ||||||||||||||||||||||||||||||||||||| ||  |||||
Db  703 GACAAGAGAGTTGAGTCCAAATATGG--------TCCCCATGCCCATCATGCCCAGCA   753

Qy  781 CCTGAACTCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840
        |||||| ||||||||| |||||||||||||||||||||||||||||||||||| ||||||
Db  754 CCTGAGTTCGAGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC   813

Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCG   873

Qy  901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   933

Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTGTCAGCGTCTGTCAGCGTCCTCCACCAG  1020
        |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG   993

Qy 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCAACAACCCCTCCCAGCCCCC   1080
        |||||||||| ||||||||||||||||||||||||| ||||||  ||||||| ||||||
Db  994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC  1053

Qy 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
        |||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||||
Db 1054 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1113

Qy 1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
        ||||||||||||||||||||| ||||||||||||||||||||||| ||||||||||||||
Db 1114 CCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1173

Qy 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1233

Qy 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC  1293
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Qy    1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTCAGCTCCCAGATGGGTGTCCCCAG    60
        ||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||
Db    1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTCAGCTCCCAGATGGGTGTTGTCCCAG    60

Qy   61 GTGAAGCTGCACGAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCGTCACC   120
        ||||| || |||||||||||||| |||| ||  |||||||||| | |||||||||||
Db   61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC   120

Qy  121 TGCGTGTCTGTGTGGTGTCCATCAGCGGTTACTCAGCGGTTACTCAGGCGGT   180
        |||||| |||||| ||||||||||||||||||||||| ||| |||||
Db  121 TGCACTGTCTCTGGTGGCTCCATCAGCAGCGGTGACTATTGGTTCTTGGATCCGGCGTCC  180

Qy  181 CCAGGGAAGGGGACTGGAGTGGATTGGGATGCCATATTTTATGGTAATGGTGACCACCAACTAC  240
        |||||||||| ||| ||||||| | ||||| | || ||||| | |||||| || ||||||||
Db  181 CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCAACTAC  240
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Qy    61 GTGAAGCTGCAGCAGTGGGCGGAAGGACTTCTGCAGCCTTCGGACCCTGTCCCGCACC       120
         ||||||||||||||||||||||||||||||||||| ||||||||||||  |||| ||
Db    61 GTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTCGGTCTCGGTGAAGGTCTCC       120

Qy   121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGAGCTGGATCCGCCAGACC       180
         || ||| ||||||||||||  |||| || |||||||||||||||||
Db   121 TGCAAGGCTTCGGAGGCACCACTACATCG---ACCAACTATCGGCTGGGTGCGACAGGCC       177

Qy   181 CCAGGGAGGGGACTGGAGTGGATCGGAT--GGATTTATGGTAATGTGGACCACCAACTAC       240
         ||||||||||  |||||||||||||  ||| || |||| || |||  || || || ||
Db   178 CCTGGACAAGGGCTTGAGTGGATGGGAGGGGATCATCCCTCTCTTCCGGTCCGCACACTAC       237

Qy   241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAGACACGTCCAAGAACCAGTTCTTC       300
         |   ||| |  |||  ||||||  |||||||||  ||| ||  ||  ||||  ||
Db   238 GCACAGAAGTTCCAGGGCAAAGTCTGATTACCGGGGACACGAGTCCACGAGCACAGCTTAC       297

Qy   301 CTGAACTTGAATTCTGTCCGACGCGGACACGGCGTCTATTACTGTGCGAGAGGGCCCT       360
         ||    ||||| | | |||  ||  ||||||||||  ||  |||||||||||||||| ||
Db   298 CTGGAACTGACCAGCCTCACATCTGAGGACACGGCCGTATATTACTGTGCGAGGGTCCTT       357

Qy   361 CGCCCTGATTGCACAACCATTGTTATGGTGCTGGGTGGTCTGGGCCGGGAGAC       420
         ||   |||||||  ||  |||| | |||||||||||  ||||  || ||||||||
Db   358 AGGGGTTATTGTCGTGGTTCCTGCTATGACTGGCTCGACCCCTGGGCCAGGGCACC       417

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC       480
         ||||||||||||||||||  |||     |||||||  |||||  |||||||||||||||||
Db   418 CTGGTCACCGTCTCCTCAGCTAGTC   CAAGGGCCCATCCGTCTTCCCCCTGGCACCCTCC       477

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC       540
         |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db   478 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCT       537

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG       600
         ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   538 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG       597

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC       660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   598 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC       657

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG       720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   658 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG       717

Qy   721 GACAAGAAAGCAGAGCCCAAAATCTTGTGACAAAAACTCACACATGCCCACCGTGCCCAGCA       780
         |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   718 GACAAGAAAGTTGAGCCCAAAATCTTGTGACAAAAACTCACACATGCCCACCGTGCCCAGCA       777

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCTC       840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   778 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCTC       837

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT       900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   838 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT       897

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAAAGCGG       960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   898 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG       957

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG       1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   958 CGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAG       1017

Qy  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC       1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1018 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC       1077

Qy  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG       1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1078 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG       1137
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Qy  1321 GTGGACAAGAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT       1380
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  1294 GTGGACAAGAGAGCAGGTGGCAGCAGGGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT       1353

Qy  1381 CTGCACCACCACACCACACGCAGAAGAGCCTCCTCCCGTCTCCGGTAAATGA       1431
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1354 CTGCACCACCACACCACACACAGAAGAGCCTCCTCCTGTCTCTGGGTAAATGA       1404
```

```
RESULT 14
AAH74680
ID    AAH74680  standard; DNA; 1428 BP.
XX
AC    AAH74680;
XX
DT    29-OCT-2001 (first entry)
XX
DE    Nucleotide sequence of a single chain antibody.
XX
KW    Complementarity determining region; CDR; single chain antibody; ScFv;
KW    hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW    envelope glycoprotein; ss.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT
FT    CDS             1..1428
FT                    /*tag=  a
FT                    /product= "single chain antibody"
XX
PN    WO200158459-A1.
XX
PD    16-AUG-2001.
XX
PF    13-FEB-2001; 2001WO-JP00967.
XX
PR    14-FEB-2000; 2000JP-0034906.
XX
PA    (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI    Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
XX
DR    WPI; 2001-496986/54.
DR    P-PSDB; AAG63640.
XX
PT    Remedies for hepatitis C containing substances with antiviral effects
PT    e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT    compounds, by inhibiting binding of hepatitis C virus envelope
PT    glycoprotein or CD81 -
XX
PS    Claim 41; Page 105-108; 138pp; Japanese.
XX
CC    The present sequence encodes a single chain antibody of the invention.
CC    The specification describes a substance can inhibit the binding between
CC    hepatitis C virus (HCV) and cells with potential HCV infection, cells
CC    with expression of CD81, or CD81. This substance is especially an
CC    antibody with affinity towards HCV E2/NS1 protein, containing amino
CC    acid sequences based on the complementarity determining region (CDR) 1,
CC    CDR2 and CDR3 of the H and L chain variable regions. The antibody
CC    inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor.
CC    The antibodies and drugs are used for treatment and/or prevention of
CC    hepatitis C, or for diagnosis of hepatitis C.
XX
SQ    Sequence 1428 BP; 315 A; 462 C; 394 G; 257 T; 0 other;
```

```
Query Match             79.3%;  Score 1135;  DB 22;  Length 1428;
Best Local Similarity   87.6%;  Pred. No. 1.4e-217;
Matches 1253;  Conservative    0; Mismatches 175;   Indels    3; Gaps    1;
```

```
Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG       60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG       60
```

```
Qy  1141  CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCTGACCTGCCTGGTCAAAGGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1138  CCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCTGACCTGCCTGGTCAAAGGC 1197

Qy  1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1198  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTAC 1257

Qy  1261  AAGACCACGGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1258  AAGACCACGGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1317

Qy  1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1318  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1377

Qy  1381  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1378  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1428
```

RESULT 15
```
AAT61241
ID   AAT61241 standard; DNA; 1428 BP.
XX
AC   AAT61241;
XX
DT   13-MAY-1997  (first entry)
XX
DE   Human anti-RSV monoclonal antibody RF-1 heavy chain DNA.
XX
KW   Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;
KW   RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;
KW   Epstein Barr virus; immortalisation; recombinant antibody; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..57
FT                   /*tag= a
FT   mat_peptide     58..1425
FT                   /*tag= b
XX
PN   WO9640252-A1.
XX
PF   06-JUN-1996;  96WO-US10070.
XX
PR   07-JUN-1995;  95US-0488376.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Brams P,  Chamat SS,  Heard CJ,  Newman RA,  Pan L;
PI   Walsh EE;
XX
DR   WPI; 1997-099892/09.
DR   P-PSDB; AAW11639.
XX
PT   Human monoclonal antibody specific for respiratory syncytial virus
PT   fusion protein - used for the prevention and treatment of RSV
PT   infection
XX
PS   Claim 9; Fig 9b-c; 85pp; English.
XX
CC   A DNA sequence (AAT61241) codes for a polypeptide (AAW11639) comprising
CC   a leader sequence. RF1 heavy chain variable region (see also
CC   AAW11637), and human gamma 1/constant region. RF1 is a human
CC   monoclonal antibody (hMAb) specific for the fusion protein of
CC   respiratory syncytial virus (RSV). The DNA sequence, in vector
CC   NEOSPLA, can be used to produce the light chain construct in
CC   transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy
CC   and light chain constructs (see also AAT61240, AAT61242, AAT61279) are
```

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CC   similarly used.  The transfected host cells provide a constant,
CC   stable supply of anti-RSV F-protein hMAbs for use in the treatment
CC   or prevention of RSV infection.
XX
SQ   Sequence 1428 BP; 326 A; 465 C; 372 G; 265 T; 0 other;

Query Match             78.6%;   Score 1125.2;   DB 18;  Length 1428;
Best Local Similarity   88.6%;   Pred. No. 1.2e-215;
Matches 1256;  Conservative   0;  Mismatches 153;  Indels   9;  Gaps   3;

Qy   17  TCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGGGTGAAGCTGCAGCAGT  76
         |||||||| ||||||| |||||   |  |||||||||  |||||||||||||||| |||||
Db   17  TCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTTGCTACGCGTGTTGCCAGGTGCAGGAGT  76

Qy   77  GGGGGAAGGACTTCGAGCCTTGGGACAACCCACAGAGACCCTTCACGGTGTTGTCTCGGTG 136
         ||||||||||||||||||||||||     |||| |   ||||||||||||||| ||||||||
Db   77  CTGGTCCTGGTGCTGGAGTGCGTGGTGAAACCCACAGAGACCCTGACCTGGTCCACCGTCTCTGGGT 136

Qy  137  GCTC---CATCAGCGGTTACTACTACTGACCTGGATCCGCCAGACCCCAGGGAGGGGGAC 193
         | |     |||||| | ||  ||  | |||||| ||  ||||| | ||| |||||||||||
Db  137  TCTCACTCAGCAACCCTAGAATGGTGTGACTGGATCCGCCAGCCCCCGGGGAAGGGGCCC 196

Qy  194  TGGAGTGGATTGGCCATATTTATGTGAAGTGGTAATGAATGTGCGACCACCAACTACAATCCCTCCTCA 253
         |||| || | ||| ||||    ||||         | ||||| || ||   |   |||  | ||| || ||
Db  197  TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAGTC---CTTCAGTCCTTCTCTGA 253

Qy  254  AGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTCCTGAACTTGAATT 313
         |||| || |||| ||||||||||||    |||||||||| |||||||||||||||| ||
Db  254  AGAGCAGACTCACCACCTCCCAGGACACACCTCCAGAGACCGGTCGTCCTTAAGCTTGACCA 313

Qy  314  CTGTGACCGACGCGGACACGGCCGTCGTGTTATTACTGTGCGAGAGGCCCTGCCCCTGATTGCA 373
         | || || || ||  || ||  |||||||| ||||      ||| | ||  |||||| || ||
Db  314  ACGTGACCCGTGGCACAGCCACCATATTACTGTGC---ACGGGTAGGACTGTATGACA 370

Qy  374  CAACCATTTGTTATGGCGCTGGGTGGATGTCTGGGGCCAGGGAGACCTGGTCACCGTCT 433
         |  |||| |  ||||  || | |  ||||  ||||   ||||  |||||||||||||||
Db  371  TCAATGCTTATTACCTATACTACCTGGATTATTGGGGCCAGGGAACCCTGGTCACCGTCT 430

Qy  434  CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCTCCAAGAGCACCT 493
         ||||||||||||||||||||||||||  ||||||||| ||| ||||||  ||||||||||||
Db  431  CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCTGCTCCTCCAAGAGCACCT 490

Qy  494  CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 553
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  491  CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 550

Qy  554  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 613
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  551  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 610

Qy  614  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGTTGGGCACCC 673
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  611  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGTTGGGCACCC 670

Qy  674  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG 733
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  671  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG 730

Qy  734  AGCCCAAATCTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 793
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  731  AGCCCAAATCTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 790

Qy  794  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 853
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  791  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 850

Qy  854  CCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA 913
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  851  CCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA 910

Qy  914  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 973
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  911  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 970
```

```
Qy    974  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1033
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1030

Qy   1034  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1093
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1090

Qy   1094  TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091  TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1150

Qy   1154  ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151  ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1210

Qy   1214  ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC  1273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211  ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC  1270

Qy   1274  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1271  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1330

Qy   1334  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1390

Qy   1394  ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
           ||||||||||||||||||||||||||||||||||||||
Db   1391  ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1428
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Search completed: April   5, 2003, 20:19:18
Job time : 396.719 secs

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OM nucleic - nucleic search, using sw model
                  GenCore version 5.1.3
           Copyright (c) 1993 - 2003  Compugen Ltd.

Run on:      April  5, 2003, 19:13:54 ; Search time 2723.68 Seconds
                                        (without alignments)
                             8508.978 Million cell updates/sec

Title:       US-09-758-173-3
Perfect score: 1431
Sequence:    1 ATGAAACACCTGTGGTTCTT..........CCCTGTCTCCGGGTAAATGA 1431

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:    16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:    32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :       EST:*
             1:  em_estba:*
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             7:  em_estro:*
             8:  em_htc:*
             9:  gb_est1:*
             10: gb_est2:*
             11: gb_htc:*
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             20: em_gss_pln:*
             21: em_gss_vrt:*
             22: em_gss_fun:*
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             26: em_gss_pro:*
             27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	902	63.0	1020	14	BQ062878	BQ062878 AGENCOURT
2	864	60.4	947	14	BQ709771	BQ709771 AGENCOURT
3	850.4	59.4	958	14	BQ706140	BQ706140 AGENCOURT
4	842.4	58.9	926	12	BQ755166	BQ755166 602711488
5	831.2	58.1	901	13	BM007892	BM007892 603617577
6	830.4	58.0	988	14	BQ708857	BQ708857 AGENCOURT
7	824.4	57.6	1029	14	BQ063185	BQ063185 AGENCOURT
8	822.8	57.5	887	14	BQ711255	BQ711255 AGENCOURT
9	822.2	57.5	918	14	BQ708022	BQ708022 AGENCOURT
10	815.2	57.0	995	14	BM914540	BM914540 AGENCOURT
11	808.8	56.5	881	14	BQ711291	BQ711291 AGENCOURT
12	800.2	55.9	1031	14	BQ064886	BQ064886 AGENCOURT
13	797.4	55.7	936	14	BQ711727	BQ711727 AGENCOURT
14	796	55.6	940	14	BQ705928	BQ705928 AGENCOURT
15	787.4	55.0	977	14	BQ710532	BQ710532 AGENCOURT
16	786.4	55.0	980	14	BM914504	BM914504 AGENCOURT
17	785.2	54.9	843	13	BM007897	BM007897 603617582
18	778.8	54.4	991	14	BQ708936	BQ708936 AGENCOURT
19	777.2	54.3	973	14	BQ706204	BQ706204 AGENCOURT
20	772.6	54.0	930	13	BM007597	BM007597 603616995
21	770.6	53.9	981	14	BM914528	BM914528 AGENCOURT
22	764.2	53.4	926	14	BQ710304	BQ710304 AGENCOURT
23	759.4	53.1	917	14	BQ708169	BQ708169 AGENCOURT
24	756.6	52.9	961	14	BQ710233	BQ710233 AGENCOURT
25	752.4	52.6	945	14	BQ712403	BQ712403 AGENCOURT
26	750.4	52.4	1012	14	BM914556	BM914556 AGENCOURT
27	750.2	52.4	783	13	BM007838	BM007838 603617519
28	748	52.3	895	14	BQ708303	BQ708303 AGENCOURT
29	741.4	51.8	1026	14	BM914288	BM914288 AGENCOURT
30	738	51.6	914	14	BQ712363	BQ712363 AGENCOURT
31	733.8	51.3	913	14	BQ707472	BQ707472 AGENCOURT
32	733.6	51.3	944	14	BQ712397	BQ712397 AGENCOURT
33	732.8	51.2	919	14	BQ709339	BQ709339 AGENCOURT
34	732.6	51.2	936	14	BQ707530	BQ707530 AGENCOURT
35	731.8	51.1	906	14	BQ711709	BQ711709 AGENCOURT
36	730.4	51.0	1014	14	BM914505	BM914505 AGENCOURT
37	729.6	51.0	973	14	BQ708902	BQ708902 AGENCOURT
38	728.8	50.9	888	12	BG757604	BG757604 602714780
39	728.4	50.9	941	14	BQ712021	BQ712021 AGENCOURT
40	728.4	50.9	925	14	BQ709853	BQ709853 AGENCOURT
41	727.6	50.8	991	14	BQ707621	BQ707621 AGENCOURT
42	726.8	50.8	855	13	BM007689	BM007689 603617119
43	726.2	50.7	870	12	BG757815	BG757815 602711335
44	725.8	50.7	925	14	BQ709152	BQ709152 AGENCOURT
45	725.8	50.7	923	14	BQ081523	BQ081523 AGENCOURT

ALIGNMENTS

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RESULT 1
BQ062878
LOCUS       BQ062878            1020 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6826949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
            5', mRNA sequence.
ACCESSION   BQ062878
VERSION     BQ062878.1  GI:19890085
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1020)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094 row: h column: 21
            High quality sequence start: 21
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
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Db    756  CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGNAGAAACTACTACTAGACC  815
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Qy   1267  ACGCCTCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC  1326
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816  ACGCCTCNCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGGA  875

Qy   1327  AAGAGCAGGTGGCAGCAGGGAACGTCTTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC  1386
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Db    876  CAGAGCAGGTGGCAGCAGGGAACGTCTTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC  935

Qy   1387  AACCACTACACGCAGAGAGAGAGCCTCTCCCTGCTCCGGGTAAA  1428
           ||||||||||||||||||||||||||||||||||||||||| ||
Db    936  AACCACTACACGCAGAGAGAGCCTCTCCCTGTCTTCGGGTAA  977
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RESULT 2
BQ709771
LOCUS   BQ709771   947 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
            5', mRNA sequence.
ACCESSION   BQ709771
VERSION   BQ709771.1 GI:21848670
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 947)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466 row: m column: 16
            High quality sequence start: 3
            High quality sequence stop: 675.
FEATURES   Location/Qualifiers
     source   1..947
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278583"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

BASE COUNT   225 a   320 c   252 g   150 t
ORIGIN

Query Match   60.4%;   Score 864;   DB 14;   Length 947;
Best Local Similarity 99.4%;   Pred. No. 1.2e-195;
Matches 867; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy    560  GGAACTCAGGCGCCCCTGACCAGCGGCGTGCACACTTCCCGGCGTGTCCTACAGTCCTCAG  619
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Db      9  GGAACTCAGGCGCCCCTGACCAGCGGCGTGCACACTTCCCGGCGTGTCCTACAGTCCTCAG  68

Qy    620  GACTTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCT  679
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Db     69  GACTTCTACTCCCTCAGCAGCGTGGTGACCGTGACCGGCGCCCCCAGCAGCGTGGGCGACCCCAGACCT  128
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Page 1 column (left side, rotated):

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                /db_xref="taxon:9606"
                /clone="IMAGE:5924420"
                /clone_lib="NIH_MGC_99"
                /tissue_type="lymphoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Size-selected >500bp for average insert size
                1.8kb. Library constructed by Ling Hong in the laboratory
                of Gerald M. Rubin (University of California, Berkeley)
                using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                II RT (Life Technologies). Note: this is a NIH_MGC
                Library."

BASE COUNT    239 a    344 c    269 g    166 t
ORIGIN

Query Match          63.0%;    Score 902;   DB 14;   Length 1020;
Best Local Similarity 98.0%;   Pred. No. 1.1e-204;
Matches 923;  Conservative  0;  Mismatches  17;  Indels  2;  Gaps  1;
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Qy    489  CACCTCTGGGGGCACAGCGGCCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGGAACCGGT  548
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Db     36  CACCTCTGGGGGCACAGCGGCCCCTGGGCTGCCTGGTCAAAGACTACTTCCCCGGAACCGGT  95

Qy    549  GACGGTGTCGTGGAACTCAGGCGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT  608
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     96  GACGGTGTCGTGGAACTCAAGCGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT  155

Qy    609  ACAGTCCTCAGGACTTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  668
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Db    156  ACAGTCCTCAAGACTTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  215

Qy    669  CACCCAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTGGACAAGAA  728
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Db    216  CACCCAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTGGACAAGAA  275

Qy    729  AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT  788
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Db    276  AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT  335

Qy    789  CCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC  848
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Db    336  CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC  395

Qy    849  CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGAGCCTGAGGTCAA  908
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Db    396  CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGAGCCCTGAGGTCAA  455

Qy    909  GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA  968
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Db    456  GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA  515

Qy    969  GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAGGACTGGCT  1028
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516  GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAGGACTGGCT  575

Qy   1029  GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA  1088
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Db    576  GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA  635

Qy   1089  AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC  1148
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Db    636  AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC  695

Qy   1149  CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC  1208
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Db    696  CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC  755

Qy   1209  CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA--GAACAACTACAAGAGACC  1266
           ||||||||||||||||||||||||||||| || |||||||
Db     69  GACTTCTACTCCCTCAGCAGCGTGGTGACCGTGACCGGCGCCCCCAGCAGCGTGGGCGACCCCAGACCT  128
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                                                     DNA Sequencing by: Agencourt Bioscience Corporation
                                                     Clone distribution: MGC clone distribution information can be
                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                     http://image.llnl.gov
                                                     Plate: LLCM2464  row: a    column: 01
                                                     High quality sequence stop: 705.
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                     /clone="IMAGE:6277512"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT    229 a   319 c   256 g   150 t   4 others
ORIGIN

Query Match         59.4%;     Score 850.4; DB 14;   Length 958;
Best Local Similarity   99.2%;     Pred. No. 2.2e-192;
Matches  865;     Conservative   0;  Mismatches   6;   Indels   1;   Gaps   1;

Qy    558 GTGGAACTCAGGCGCCTGACCAGCGGCGGTGCACACCTTCCGGCTGTCCTACAGTCCTC 617
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Db     11 GTGGAACTCAGGCGCCTGACCAGCGGCGGTGCACACCTTCCGGCTGTCCTACAGTCCTC  70

Qy    618 AGGACTCTACTCCCTCCTCAGCAGCGGTGACCGTGCCTCCTCCAGCAGCTTGGGCACCCGAC 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 AGGACTCTACTCCCTCCTCAGCAGCGGTGACCGTGCCTCCTCCAGCAGCTTGGGCACCCGAC 130

Qy    678 CTACATCTGCACGTGAATCACAAGCCCAGCAACACCAAGGTGACAACAAGCAGAGCC 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CTACATCTGCACGTGAATCACAAGCCCAGCAACACCAAGGTGACAACAAGAAGTTGAGCC 190

Qy    738 CAAATCTTGTGACAAAACTCACACATGCCCCACCGTGCCCAGCACACTGAACTCCTGGGGG 797
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Db    191 CAAATCTTGTGACAAAACTCACACATGCCCCACCGTGCCCAGCACACTGAACTCCTGGGGG 250

Qy    798 ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC 310

Qy    858 TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG 917
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Db    311 TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG 370

Qy    918 GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA 977
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Db    371 GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA 430

Qy    978 CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA 1037
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Db    431 CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA 490

Qy   1038 GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC 1097
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Db    491 GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC 550

Qy   1098 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA 1157
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Db    551 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA 610

Qy   1158 GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCATCCCCAGCGACAT 1217
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Db    611 GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTATCCCAGCGACAT 670

Qy    680 ACATCTGCACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCA 739
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Db    129 ACATCTGCAAGTGCAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCA 188

Qy    740 AATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGCCCAGCTCCTGGGGGAC 799
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Db    189 AATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGCCCAGCTCCTGGGGGAC 248

Qy    800 CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG 859
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Db    249 CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG 308

Qy    860 AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 368

Qy    920 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 979
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Db    369 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 428

Qy    980 GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 1039
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Db    429 GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 488

Qy   1040 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1099
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Db    489 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 548

Qy   1100 AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC 1159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC 608

Qy   1160 TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCATCCCCAGCGACATCG 1219
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Db    609 TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTATCCCAGCGACATCG 668

Qy   1220 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC 1279
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Db    669 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC 728

Qy   1280 TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 1339
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Db    729 TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 788

Qy   1340 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC 1399
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Db    789 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGC 848

Qy   1400 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db    849 AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 880

RESULT 3
BQ706140
LOCUS       BQ706140                 958 bp    mRNA       linear      EST 16-JUL-2002
DEFINITION  AGENCOURT_8352177 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277512
            5', mRNA sequence.
ACCESSION   BQ706140
VERSION     BQ706140.1  GI:21845039
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 958)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
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Qy  1218  CGCCGTGAGTGGGAGAGCAATGGGCAGCCCGGAGAACAACTACAGAGACCACGCCTCCCGT 1277
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Db   671  CGCCGTGAGTGGGAGAGCAATGGGCAGCCCGGAGAACAACTACAGAGACCACGCCTCCCGT 730

Qy  1278  GCTGGACTTCCGACGGCGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAGAGAGGTG 1337
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Qy  1338  GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCTCCGTGATGAGGCTCTGCACAAACCACTACAC 1397
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Db   791  GCAGCAGGGGAAGGTCTTCTCATGCTCCGTGATGCTCCGTGATGAGGCTCTGCACAACCACTACAC 850

Qy  1398  GCAG-AAGAGCCCTCCCTGTCTCCGGGTAAA 1428
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Db   851  ACAGAAAGAGCCCTCCCTGTCTCCCGGGTAA 882
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RESULT 4
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LOCUS   BG755166   926 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602711488F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',
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ACCESSION   BG755166
VERSION   BG755166.1 GI:14065819
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 926)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1695 row: o column: 21
FEATURES   Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

BASE COUNT   225 a   309 c   244 g   148 t
ORIGIN

Query Match   58.9%; Score 842.4; DB 12; Length 926;
Best Local Similarity 98.2%; Pred. No. 1.8e-190;
Matches 852; Conservative   0; Mismatches 16; Indels   0; Gaps   0;

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Qy   564  CTCAGGCGCCCTGACCAGCGGCGGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACT 623
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[rotated sequence alignment block — RESULT 5]

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Db    62  CTACTCCCTCAGCAGCGGTGGTGACCGTGCCCTGCCCCCAGCAGTTGGGCACCCAGACCTACAT 121

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Qy   744  TTGTGACAAAACTACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTC 803
Db   182  TTGTGACAAAACTACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTC 241

Qy   804  AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 863
Db   242  AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT 301

Qy   864  CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 923
Db   302  CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 361

Qy   924  GGACGGCGTGGAGGTGCATATGCCAAGACAAAGCCGCGGGAGGAGCAGTACACAGACAC 983
Db   362  GGACGGCGTGGAGGTGCATATGCCAAGACAAAGCCGCGGGAGGAGCAGTACACAGACAC 421

Qy   984  GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 1043
Db   422  GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 481

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Qy  1104  CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC 1163
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Qy  1164  CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT 1223
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Qy  1224  GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 1283
Db   662  GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 721

Qy  1284  CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 1343
Db   722  CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 781

Qy  1344  GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 1403
Db   782  GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGACAAACACTTACACGCAGAA 841

Qy  1404  GAGCCTCTCCCGTGTCTCCGGGTAAATGA 1431
Db   842  AAAGCCTCTCCGTGTCTCCGGGTAAATGA 869
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RESULT 5
BM007892
LOCUS   BM007892   901 bp   mRNA   linear   EST 30-OCT-2001
DEFINITION 603617577F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450611 5',
            mRNA sequence.
ACCESSION   BM007892
VERSION   BM007892.1 GI:16522233
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 901)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.

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Db    619 CGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC 678
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Qy   1068 CCTCCCAGCCCCATGAGAAAACCATCTCAAAGCCAAAGGCAGCCCCGAGAACCACA 1127
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Db    679 CCTCCCAGCCCCATGAGAAAACCATCTCCAAAGCC-AAGGGCAGCCCCGAGAACCACA 737
Qy   1128 GGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG 1187
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Qy   1188 CCTGGTCAAAGGCTTCTATCCCAGCGACATCG-CCGTGGAGTGGGAGAGCAATGGGCAGC 1246
          ||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||||
Db    798 CCTGGTCAAAGGCTTCTATCCCAGCGACATCCGTGGAGTGCGAGAGCATCCGGACCAGC 857
Qy   1247 CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC 1290
          ||||||||| |||||||||||||||||||||||||||||||||||
Db    858 CGGAGAACAACTACAAGACCACGCCTCCCGTGCTCCGTGGACTCCGAC 901
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RESULT 6
BQ708857
LOCUS   BQ708857   988 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8352194 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277561
            5', mRNA sequence.
ACCESSION   BQ708857
VERSION   BQ708857.1 GI:21847756
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 988)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464 row: c column: 02
            High quality sequence stop: 716.
FEATURES   Location/Qualifiers
     source   1..988
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6277561"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   230 a   338 c   258 g   162 t
ORIGIN

Query Match   58.0%;   Score 830.4; DB 14; Length 988;
Best Local Similarity 94.6%;   Pred. No. 1.3e-187;
Matches 904; Conservative   0; Mismatches 46; Indels 6; Gaps 4;

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Qy    393 CTGGGTCGATGTCTGGGCCCGGGAGACCTGGTCACCGTCTCCAGCTAGCACCAAGGG 452
          ||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||
Db      5 CTACTTTGACTACTGGGGCCAGGGAACGCTGGTCACCGTCTCCTCGGCCTCCACCAAGGG 64
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: j column: 20
High quality sequence stop: 834.
FEATURES   Location/Qualifiers
     source   1..901
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5450611"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   209 a   315 c   234 g   143 t
ORIGIN

Query Match   58.1%;   Score 831.2; DB 13; Length 901;
Best Local Similarity 97.7%;   Pred. No. 8.3e-188;
Matches 864; Conservative   0; Mismatches 18; Indels 2; Gaps 2;

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Qy    408 GGGCCCGGGAGACCTGGTCACCGTCTCCAGCTAGCACCAAGGGCCCATCGGTCTTCCC 467
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     19 GGGGCCAGGGAACCCTGGTCACCGTCTCCAGCCTCCACCAAGGGCCCATCGGTCTTCCC 78
Qy    468 CCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAA 527
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 CCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCAGCCCTGGGCTGCCTGGTCAA 138
Qy    528 GGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGCGCCCTGACCAGCGGCGT 587
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    139 GGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGCGGCCCTGACCAGCGGCGT 198
Qy    588 GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC 647
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAC 258
Qy    648 CGTGCCCTCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG 707
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 CGTGCCCTCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG 318
Qy    708 CAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCC 767
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 CAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCC 378
Qy    768 ACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC 827
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Db    379 ACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC 438
Qy    828 CAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAG 887
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 CAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAG 498
Qy    888 CCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC 947
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 CCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC 558
Qy    948 CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCAC 1007
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCAC 618
Qy   1008 CGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC 1067
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REFERENCE   1 (bases 1 to 1029)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2095 row: g column: 10
             High quality sequence stop: 723.

FEATURES   Location/Qualifiers
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                     /clone="IMAGE:5924769"
                     /clone_lib="NIH_MGC_99"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."

BASE COUNT   237 a   350 c   276 g   165 t   1 others
ORIGIN

Query Match   57.6%; Score 824.4; DB 14; Length 1029;
Best Local Similarity   99.0%; Pred. No. 3.7e-186;
Matches   861; Conservative   0; Mismatches   0; Indels   6; Gaps   3;

Qy   453 CCCATCGTCTTCCCCCTGGCACCTCTGGGGCACAGCGGCCCT 512
          ||||||||||||||||||||||||||||||||||||||||||
Db   65 CCCATCGTCTTCCCCCTGGCACCTCTGGGGCACAGCGGCCCT 124

Qy   513 GGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125 GGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 184

Qy   573 CCTGACCAGCGGCGGCGTGCACACTTCCGGCGTGTCTACAGTCCTCCAGTCTTCCCT 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 CCTGACCAGCGGCGGCGTGCACACTTCCGGCGTGTCTACAGTCCTCCAGTCTTCCCT 244

Qy   633 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT 304

Qy   693 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAA 752
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA 364

Qy   753 AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCT 812
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Db   365 AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCT 424

Qy   813 CTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT 872
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Db   425 CTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT 484

Qy   873 GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT 932
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Db   485 GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT 544

Qy   933 GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT 992
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Db   545 GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT 604

Qy   993 GGTCAGCGTCCTCACCGTCCTGCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA 1052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   605 GGTCAGCGTCCTCACCGTCCTGCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA 664

Qy   1053 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA 1112
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Db   665 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA 724

Qy   1113 GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCA 1172
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   725 GCCCCGAGAAACACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGA-CA 783

Qy   1173 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA 1232
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   784 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA 843

Qy   1233 GAGCAATGGGCAG-CCGGAGAACAACTACAAGACCACGCCTCCCGTG---CTGGACTCCG 1288
          |||||||||||| || |||||||||||||||||||||||||||||| ||||||||||
Db   844 GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCG 903

Qy   1289 ACGGC-TCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 1343
          ||||| ||| ||||||||||||||||||||||||||||| ||| |||||||||||
Db   904 ACGGCTTCCTTCTTCCTCTACAGCAAGAAAGTCCCCGGGGGAACAAAGCAGGGTGGCA 959

RESULT 7
BQ063185
LOCUS   BQ063185 1029 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6876667 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924769
            5', mRNA sequence.
ACCESSION   BQ063185
VERSION   BQ063185.1 GI:19890681
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

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Best Local Similarity  97.6%;  Pred. No. 8.3e-186;
Matches  866;  Conservative  0;  Mismatches  18;  Indels  3;  Gaps  3;

Qy    541 GAACCGGTGACGGTGTCGTGGAACTCAGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAACCGGTGACGGTGTCGTGGAACTCAGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 60

Qy    601 GCTGTCCTACAGTCCTCCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGCCCTCCAGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCTGTCCTACAGTCCTCCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGCCCTCCAGC 120

Qy    661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACCAAGGTG 180

Qy    721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    181 GACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 240

Qy    781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCAAGGACACCCTC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCAAGGACACCCTC 300

Qy    841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 360

Qy    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 420

Qy    961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 480

Qy   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 540

Qy   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 600

Qy   1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCGTGACCTGCCTGGTCAAAGGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCGTGACCTGCCTGGTCAAAGGC 660

Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 720

Qy   1261 AAGA-CCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC 1319
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Db    721 NAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC 780

Qy   1320 CGT-GGACAAGAGCAGGTGGCAGC-AGGGGAAGTCTTCTCATGCTCCGTGATGCATGAG 1377
          ||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    781 CGTGGGACAAAAGCAAGTGGCAGCAAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAA 840

Qy   1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1424
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Db    841 GCTCTGCACAACCACTACCCGCAGAAGAGCCTCTCCCTGGTCTCGG 887
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Db    484 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1023 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1082

Db    544 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 603
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Qy   1083 CGAGAAAACCATCTCCAAAGGCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC 1142

Db    604 CGAGAAAACCATCTCCAAAGGCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC 663
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Qy   1143 CCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTT 1202

Db    664 CCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTT 723
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Qy   1203 CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAA 1262

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Qy   1263 GACCACGCCT-CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACA-GCAAGCTCACC 1320

Db    784 GAACACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGGCAAGCTCACC 843
          ||||||||| |||||||||||||||||||||||||||||||||||| ||||||||||
Qy   1321 GTGACAAGAGCA-GGTGGCAGCAGGGGGAA 1349

Db    844 GTGGACCAGAGCAGGGGTGGCAGCAGGGGGGA 873
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RESULT 8
BQ711255
LOCUS   BQ711255   887 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_8443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
             5', mRNA sequence.
ACCESSION   BQ711255
VERSION   BQ711255.1 GI:21850154
KEYWORDS   EST.
SOURCE   human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 887)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2474 row: m column: 20
             High quality sequence stop: 681.
FEATURES   Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   218 a   295 c   230 g   143 t   1 others
ORIGIN

Query Match   57.5%; Score 822.8; DB 14; Length 887;

RESULT 9
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LOCUS   BQ708022   918 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   AGENCOURT_8353641 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279643
             5', mRNA sequence.
ACCESSION   BQ708022
VERSION   BQ708022.1 GI:21846921
KEYWORDS   EST.
SOURCE   human.

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ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 918)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469 row: i column: 20
            High quality sequence stop: 667.
FEATURES    Location/Qualifiers
   source   1..918
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:6279643"
            /clone_lib="NIH_MGC_113"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
BASE COUNT    208 a    316 c    245 g    147 t    2 others
ORIGIN

Query Match      57.5%;  Score 822.2;  DB 14;  Length 918;
Best Local Similarity  95.4%;  Pred. No. 1.2e-185;
Matches 867;  Conservative 0;  Mismatches 40;  Indels 2;  Gaps 2;

Qy  398 TCGATGTCTGGGGCCCGGGAGACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCAT 457
         ||||||||||  |||||||||  ||||||||||||||||  ||||||||||||||||||
Db    1 TTGACCGCTGGGGCCAAGGGAACGCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCAT 60
Qy  458 CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACTTCTGGGGGCACAGCGGCCCTGGGCT 517
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   61 CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT 120
Qy  518 GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGTGTCGTGGAACTCAGGCGCCCTGA 577
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGTGTCGTGGAACTCAGGCGCCCTGA 180
Qy  578 CCAGCGGCGTGCACACCTTCCCGGCTGTGTCCACAGTCCTACAGTCCTCCTCAGCA 637
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  181 CCAGCGGCGTGCACACCTTCCCGGCTGTCTCCACAGTCCTACAGTCCTCCTCAGCA 240
Qy  638 GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC 697
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC 300
Qy  698 ACAAGCCCAGCAACACCAAGGTGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTC 757
         |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db  301 ACAAGCCCAGCAACACCAAGGTGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTC 360
Qy  758 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 817
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 420
Qy  818 CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 877
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 480
Qy  878 TGGACGTGÁGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 937
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Db  481 TGGACGTGAGCCACGAGGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 540
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Qy  938 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGGTCA 997
         ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db  541 TGCATAATGCCAAGACAACAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGGTCA 600
Qy  998 GGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1057
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 660
Qy 1058 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1117
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 720
Qy 1118 GAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1177
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GAGAACCACCAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGGACCAGGTCA 780
Qy 1178 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT-GGAGTGGGAGAGC 1236
         ||||| ||||||||||||||||||||||||||||||||||||  ||| |||||||||||
Db  781 GCCTGGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCNCCGNGGGAGTGGGAGAGC 840
Qy 1237 AATGGGCAG-CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC 1295
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Db  841 ATGGGGCAGCCCGGAGAACAACTACAAGACCACGCCTCCCGGGCTGGACTCCGACGG 900
Qy 1296 CTTCTTCCT 1304
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Db  901 GTCCTTTCT 909
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RESULT 10
BM914540
LOCUS       BM914540  995 bp  mRNA  linear  EST 12-MAR-2002
DEFINITION  AGENCOURT_6615506 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480223
            5', mRNA sequence.
ACCESSION   BM914540
VERSION     BM914540.1  GI:19364919
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 995)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2002  row: l  column: 16
            High quality sequence stop: 718.
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            /db_xref="taxon:9606"
            /clone="IMAGE:5480223"
            /clone_lib="NIH_MGC 113"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
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ACCESSION    BQ711291
VERSION      BQ711291.1  GI:21850190
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 881)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
  COMMENT    Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2468  row: c  column: 01
             High quality sequence stop: 721.
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT         220 a      285 c      237 g      139 t
ORIGIN
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Query Match        56.5%;  Score 808.8;  DB 14;  Length 881;
Best Local Similarity    99.8%;  Pred. No. 1.8e-182;
Matches 810;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   612  GTCCTCAGGACTCTTACTCCCTCAGCAGCGTCGTGTGTGACCGTGCCCTCCAGCAGCTTGGGCAC  671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GTCCTCAGGACTCTTACTCCCTCAGCAGCGTCGTGTGTGACCGTGCCCTCCAGCAGCTTGGGCAC   60

Qy   672  CCAGACCTTACATCTGCAACGTGAATCACAAGTGACAAGCCCAGCAACACCAAGGTGACAAGAAAGC  731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CCAGACCTTACATCTGCAACGTGAATCACAAGTGACAAGCCCAGCAACACCAAGGTGACAAGAAAGT  120

Qy   732  AGAGCCCAAATCTTGTGACAAAATCACAACATGCCACCGTGCCCAGCCACCTGAACTCCT  791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TGAGCCCAAATCTTGTGACAAAATCACAACATGCCACCGTGCCCAGCCACCTGAACTCCT  180

Qy   792  GGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGACACCCTTCCCATGATCTCCCG  851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGACACCCTTCCCATGATCTCCCG  240

Qy   852  GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT  911
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT  300

Qy   912  CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA  971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA  360

Qy   972  GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA  1031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA  420
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BASE COUNT         241 a      330 c      259 g      165 t
ORIGIN

Query Match        57.0%;  Score 815.2;  DB 14;  Length 995;
Best Local Similarity    96.1%;  Pred. No. 5.7e-184;
Matches 857;  Conservative    0;  Mismatches   33;  Indels    2;  Gaps    2;

Qy   393  CTGGTCGATGTCTGGGGCCCGGAGACCTGGTCACCGTCTCCTCAGTGACCACCAGGG  452
          ||||||||||||||||||||||||||||||| |||||
Db     6  CTACTTTGACGATTGGGGCCCAGGGAACGCTGGTCACCGTCTCCTCAGCCTCCACCAAGGG   65

Qy   453  CCCATCGGTCTTCCCCCTGGCACCCTCTGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCT  512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66  CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT  125

Qy   513  GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC  572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC  185

Qy   573  CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT  632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT  245

Qy   633  CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT  692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246  CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT  305

Qy   693  GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAA  752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306  GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAA  365

Qy   753  AACTCACACATGCCCACCGTGCCCAGCACTCCTGGGGGGACCGTCAGTCTTCCT  812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366  AACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCT  425

Qy   813  CTTCCCCCCAAAACCCAAGGACACACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT  872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426  CTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT  485

Qy   873  GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT  932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486  GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT  545

Qy   933  GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT  992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546  GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT  605

Qy   993  GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA  1052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606  GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA  665

Qy  1053  GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA  1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666  GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA  725

Qy  1113  GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCA  1172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726  GCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCA  785

Qy  1173  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG-  1231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACTTCCCCGTGGAGTGGGA  845

Qy  1232  AGAGCAATGGGCAGCCGGAGAACAACTACAAGA-CCACGCCTCCCGTGCTGG  1282
          |||||||||||||||| |||||||||||||||||       |||||||||||||
Db   846  AAAGCAATGGGAGAGCCGGAAAAAACTACAAGACCACAGACCCCCCGCCTCCCGTGCTGTTG  897
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RESULT 11
BQ711291     BQ711291
LOCUS        AGENCOURT_8347186 NIH_MGC_113     881 bp    mRNA    linear    EST 16-JUL-2002
DEFINITION   NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
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BASE COUNT      248 a      349 c      271 g      162 t      1 others
ORIGIN

           Query Match        55.9%;   Score 800.2;  DB 14;  Length 1031;
           Best Local Similarity  94.4%;  Pred. No. 2.2e-180;
           Matches  840;  Conservative  0;  Mismatches  49;  Indels  1;  Gaps  1;

Qy      491  CCTCTGGGGCACAGCGGCCCTGGGTCGTCCTGGTCAAGGACTACTTCCCGAACCGGTGA  550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       11  CCTCTGGGGCACAGCGGCCCTGGGTCGTCCTGGTCAAGGACTACTTCCCGAACCGGTGA  70

Qy      551  CGGTGTCGTGGAACTCAGGCGGCCGCCTGCACAGCGGCGTGCACACCTTCCGGCGTGTCCTAC  610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       71  CGGTGTCGTGGAACTCAGGCGGCCGCCTGCACAGCGGCGTGCACACCTTCCGGCGTGTCCTAC  130

Qy      611  AGTCCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACGCGTGGCCCCCAGCAGCTTGGGCA  670
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      131  AGTCCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGGCCCCTCAGCAGCTTGGGCA  190

Qy      671  CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGACAAGAAAG  730
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      191  CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGACAAGAAAG  250

Qy      731  CAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC  790
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      251  TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC  310

Qy      791  TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCAAGGACACCCTCATGATCTCCC  850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      311  TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCAAGGACACCCTCATGATCTCCC  370

Qy      851  GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAGT  910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371  GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAGT  430

Qy      911  TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC  970
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Db      431  TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC  490

Qy      971  AGTACAACAGCACGTACCGTGTGTCAGCGTCCTCCACCGTCCTGCACCAGGACTGGCTGA  1030
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Db      491  AGTACAACAGCACGTACCGTGTGTCAGCGTCCTCCACCGTCCTGCACCAGGACTGGCTGA  550

Qy     1031  ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA  1090
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      551  ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA  610

Qy     1091  CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC  1150
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Db      611  CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC  670

Qy     1151  GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA  1210
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      671  GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA  730

Qy     1211  GCGACATCGCCGT-GGAGTGGGAGAGCAATGGCAGCCCGGAGAACAACTACAAGACCACG  1269
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      731  GCGACATCCCCNTGGGAGTGGGAGAAACCAATGGCAGCCCGGAGAACAACTACAAGAACCCG  790

Qy     1270  CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG  1329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      791  CCTCCCGTGCTGAACTCCGACGCGCTCCTTCTTCCTCTACAGCAAAGCTCACCGGGGGACA  850

Qy     1330  AGCAGGTGGCAGCAGGGGAACGTCTTTCAATGCTCCGTGATGCATGAGGC  1379
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Db      851  AAAGCAGGGGGGCAACCGGGGGAACGTCTTTTCCAATGCTCCGTGATGC  900
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RESULT 12
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BQ064886
LOCUS       BQ064886                1031 bp    mRNA     linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343
            5', mRNA sequence.
ACCESSION   BQ064886
VERSION     BQ064886.1  GI:19893932
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1031)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2107  row: e    column: 24
            High quality sequence stop: 573.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
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RESULT 13
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BQ711727
BQ711727
LOCUS       BQ711727                 936 bp    mRNA     linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
            5', mRNA sequence.
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ACCESSION    BQ711727
VERSION      BQ711727.1  GI:21850626
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 936)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2518  row: k  column: 18
             High quality sequence stop: 547.
FEATURES             Location/Qualifiers
source               1..936
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT    231 a   306 c   245 g   152 t   2 others
ORIGIN
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Query Match          55.7%;  Score 797.4;  DB 14;  Length 936;
Best Local Similarity  98.3%;  Pred. No. 9.9e-180;
Matches   826;  Conservative    0;  Mismatches   12;  Indels    2;  Gaps    2;

Qy    593 CCTTCCCGGCGTCCTACAGTCCTCCAGGACTCTACTCCCTCCAGGAGCGGTGGTGACCGTGC 652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 CCTTCCCGGCGTCCTACAGTCCTCCAGGACTCTACTCCCTCCAGGAGCGGTGGTGACCGTGC 69

Qy    653 CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGAGCCCAGCAACA 712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 CCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAGAGCCCAGCAACA 129

Qy    713 CCAAGGTGACAAGAAAGCAGAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT 772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 CCAAGGTGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT 189

Qy    773 GCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCCTCTTCCCCCCAAAACCCAAGG 832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 GCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCCTCTTCCCCCCAAAACCCAAGG 249

Qy    833 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGGCGTGGTGGACGTGAGCCACG 892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGGCGTGGTGGACGTGAGCCACG 309

Qy    893 AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 952
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Db    310 AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 369

Qy    953 CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC 1012
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Db    370 CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC 429

Qy   1013 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC 1072
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Db    430 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC 489
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Qy   1073 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT 1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT 549

Qy   1133 ACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 ACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGG 609

Qy   1193 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA 1252
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Db    610 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA 669

Qy   1253 ACAACTACAAGACCA-CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 1311
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Qy   1312 AAGCTCACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTTCTCATGCTCCGTGATG 1371
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Db    730 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTTCTCATGCTCCGGGATG 789

Qy   1372 CATGAGGGTCTGCACAACCACCACTACACGCAGAAGAGCCTCTCCCGTGCTCCGGGTAAATGA 1431
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    790 CATGAGGGTCTGGAC-ACCAGTAACCCAGAGAAGAGCCTCTCCTCCTCCGTGCTCCGGGAAATGA 848
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RESULT 14
BQ705928
LOCUS       BQ705928   940 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214795
            5', mRNA sequence.
ACCESSION   BQ705928
VERSION     BQ705928.1  GI:21844827
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 940)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2382  row: k  column: 20
            High quality sequence stop: 619.
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                    /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Library constructed by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC Library."
BASE COUNT   235 a   318 c   240 g   147 t
ORIGIN
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RESULT 15

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BQ710532
LOCUS       BQ710532                 977 bp    mRNA    linear    EST 16-JUL-2002
DEFINITION  AGENCOURT_8352211 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277538
            5', mRNA sequence.
ACCESSION   BQ710532
VERSION     BQ710532.1  GI:21849431
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 977)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464 row: b  column: 03
            High quality sequence stop: 749.
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                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT      227 a    331 c    264 g    154 t    1 others
ORIGIN
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Qy    535 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGAACTCAGGGCGTGCACACC 594
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Db     71 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGAACTCAGGGCGTGCACACC 130

Qy    595 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGCCC 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGCCC 190

Qy    655 TCCAGCAGTTGGGCACCCAGCAGCTCCAACGTGAATCACAGCGAATCACAACACC 714
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Db    191 TCCAGCAACTTCGGCACCCAGCAGCTCCAACGTCAACGTAGATACAACACCAACAACC 250

Qy    715 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAATCACACATGCCCACCGTGC 774
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Db    251 AAGGTGGACAAGACAGTTGAGCGCAAATGTGTCGA--------GTGCCCACCGTGC 301

Qy    775 CCAGCACCTGAACTCCTGGGGGACCCGTCAGTCTTCCCCCCAAAACCCAAGGAC 834
              |||||||||      |||||||||||||||||||||||||||||||||||||
Db    302 CCAGCACC---ACCTGTGCAGGACCCGTCAGTCTTCCCCCCAAAACCCAAGGAC 358

Qy    835 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 894
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Db    359 ACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAA 418

Qy    895 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 954
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Db    419 GACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 478

Qy    955 AAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 1014
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Query Match   55.6%; Score 796; DB 14; Length 940;
Best Local Similarity 99.3%; Pred. No. 2.1e-179;
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Qy    677 CCTACATCTGCAACGTGAATCACAAGAGCCAGCAACAACCAAGGTGGACAAGAGAGAGC 736
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Db    181 GACCGTCAGTCTTCCTCCTCTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC 240

Qy    857 CTGAGGTGACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT 916
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Db    241 CTGAGGTGACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT 300

Qy    917 GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACA 976
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Db    301 GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACA 360

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Qy   1157 AGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA 1216
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Qy   1277 TGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGT 1336
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Db    661 TGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGT 720

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Db    721 GGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAAGCTCTGCACAACCACTACA 780

Qy   1397 CGC-AGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA 1431
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Db    781 CGCAGAAAAGAGCCTCTCCGTGTCTCCGGGTAAATGA 816
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Qy  1015 CACCAGGACTGGCTGAATGGCTGCAAGGAGTACAAGTGCAAGGTCTTCCAACAAAGCCCTCCCA 1074
              ||||||||||||||||||| |||||||||||||||||||||||||||| |||||| ||||||
Db   539 CACCAGGACTGGCTGAACGGCTGCAAGGAGTACAAGTGCAAGGTCTTCCAACAAAGCCCTCCCA 598

Qy  1075 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTAC 1134
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Db   599 GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGGGCAGCCCGAGAACCACAGGTGTAC 658

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Qy  1374 TGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db   898 TGAGGCTCTGCGCCCCCTACACACA-AAGAGCCTCTCCCTGGTCTCGGGTAAATGA 954
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Job time : 2734.68 secs

OM nucleic - nucleic search, using sw model

Copyright   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: April 5, 2003, 19:13:05 ; Search time 4490.25 Seconds
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Perfect score: 1431
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Scoring table: IDENTITY.NUC
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Searched: 2054640 seqs, 1455140878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1234.8	86.3	1431	1567	6	AR135359	AR135359 Sequence
5	1227.6	85.8	1596	1596	9	AK098516	AK098516 Homo sapi
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7	1215.2	84.9	1594	1594	6	AK057754	AK057754 Homo sapi
8	1210.4	84.6	1418	1418	6	AR176296	AR176296 Homo sapi
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10	1171.2	81.9	1566	1566	9	AR135375	AR135375 Sequence
11	1170	81.8	1566	1566	9	AK097365	AK097365 Homo sapi
12	1168.2	81.6	1404	1404	6	AR135377	AR135377 Sequence
13	1166.6	81.5	1404	1404	6	AR135376	AR135376 Sequence
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18	1123.6	78.5	1428	1428	6	AR059282	AR059282 Sequence
19	1123.6	78.5	1428	1428	6	AR076260	AR076260 Sequence
20	1122.8	78.5	1430	1430	6	AX419496	AX419496 Sequence
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22	1117.2	78.1	1437	1437	6	AR108865	AR108865 Sequence
23	1116.2	78.0	1624	1624	9	HSIGG1KH	Y14735 Homo sapien
24	1115.4	77.9	1630	1630	9	BC024289	BC024289 Homo sapi
25	1113.2	77.8	1673	1673	9	HSIGG1LH	Y14737 Homo sapien
26	1113.2	77.8	3143	3143	9	BC019046	BC019046 Homo sapi
27	1112.4	77.7	1428	1428	6	AR031186	AR031186 Sequence
28	1112.4	77.7	1428	1428	6	AR042591	AR042591 Sequence
29	1112.4	77.7	1428	1428	6	AR059284	AR059284 Sequence
30	1112.4	77.7	1428	1428	6	AR076262	AR076262 Sequence
31	1112.4	77.7	1990	1990	9	AK098817	AK098817 Homo sapi
32	1109.2	77.5	1631	1631	9	AK097010	AK097010 Homo sapi
33	1104.6	77.2	1465	1465	10	S79307	S79307 Ig gamma =i
34	1103.2	77.1	1617	1617	6	A29585	A29585 H.sapiens c
35	1102	77.0	1599	1599	6	AX330501	AX330501 Sequence
36	1102	77.0	1599	1599	6	AX333307	AX333307 Sequence
37	1102	77.0	1599	1599	6	AX334122	AX334122 Sequence
38	1102	77.0	1599	1599	6	HUMIGHEPAH	M87789 Human (hybr
39	1096.4	76.6	1633	1633	9	AK097367	AK097367 Homo sapi
40	1096	76.6	7521	7521	9	AK080951	AK080951 Sequence
41	1095.6	76.6	1549	1549	6	A21385	A21385 Plasmid DNA
42	1092.6	76.4	6557	6557	6	I26929	I26929 Sequence 3
43	1092.4	76.3	1666	1666	9	BC006402	BC006402 Homo sapi
44	1091.8	76.3	1341	1341	6	A07562	A07562 DNA sequenc
45	1091.4	76.3	1639	1639	9	AK097950	AK097950 Homo sapi

ALIGNMENTS

RESULT 1
AR108863
LOCUS   AR108863   1431 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6113898.
ACCESSION   AR108863
VERSION   AR108863.1   GI:12825139
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1431)
AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE   Human B7.1-specific primatized antibodies and transfectomas
            expresing said antibodies
JOURNAL   Patent: US 6113898-A 3 05-SEP-2000;

Pred. No. is the number of results predicted by chance to have a

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FEATURES         Location/Qualifiers
   source        1..1431
                 /organism="unknown"
BASE COUNT     322 a    469 c    380 g    260 t
ORIGIN

Query Match           100.0%;   Score 1431;   DB 6;   Length 1431;
Best Local Similarity 100.0%;   Pred. No. 4.6e-280;
Matches 1431;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAG   60
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Db     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAG   60

Qy    61 GTGGTTGTCTGGTGCTCCATCAGCGGTTACTACTACTGGTGGATCCGGCCACCAACTAC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTGGTTGTCTGGTGCTCCATCAGCGGTTACTACTACTGGTGGATCCGGCCACCAACTAC  120

Qy   121 TGGGTTGTCTCTGGTGCTCCATCAGCGGTTACTACTGACCTGGATCCGGCCACCAACTAC  180
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Db   121 TGCGTTGTCTCTGGTGCTCCATCAGCGGTTACTACTGACCTGGATCCGGCCACCAACTAC  180

Qy   181 CCAGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGTGCGACCACCAACTAC    240
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Db   181 CCAGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGTGCGACCACCAACTAC    240

Qy   241 AATCCCCTCCCTCAAAGAGTCGAGTCACCATTCAAAAGACAGTCCAAGAACCAGTTCTTC  300
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Db   241 AATCCCCTCCCTCAAAGAGTCGAGTCACCATTCAAAAGACAGTCCAAGAACCAGTTCTTC  300

Qy   301 CTGAACTTGAATTCTGACCGAGTCCGATCAAACCATTGTCACAACCATTGTTGGGGCCCT  360
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Db   301 CTGAACTTGAATTCTGACCGAGTCCGATCAAACCATTGTCACAACCATTGTTGGGGCCCT  360

Qy   361 CGCCTCGATTGCACAACCATTGTTATGGCCGGCTGGGTCGATGTCTGGGGCCCGGGAGAC  420
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Db   361 CGCCTCGATTGCACAACCATTGTTATGGCCGGCTGGGTCGATGTCTGGGGCCCGGGAGAC  420

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480
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Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
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Db   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540

Qy   541 GAACCGGTGACGGTGTCGTGAACTCAGGCGCCTGACCAGCGGCGTGCACACCTTCCCG   600
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Db   541 GAACCGGTGACGGTGTCGTGAACTCAGGCGCCTGACCAGCGGCGTGCACACCTTCCCG   600

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTCACCGTGCCCTCCAGC  660
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Db   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTCACCGTGCCCTCCAGC  660

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
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Db   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720

Qy   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
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Db   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
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Db   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACAGTGGTGGTGGACGTGAGCCACGAAGACCCT    900
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Db   841 ATGATCTCCCGGACCCCTGAGGTCACAGTGGTGGTGGACGTGAGCCACGAAGACCCT    900

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
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Db   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
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Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
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Db  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
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Db  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
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Db  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
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Db  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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Db  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
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Db  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA         1431
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Db  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA         1431
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RESULT 2
AR108867
LOCUS       AR108867          1431 bp    DNA       linear    PAT  14-FEB-2001
DEFINITION  Sequence 11 from patent US 6113898.
ACCESSION   AR108867
VERSION     AR108867.1   GI:12825143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1431)
  AUTHORS   Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
  TITLE     Human B7.1-specific primatized antibodies and transfectomas
            expressing said antibodies
  JOURNAL   Patent: US 6113898-A 11 05-SEP-2000;
FEATURES         Location/Qualifiers
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                 /organism="unknown"
BASE COUNT     319 a    462 c    385 g    265 t
ORIGIN

Query Match           91.9%;   Score 1315.8;   DB 6;   Length 1431;
Best Local Similarity 95.0%;   Pred. No. 1.1e-256;
Matches 1359;  Conservative   0;  Mismatches   72;  Indels   0;  Gaps   0;

Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAG   60
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Db     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGCAGCTCCCAGATGGGTCCTGTCCCAG   60

Qy    61 GTGAAGCTGCAGCAGTGGGGCGAAGGCTTCGCAGCCTTCGGAGACCTTCGGCCACC      120
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Db    61 GTGCAGCTGCAGCAGTGGGGCGAAGGCTTCGCAGCCTTCGGAGACCTTCGGCCACC      120

Qy   121 TGGGTTGTCTCTGGTGCTCCATCAGCGGTTACTACTACTGGGGATCCGGCCACCAACTAC  180
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Db   121 TGCGTTGTCTCTGGTGCTCCATCAGCGGTTACTACTACTGGGGATCCGGCCACCAACTAC  180

Qy   181 CCAGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTTATGGCGGTGGG      240
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Db   181 CCAGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTTATGGCGGTGGG      240
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Qy  1321 GTGACAAGAGACGAGGTGGCAGCAGGGGAAGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
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Db  1321 GTGACAAGAGACGAGGTGGCAGCAGGGGAAGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380

Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTTCCCTGTCCGGGTAAATGA 1431
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Db  1381 CTGCACAACCACTACACGCAGAAGAGCCTCCCTGTCCGGGTAAATGA 1431
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RESULT 3
E10697
LOCUS   E10697   1431 bp   RNA   linear   PAT 29-SEP-1997
DEFINITION   cDNA encoding heavy chain of human monoclonal antibody against
             human cytomegalovirus 65kD antigen.
ACCESSION   E10697
VERSION   E10697.1 GI:22027790
KEYWORDS   JP 199603B178-A/20.
SOURCE   Homo sapiens
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1431)
  AUTHORS   Tanaka,S., Niwa,H. and Tanaka,H.
  TITLE   HUMAN MONOCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR
             CLONING OF GENE THEREOF
  JOURNAL   Patent: JP 199603B178-A 20 13-FEB-1995;
             TANAKA HIDEYUKI, NISSHINBO IND INC
COMMENT   OS   Homo sapiens (human)
             PN   JP 199603B178-A/20
             PD   13-FEB-1996
             PF   20-FEB-1995 JP 1995030742
             PR   18-FEB-1994 JP 94P   21628
             PI   TANAKA SHIGEAKI, NIWA HIRONUKI, TANAKA HIDEYUKI PC
             C12N15/09,C07K16/08,C12N1/21,C12N15/02,C12P21/08,C12Q1/68, PC
             G01N33/53,
             PC   G01N33/531,G01N33/577,(C12N1/21,C12R1:19),(C12P21/08, PC
             C12R1:19);
             CC   strandedness: Single;
             CC   topology: Linear;
             CC   hypothetical: No;
             CC   anti-sense: No;
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             FT   /organism='Homo sapiens'
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             FT   sig_peptide   1..57
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             FT   human monoclonal
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             FT   antibody against
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FEATURES   Location/Qualifiers
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Query Match   86.5%; Score 1237.2; DB 6; Length 1431;
Best Local Similarity 92.9%; Pred. No. 9.1e-241;
Matches 1332; Conservative 0; Mismatches 93; Indels 9; Gaps 3;

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Qy     1 ATGAAACACCTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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Db  181 CCAGGGAAGGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTAGTGGAAACACCTACTAC 240

Qy  241 AATCCCTCCCTCCAAGAGTCAGAGTCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTC 300
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Db  241 AACCCCTCCCTCCAAGAGTCAAGTCAAGTCACCATTCACAGAACACCAGTTCTCC 300

Qy  301 CTGAACTTGAATTCTGTGACCGACACGGCCGTGTATTACTGTGCGAGAGGCCCT 360
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Db  301 CTGAAGCTGAACTCTATGACCGCGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360

Qy  361 CGCCCTGATTGCACAACCATTGTTATGGCGGCTCGGGTCTCGGGCCCCGGGAGAC 420
        ||| ||| | ||||||  ||| ||| |||| |||||||||||||||||||||||
Db  361 CTTTTTCAGTTGTGTGGAATGGTTTACACAACTGGTTCGGATGTCTGGGCCCGGGGAGTC 420

Qy  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480

Qy  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
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Db  481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540

Qy  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
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Db  541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600

Qy  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
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Db  601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660

Qy  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
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Db  661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720

Qy  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
        ||| || |||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780

Qy  781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
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Db  781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840

Qy  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
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Db  841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900

Qy  901 GAGGTCAAGTTCAACTGGTACGTGACGGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
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Db  901 GAGGTCAAGTTCAACTGGTACGTGACGGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960

Qy  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
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Db  961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

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Db 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
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Db 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy 1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
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Qy 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
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Db 1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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Db 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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Db 1075 CCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1134
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Qy 1138 CTGCCCCCATCCCGGGATGAGCTGACCCAGGCTCAGCCTGACCTGCCTGGTCAAA 1197
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Db 1135 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1194
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Qy 1198 GGCTTCTATCCCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCGGAGAACAAC 1257
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Db 1195 GGCTTCTATCCCGACGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCGGAGAACAAC 1254
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Qy 1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317
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Db 1255 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1314
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Qy 1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377
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Db 1315 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1374
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Qy 1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db 1375 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428
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RESULT 4
AR135359
LOCUS   AR135359   1567 bp   DNA   linear   PAT 16-JUN-2001
DEFINITION Sequence 17 from patent US 6135941.
ACCESSION   AR135359
VERSION   AR135359.1 GI:14476031
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1567)
  AUTHORS   Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J.,
            Corley,N.C., Guegler,K.J. and Baughn,M.R.
  TITLE   Human immune system associated molecules
  JOURNAL   Patent: US 6135941-A 17 24-OCT-2000;
FEATURES   Location/Qualifiers
     source   1..1567
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BASE COUNT   346 a   503 c   428 g   289 t   1 others
ORIGIN

Query Match   86.3%; Score 1234.8; DB 6; Length 1567;
Best Local Similarity 92.9%; Pred. No. 2.8e-240;
Matches 1332; Conservative 0; Mismatches 87; Indels 15; Gaps 3;

Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGGTCCTGTCCCAG 60
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   78 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGGTCCTGTCCCAG 137
```

```
Qy   61 GTGAAGCTGCAGCAGTGGGGAAGGACTTCTGCAGCCTTCGCAGCCTGGAGCCCGTGCACC 120
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db 138 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGCAGACCCTGTCCCGCACC 197
```

```
Qy 121 TGCGTGTCTCTGGTGCTCCATCAGC---AGGGTTACTACTGGAGCTGGATCCGCCAG 177
```
          |||  |||| |||||  |||| || |    |||  |||||||| ||| ||||||||||
```
Db 198 TGCGGTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGCCAG 257
```

```
Qy 178 ACCCCAGGGAAGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGACCACCAAG 237
```
          |||||||||||||||  |||||||||||||| |||||||| | | |||||
```
Db 258 CCCCCAGGGAAGGGGCTGGAGTGGATTGGTTACATCTA---TTACAGTGGGAGCACCCTC 314
```

```
Qy 238 TACAATCCCTCCCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTC 297
```
          |||| ||| |||| ||||||| || || || |||| |||||| || |||||||||||
```
Db 315 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTC 374
```

```
Qy 298 TTCCTGAACTTGAATTCTGTGACCGCCGACACGGCCGTCTATTACTGTGCGAGAGGC 357
```
          |||||||||||| ||| ||||||| |||||| || ||||||| ||||||| ||||||
```
Db 375 TCCCTGAAGCTGAGCTCTGTGACTGCCGCAGACACGGCCGTGTATTACTGTGCCAGAG-- 432
```

```
Qy 358 CCTGCCCCTGATTGCACAACCATTTGTTATGGCGGCTGGGTGCGATGCTGCTGGGGCCCGGGA 417
```
          ||||||||||||||||
```
```

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Db   1
```
          ||||| |||||||||||||| |||||||| |||||||||||||||||||||||||
```
Qy   1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCTCCCAGATGGGGTCCTGTCCCCAG 60
```

```
Qy   61 GTGAAGCTGCAGCAGTGGGGGCAGGAGGACTTCTGCAGCCTTCGCAGCCTGGAGACCGCCACC 120
```
          |||| ||||||||| ||||||||| |||||||||||| |||||||||||||
```
Db   61 CTGCGGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
```

```
Qy  121 TGCGTGTCTCTGGTGGCTCCATCAGC---GGTTACTACTGGAGCTGGATCCGCCAG 177
```
          ||| |||| ||||| |||| || | ||| |||||| ||| ||||||||||
```
Db  121 TGCACTGTCTCTGGTGGCTCCATCAGCAGGGGTGAGTAGTTACTCCTGGGGCTGCATCCGCCAG 180
```

```
Qy  178 ACCCCAGGGAAGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGACCACCAAAC 237
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          ||||||||||||| |||||||||||||| |||||||| | | |||||
```
Db  181 CCCCCGGGGAAGGGGCTGGAGTGGATTGGGGACTCA---TTATAGTGGGGAGCACTTAC 237
```

```
Qy  238 TACAATCCCTCCCAAGAGTCGAGTCACCATTCAAAGATGCAGTGTCCAAGAACCAGTTC 297
```
          || |||| ||| ||||||| || |||||| |||||| || |||||||||||
```
Db  238 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACGCGTCCAACAACCAGTTC 297
```

```
Qy  298 TTCCTGAACTTGTGCACACAACCATTTGTTATGGCGGCTGGGTCGATGTCTGATCTGGGGCCCGGGA 357
```
          |||| |||| ||| || ||||||||||||||||||||||||||||||||||||
```
Db  358 TCGCGGCAGTATTACGA---TCTTTTGACTGGTTCTTTCCCTCATACTGGGGCCAGGGA 414
```

```
Qy  358 CCTGCGCCTGAGTTGACACCACCATTTGTTATGGCGGCTGGGTCGATGTCTGATCTGGGGCCCGGGA 417
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          |||| ||| || || || |||||||||||||||||||||||
```
Db  415 ACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATGGTCTTCCCCTGGCACCTC 474
```

```
Qy  418 GACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATGGTCTTCCCCCTGGCACCC 477
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db  475 TCCTCCAAGAGCACACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 534
```

```
Qy  478 TCCTCCAAGAGCACACCTCTGGGGGCACAGCGGCCCCTGGGCTGCCTGGTCAAGGACTACTTC 537
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db  538 CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
```

```
Qy  538 CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCCTGACCAGCGGCGTGCACACCTTC 597
```
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db  535 CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 594
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```
Qy  598 CCGGCTGTCCTACAGTCCTCACTCCTCCTCAGCAGCGGTGTGACCGTGCCCTCC 657
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db  595 CCGGCTGTCCTACAGTCCTCACTCCTCCTCAGCAGCGGTGTGACCGTGCCCTCC 654
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```
Qy  658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db  655 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 714
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```
Qy  718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
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          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
```
Db  715 GTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA 774
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Qy  778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACAC 837
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  775 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 834
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Qy  838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 897
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  835 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC 894
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```
Qy  898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db  895 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 954
```

```
Qy  958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
```
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db  955 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1014
```

```
Qy 1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1015 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1074
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Qy 1078 CCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1137
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          |||||||||||||||||
```
```

```
AK098516
LOCUS       AK098516           1596 bp    mRNA      linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ25650 fis, clone SYN01104, highly similar to
            Ig gamma =immunoglobulin heavy chain.
ACCESSION   AK098516
VERSION     AK098516.1  GI:21758543
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens synovial membrane (knee) cDNA to mRNA, clone_lib:SYN
            clone:SYN01104.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta.T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S.,
            Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
            Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1596)
  AUTHORS   Sugano,S. and Suzuki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure, Human Genome
            Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
            (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction and 5'-end one pass sequencing: Institute of Medical
            Science, University of Tokyo, Laboratory of Genome Structure, Human
            Genome Center; 3'-end one pass sequencing: RAB; clone selection for
            full insert sequencing: RAB and Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1..1596
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="SYN01104"
                     /tissue_type="synovial membrane (knee)"
                     /clone_lib="SYN"
                     /note="cloning vector: pME18SFL3"
BASE COUNT      342 a    540 c    426 g    288 t
ORIGIN
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Query Match         85.8%;  Score 1227.6;  DB 9;  Length 1596;
Best Local Similarity  92.5%;  Pred. No. 8e-239;
Matches 1326;  Conservative  0;  Mismatches  99;  Indels  9;  Gaps  3;

Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGGTCCTGTCCCAG  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     36 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGGTCGTGTCCCCAG  95

Qy     61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCAGCCTGTCCCGCACC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 GTGCACCTGCAGGAGTCCGGCTCAGGACTGGTGAGGCCTTCACAGACTCTGTCCTCACC  155

Qy    121 TGCCGTTGTCTGTGGCTCCAT---CAGCGGTTACTACTACTGGACCTGGACTCCGGCCAG  177
          ||||||||||||||||||||      |||||||||||||||||||||||||||||||||||
Db    156 TGCGCTGTCTCTGGTGACTCCATCACCAGTGGTGCTCACTCCTGGAGCTGGATCCGGCCAG  215

Qy    178 ACCCAGGGAGGGGACTGGAGTGGATTGGCCCATATTTATGGTAATGGTGCGACCACCAAC  237
          |||||||||||||||||||||||||||||||||||||||||||||||||    |||||||
Db    216 CCACCAGGGAAGGGCCTGGAGTGGATTGGGCTACGGTCTATCTCA---GTGGGAGCACCTCT  272

Qy    238 TACAATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTC  297
          |||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db    273 TACAATCCGTCCCTCAAGAGTCGACTCACCATGTCAATAGACAGGTCCAACAACCAGTTC  332

Qy    298 TTCCTGAACTTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGC  357
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Db 1410 GGTCTGCACAACCACTACACGCAGAGAGCCTCTCCGTGTCTCCGGGTAAATGA 1463

RESULT 6
LOCUS   A49389
DEFINITION A49389
            Sequence 7 from Patent WO9607740.
ACCESSION   A49389   1418 bp   DNA   linear   PAT 07-MAR-1997
VERSION   A49389.1   GI:2202866
KEYWORDS   .
SOURCE   unidentified
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 1418)
  AUTHORS   Edelman,L., Margaritte,C., Kaczorek,M. and Chaabihi,H.
  TITLE   MONOCLONAL RECOMBINANT ANTI-RHESUS D (D7C2) ANTIBODY
  JOURNAL   Patent: WO 9607740-A 7 14-MAR-1996;
            PASTEUR INSTITUT (FR)
COMMENT   Other publication FR 2724182 960308.
FEATURES   Location/Qualifiers
     source   1..1418
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     CDS   1..>1418
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA03180.1"
                     /db_xref="GI:2302867"
                     /translation="MGWSCIILFLVATATGVHSQVQLQQWGAGLLKPSETLSLTCTVY
                     GGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLN
                     SVTAADTAVYYCARAPEYKKYHGWFDPWGQGTTVTVSSASTKGPSVFPLAPSSKST
                     SGGTALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL
                     GTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL
                     MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLKVL
                     HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
                     LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
                     SVMHEALHNHYTQKSLSLSPGK"
     sig_peptide   1..57
     mat_peptide   58..1418
                     /product="IMMUNOGLOBULIN, HEAVY CHAIN"
BASE COUNT   333 a   458 c   378 g   249 t
ORIGIN

Query Match   85.4%;   Score 1221.6; DB 6; Length 1418;
Best Local Similarity   92.9%;   Pred. No. 1.3e-237;
Matches 1317; Conservative   0; Mismatches   89; Indels   12; Gaps   3;

Qy   13 TGGTTCTTCCTCCTCCTGGTTGCAGCTCCCAGATGGGTCCTGTCCCAGTGAAGCTGCAG 72
         ||||| || | ||| |||||| |||| | | ||||||||||||| |||||||||||||
Db   13 TGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCCAGGTCCAACTGCAG 72

Qy   73 CAGTGGGGCGGAAGGACTTCTGCAGCCTTCGGAGACCCGTCCCGGACACTTGCGTTGTCT 132
         ||||||||||||||||||||||||||||| ||||||||||||||||| ||||||| |||||
Db   73 CAGTGGGGCGGAGGACTGTTGAAGCCTTCGGAGACCCGTCCCTCACCTGCACTGTCTAT 132

Qy   133 GGTGGCTCCATCAGCGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAGGGGA 192
         |||||| |||||||||| |||||||||||| ||| |||||| ||| ||||| |||
Db   133 GGTGGGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGG 189

Qy   193 CTGGAGTGGATTGGCCATATTATGTGGAGTAATGGTGCGACCACCAACTACAATCCCTCCTC 252
         |||||||||||||||||| ||| | ||||| ||||| ||||||||||||| ||||||
Db   190 CTGGAGTGGATTGGGGAAATCAA---TCATAGTGGAAGCACCAACTACAACCCGTCCCTC 246

Qy   253 AAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTCGAACTTGAAT 312
         |||||||||| || |||||||| ||||| |||||||| |||| ||| ||||| |||
Db   247 AAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAACTGAAC 306

Qy   313 TCTGTGACCGACAGCAGGTGCGACACGGCCGTCTATTACTGTGCAGAGGCCCTGATTGC 372
         | | ||| |||||| || | ||||||| ||||| |||||||| |||||| |||
Db   307 TCTGTGACCGCCGCCGACACGGCCGTGTATTACTGTGCAGGG------CCCCAGAGTAT 360

Qy   373 ACAACCATTTGTTATGGCGGCATGGCCTCGATGCTGTCGGGGACCTGGTCACCGTC 432
         | | || ||| |||| | || || ||| | | | ||| |||| |||||

```
Db    361  AAATGGAGTATCATGGGACTGGTTCGACCCCTGGGGCCAAGGTACCACTGTCACCGTC  420
           ||||||||                |||||||||||||||||||||||||||||||||||||
Qy    433  TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC  492
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TCCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC  480

Qy    493  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG  552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG  540

Qy    553  GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG  612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG  600

Qy    613  TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCAGCAGCTTGGGCACC  672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCAGCAGCTTGGGCACC  660

Qy    673  CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA  732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA  720

Qy    733  GAGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG  792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GAGCCCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG  780

Qy    793  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTCATGATCTCCGG  852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTCATGATCTCCGG  840

Qy    853  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC  912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC  900

Qy    913  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG  972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG  960

Qy    973  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT  1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT  1020

Qy    1033 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC  1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC  1080

Qy    1093 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG  1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG  1140

Qy    1153 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC  1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC  1200

Qy    1213 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT  1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT  1260

Qy    1273 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC  1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC  1320

Qy    1333 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC  1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC  1380

Qy    1393 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG  1430
           ||||||||||||||||||||||||||||||||||||||
Db    1381 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG  1418
```

RESULT 7
AK057754

LOCUS   AK057754   1594 bp   mRNA   linear   PRI 27-MAR-2002
DEFINITION Homo sapiens cDNA FLJ25025 fis, clone CBL01928, highly similar to
            Ig gamma immunoglobulin heavy chain.
ACCESSION   AK057754
VERSION   AK057754.1 GI:16553681
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL01928.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
            Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M.,
            Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
            Sugano,S.
  TITLE   NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1594)
  AUTHORS   Sugano,S. and Suzuki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure, Human Genome
            Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
            (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction and 5'-end one pass sequencing: Institute of Medical
            Science, University of Tokyo, Laboratory of Genome Structure, Human
            Genome Center; 3'-end one pass sequencing: RAB; clone selection for
            full insert sequencing: RAB and Helix Research Institute.
FEATURES   Location/Qualifiers
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                     KAQFFLTLSVTAADTAVYYCARHWVPRVLGVDAWFDPWGPGILVTVSSASTKGPSVF
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                     FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
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BASE COUNT   338 a   532 c   437 g   287 t
ORIGIN

Query Match   84.9%; Score 1215.2; DB 9; Length 1594;
Best Local Similarity   92.0%; Pred. No. 2.6e-236;
Matches 1319; Conservative   0; Mismatches 103; Indels 12; Gaps   3;

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Qy    1  ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGCTCCCAGATGGGTCCTGTCCCAG  60
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Db   36  ATGAAGCACCTGTGGTTCTTCCTCCTGCTGGTGGCGGCCCCCAGATGGGTCCTGTCCCAG  95

Qy   61  GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCGCAGCCTTCCAGCCTGTCCCGCACC  120
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Db   96  TTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCAGTGACCCTGTCCCTCACG  155

Qy   121 TGCGTTGTGTCTGGTGGCTCCAT---CAGCGGTTACTACTACTGGAGCTGGATCCGCCAG  177
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Qy 1258 TACAAGACCACGCCTCCCGTCTGACTCCGACGGCTCCTCTTCCTCTACAGCAAGCTC 1317
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Db 1287 TACAAGACCACGCCTCCCGTCTGACTCCGACGGCTCCTCTTCCTCTACAGCAAGCTC 1346

Qy 1318 ACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTTCTCATGCTCCGTGATGCATGAG 1377
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Db 1347 ACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTTCTCATGCTCCGTGATGCATGAG 1406

Qy 1378 GCTCTGCACAACCACCACTACACGCCAGAAGAGAGCCTCTCCCTGCTCCGGGTAAATGA 1431
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RESULT 8
AR176296
LOCUS   AR176296   1418 bp   DNA   linear   PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6312690.
ACCESSION   AR176296
VERSION   AR176296.1 GI:17918651
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1418)
  AUTHORS   Edelman.L., Margaritte.C., Kaczorek.M. and Chaabihi.H.
  TITLE   Monoclonal recombinant anti-rhesus D (D7C2) antibody
  JOURNAL   Patent: US 6312690-A 7 06-NOV-2001;
FEATURES   Location/Qualifiers
     source   1..1418
                     /organism="unknown"
BASE COUNT   332 a   454 c   379 g   253 t
ORIGIN

Query Match   84.6%; Score 1210.4; DB 6; Length 1418;
Best Local Similarity   92.4%; Pred. No. 2.5e-235;
Matches 1310; Conservative   0; Mismatches 96; Indels 12; Gaps 3;

Qy   13 TGGTTCTTCCTCCTCGGTGGCAGCTCCCAGATGGGTCTGTCCAGTGAAGCTGCAG   72
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Db   13 TGTATCATCCTCCTTCTTGGTGACAACAGTCACAGTGTCCACTCCCAGTCCAACTGGAG   72

Qy   73 CAGTGGGCGAAGGACTTCTGCAGCCTTGCAGCCTTCTGACTACTACTACTCAGCCCAGGGAGGGGA 132
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Db   73 CAGTGGGGCGCGGAGGACCTGGGGCTTGGAGGCCTTCGGAGCCCTGTCCCTCACCTGCACTGTCTAT 132

Qy 133 GGTGGCTCCATCAGCGGTTACTACTGGAGCTGGATCCGCCAGCCCCAGGGAGGGGA 192
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Db 133 GGTGGGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGG 189

Qy 193 CTGGAGTGGATTGGCCATATTTATGGTAATGGTGCAGACTACAATCCCTCCCTC 252
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Db 190 CTGGAGTGGATTGGGGAAATCAA---TCATAGTGGAAGCACAACTACACACCCGTCCCTC 246

Qy 253 AAGAGTCGAGTCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTCCTGAACTTGAAT 312
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Db 247 AAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAACTGAAC 306

Qy 313 TCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCTCGCCCTGATTGC 372
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Db 307 TCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGGG-----CCCCAGAGTAT 360

Qy 373 ACAACCATTTGTTATGGCGGCTCGGTCGATGTCTGGGCGCCCGGGAGACCTGGTCACCGTC 432
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Db 361 AAATGGAAGTATCATGGGACTGGTTCGACCCTCGGCTCACCGTCTCCTCAGGGCAAGTGTCACCGTC 420

Qy 433 TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCTGGGTCAAA 492
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Db 421 TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 480

Qy 493 TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG 552
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Db 481 TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG 540

Db 156 TGCAGTGTCTCTGGTGACTCCATCGCCACAACTGGCTATTCTGGGGGTGGTTCCGCCAG 215

Qy 178 ACCCCAGGGAGGGGACTTGGAGTGGGATTGGCCATATTTATGGTGTAATGTGCGACCACCAAC 237
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Db 216 CCCCAGGGAAGGGGACTCGCAATTTATAGGGAGTGTGTATTATACTGG---GACCCCCCAC 272

Qy 238 TACAATCCCTCCCTCCAAGAGTCGAGTCACCATTCAAAAGACAGTCCAAGAGAACCAGTTC 297
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Db 273 CACAACCCGTCCCTCCAAGCGCCCAGTCACATATCCGCAGACACGTCCAAGGCCCAGTTC 332

Qy 298 TTCCTGAACTTGAATTCTGTGACCGACACGGGCCGTCTATTACTGTGCGAGAGGC 357
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Qy 358 CCTCGCCCTGATTGCACAACCATTTGTTATGGCGGCTCGGTCGATGTCTGGGGCCCGGGA 417
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Db 507 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 566

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Db 567 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 626

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Db 627 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC 686

Qy 658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 717
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Db 687 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG 746

Qy 718 GTGGACAAGAAAGCAGAGCCCAAAATCTGTGACAAAACTCACACATGCCCACCGTGCCCA 777
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Db 747 GTGGACAAGAAAGTTGAGCCCAAAATCTTGTGACAAAACTCACACACATGCCCACCGTGCCCA 806

Qy 778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 837
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Db 807 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC 866

Qy 838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGGAC 897
         |||||||||||||||||||| ||||| || |||||||||| ||||||||||||||||||||
Db 867 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGGGG 926

Qy 898 CGTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 957
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Db 927 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 986

Qy 958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
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Db 987 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1046

Qy 1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCTCCAGCC 1077
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Db 1047 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCTCCAGCC 1106

Qy 1078 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1137
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Qy 1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
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Db 1167 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1226

Qy 1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
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REFERENCE 1
AUTHORS   Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
           Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M.,
           Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
           Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
           Sugano,S.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1589)
AUTHORS   Sugano,S. and Suzuki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
           University of Tokyo, Laboratory of Genome Structure, Human Genome
           Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
           (E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
           Fax:81-3-5449-5416)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
           Economy, Trade and Industry of Japan; cDNA full insert sequencing:
           Research Association for Biotechnology (RAB); cDNA library
           construction and 5'-end one pass sequencing: Institute of Medical
           Science, University of Tokyo, Laboratory of Genome Structure, Human
           Genome Center; 3'-end one pass sequencing: RAB; clone selection for
           full insert sequencing: RAB and Helix Research Institute.
FEATURES   Location/Qualifiers
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                     /clone="CBL03624"
                     /tissue_type="cerebellum"
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                     /note="Cloning vector: pME18SFL3"
BASE COUNT   338 a   532 c   430 g   289 t
ORIGIN

Query Match   84.5%;   Score 1209.6; DB 9;   Length 1589;
Best Local Similarity 91.8%;   Pred. No. 3.6e-235;
Matches 1317; Conservative   0; Mismatches 99; Indels 18; Gaps 3;

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Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTCGGTGCAGCTGCCAGATGGTCCTGTCCCAG   60
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Db    38 ATGAAGCAGATGTGGTTCTTCCTCCTCGGTGCAGCTGCCAGATGGTCCTGTCCCAG   97

Qy    61 GTGAAGCTGCAGCAGTGGGGGAAGGACTTCTGCAGCCTGGAGAAGACCTGTCCCGACACC  120
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Db    98 CTGCAGCTGCAGGAGTCGGGCCCAGGACTCGGCCCTGGAGGTCCTGTCCTCACC  157

Qy   121 TGGGTGTCTCTGGTGGCTCCAT---CAGCGGTTACTACTGGACCTGGCCCAG  177
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Db   158 TGCGCTGTGTCTGGTGTGGCTCCATTACCACCAGCAATGACAATGCTGCTGGATCGGATCGGATCGGCCCAG  217

Qy   178 ACCCCAGGGAGGGGACTGGAGTGATTGGCCATATTTATGGTAATGGTGCGACCACCAAC  237
         ||||||||| |||||||||||||||||||||||||||||||||||      |||||||||
Db   218 CCCCCAGGGAAGAGACTACAGGCTCTGGTGTTTGG------ATGTCATGAAGAACACGTCCAAGAACCAGTTC  271

Qy   238 TACAATCCCTCCCCAAGAGTCGAGTCACCATTTCAAAAGACATTCAAAAGACCAGTTC  297
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Db   272 TACAGCCGTCCCTCGGGAGTCGAGTCACCATATCCGCAGAGACGTCAAGAACCAATTC  331

Qy   298 TTCCTGAACTTGAATTCTGTGACCGACCTGCCTCCCCGACACGGCCGTCTATTACTGTGCGAGAGGC  357
         ||||  |||||||||||||||||||||||||||||||||||||||||||||||| ||| || ||||| ||
Db   332 TCCCTGAGCGTGACCTCTGCCTCGCTCCCGCCAGACACGGCCGTCTGTTTATTATTGTGCGAGCGTC  391

Qy   358 CCTCGCCCTGATTGCACAACCATTTGTTATGGGGTCGTCGGTCGGGCCCGGGA  417
         ||              | ||| |||||||||||||||||||||| |||||||||
Db   392 C-------GTGTTTCCAGGGTTCGCGGAGTCCTTTCTTTGACTTCTGGGGCCAGGGG  442

Qy   418 GACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  477
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Db   443 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  502

Qy   478 TCCTCCAAGAGCACCTCTGGGGGACACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  537
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Qy   553 GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG 612
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Db   541 GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG 600

Qy   613 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 672
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Db   601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 660

Qy   673 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA 732
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA 720

Qy   733 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 792
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Db   721 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG 780

Qy   793 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 852
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Db   781 GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 840

Qy   853 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 912
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Db   841 ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC 900

Qy   913 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 972
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Db   901 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG 960

Qy   973 TACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTCCTCAAAGTCCTGGCTGAAT 1032
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Db   961 TACAACAGCACTTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT 1020

Qy 1033 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1092
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Db 1021 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATTGAGAAAACC 1080

Qy 1093 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1152
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Db 1081 ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG 1140

Qy 1153 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC 1212
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Db 1141 GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGTTTCTATCCTAGC 1200

Qy 1213 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1272
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Db 1201 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1260

Qy 1273 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1332
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Db 1261 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1320

Qy 1333 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1392
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Db 1321 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC 1380

Qy 1393 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG 1430
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Db 1381 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG 1418

RESULT 9
AK057775
LOCUS   AK057775   1589 bp   mRNA   linear   PRI 26-MAR-2002
DEFINITION Homo sapiens cDNA FLJ25046 fis, clone CBL03624, highly similar to
            Ig gamma immunoglobulin heavy chain.
ACCESSION   AK057775
VERSION   AK057775.1 GI:16553709
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL03624.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE   1  (bases 1 to 1404)
AUTHORS     Hanna,N., Newman,R.Anthony, and Reff,M.Elliot.
TITLE       Recombinant anti-CD4 antibodies for human therapy
JOURNAL     Patent: US 6136310-A 7 24-OCT-2000;
FEATURES             Location/Qualifiers
     source          1..1404
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BASE COUNT      312 a    448 c    377 g    267 t
ORIGIN

Query Match            81.9%;  Score 1171.4;  DB 6;  Length 1404;
Best Local Similarity  90.0%;  Pred. No. 2e-227;
Matches 1288;  Conservative    0;  Mismatches 116;  Indels 27;  Gaps  2;

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Db     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGTCCCAGCAGCCCCAGATGGGTCTTGTCCCAG    60

Qy    61 GTGAAGCTGCAGCAGTGGGCGGAAGGACTTCTGCAGCCTTCGGAGGACCCTGTCCGTGCACC   120
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Qy   121 TGCGGTGTCTCTGGTGGCTCCATCAGCCGGTTACTACTACTGGAGCTGGATCCGCCAGCCC   180
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Qy   181 CCAGGGAGGGGACTGGAGTGGATTGGGAGTATATTTATGGTAATGTGCGACCACCAACTAC   240
           |||||||||||||||||||||||||||||||    ||||   |||||||||||||||| ||
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Db   301 CTGAACTTGAGGTCTGTGACCGCTGAGGACACGGCCGTCTATTACTGTGCGA    352

Qy   361 CGCCCTGATTGCACAACCATTGTTATGGCGGCCCGGGAGAC   420
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Db   353 GTAATATATGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTC    402

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC   480
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Db   403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGC   462

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC   540
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Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC   840
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Db   841 ...
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Qy   538 CCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC   597
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Qy   658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG   717
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Qy   718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA   777
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Db  1343 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG   1402

Qy  1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCGTCTCCGGGTAAATGA   1431
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RESULT 10
AR135375
LOCUS       AR135375                1404 bp    DNA      linear       PAT 16-JUN-2001
DEFINITION  Sequence 7 from patent US 6136310.
ACCESSION   AR135375
VERSION     AR135375.1  GI:14476047
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
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Qy   961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTGCACCAG 1020
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Qy  1261  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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Db  1294  GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy  1381  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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RESULT 11
AK097365

LOCUS   AK097365   1566 bp   mRNA   linear   PRI 15-JUL-2002
DEFINITION   Homo sapiens cDNA FLJ40046 fis, clone SYNOV2001300, highly similar
              to Ig gamma =immunoglobulin heavy chain.
ACCESSION   AK097365
VERSION   AK097365.1 GI:21757092
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens synovial membrane tissue from rheumatoid arthritis
              cDNA to mRNA, clone_lib:SYNOV2 clone:SYNOV2001300.
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
              Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
              Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
              Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
              Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
              Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
              Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
              Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
              Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1566)
AUTHORS   Isogai,T. and Yamamoto,J.
TITLE   Direct Submission
JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
              Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
              (E-mail:genomics@hri.co.jp Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
              Economy, Trade and Industry of Japan; cDNA full insert sequencing:
              Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

FEATURES   Location/Qualifiers
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                     /note="cloning vector: pME18SFL3"
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BASE COUNT   341 a   529 c   410 g   286 t
ORIGIN

Query Match   81.8%;   Score 1170; DB 9; Length 1566;
Best Local Similarity 90.4%;   Pred. No. 3.8e-227;
Matches 1296; Conservative   0; Mismatches 105;   Indels 33; Gaps 3;

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Qy    1  ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGACAGCTCCCAGATGGGTCCTGTCCCAG  60
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Qy   61  GTGAAGCTGCAGCAGTCTGGGGCCGAAGACTTCTCAGCCTCTGGATACTCTGGTCCACC 120
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Db   90  GTCCGATTACAGGAGTCGGGGCCCAGGGCTCGTGAAGCCTCACAAACCCTGGTCCCTCACC 149

Qy  121  TGCGTTGTCTCCGGTGGCTCCATCAGCG---GTTACTACTGACAGCTGGATCCGGCCAG 177
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Qy  418  GACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC 477
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Qy  538  CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC 597
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ORIGIN

Query Match     81.6%;   Score 1168.2;  DB 6;  Length 1404;
Best Local Similarity   89.9%;
Matches 1286;   Conservative   0;   Mismatches 118;   Indels 27;   Gaps 2;

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         |||  | |  |   |||||     ||  |           | ||  ||||||||| |
Db   353 ---------GTAATATATTGGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTC  402

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC  480
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Db   583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  642

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Left-column continuation (positions 540–1433):

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Qy  1078 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC  1137
Db  1080 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC  1139

Qy  1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA  1197
Db  1140 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA  1199

Qy  1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1257
Db  1200 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC  1259

Qy  1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC  1317
Db  1260 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC  1319

Qy  1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG  1377
Db  1320 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG  1379

Qy  1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
Db  1380 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1433
```

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RESULT 12
AR135377
LOCUS       AR135377                1404 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 11 from patent US 6136310.
ACCESSION   AR135377
VERSION     AR135377.1  GI:14476049
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1404)
AUTHORS     Hanna,N., Newman,R.Anthony. and Reff,M.Elliot.
TITLE       Recombinant anti-CD4 antibodies for human therapy
JOURNAL     Patent: US 6136310-A 11 24-OCT-2000;
```

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Qy   241  AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC  300
          ||||||||||||||||||||||||||||| ||||||||   |||||  |||| ||||| |
Db   241  AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCAAGAACCTCTTCTCC   300

Qy   301  CTGAACTTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTACTGTGCGAGAGGGCCCT  360
          |||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTGAAACTGAGGTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGA--------  352

Qy   361  CGCCCTGATTGCACAACCATTTGTTATGGCGGTCGATGTCTGGGCCCGGAGAC  420
                        |||||||||||   || ||  |||  ||   |||| ||| |
Db   353  -------GTAATATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTC  402

Qy   421  CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCACCCTCC  480
          ||||||||||||||||||||||||||||||||||||||||||||||   |||| ||| |
Db   403  CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCGGCCCTGC  462

Qy   481  TCCAAGAGCACCTGTGGGGCGCACGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   463  TCCAGGAGCACCTGCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  522

Qy   541  GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   523  GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  582

Qy   601  GCTGTCCTACAGTCCTCACTGGACTCCTCCCTCAGCAGCGTCGTGACCGTGCCCTCCAGC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   583  GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  642

Qy   661  AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
          ||||   |||||  | |||||    ||||| | |||||
Db   643  AGCTTGGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG  702

Qy   721  GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
          |||||||  |||| |||  ||     ||||    |||| |||||||||||||||||||||
Db   703  GACAAGAGAGTTGAGTCCAAATATGG-------TCCCCATGCCCATCATGCCCAGCA  753

Qy   781  CCTGAACTTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
          |||||||||| |||||  |||||||||||||||||||||||||||||||||||||||||||
Db   754  CCTGAGTTCGAGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC  813

Qy   841  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   814  ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC  873

Qy   901  GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
          |||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||||
Db   874  GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  933

Qy   961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   934  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  993

Qy  1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
          |||||||||||| || ||||||||||||||||||||||||||||||||  |||||| ||
Db   994  GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC  1053

Qy  1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
          |||||||||| ||||||||||||||||||| ||||||||||||||||||||||||||| |
Db  1054  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG  1113

Qy  1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  1114  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1173

Qy  1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  1174  TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1233

Qy  1261  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320
          ||||| ||||||||||||| |||||| ||||||||||||||||||||||||||||| |||
Db  1234  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC  1293
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Qy   961  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   934  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  993

Qy  1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
          |||||||||||| || |||||||||||||||||||||||||||||||||  ||||| ||
Db   994  GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC  1053

Qy  1081  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  1140
          |||||||||| ||||||||||||||||||| |||||||||||||||||||||||||| |
Db  1054  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTG  1113

Qy  1141  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1114  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  1173

Qy  1201  TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1260
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  1174  TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  1233

Qy  1261  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC  1320
          ||||| ||||||||||||| |||||| |||||||||||||||||||||||||||||| ||
Db  1234  AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACC  1293

Qy  1321  GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1294  GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT  1353

Qy  1381  CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1354  CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1404
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RESULT 13
AR135376
LOCUS   AR135376   1404 bp   DNA   linear   PAT 16-JUN-2001
DEFINITION Sequence 9 from patent US 6136310.
ACCESSION   AR135376
VERSION   AR135376.1 GI:14476048
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1404)
  AUTHORS   Hanna,N., Newman,R.Anthony. and Reff,M.Elliot.
  TITLE   Recombinant anti-CD4 antibodies for human therapy
  JOURNAL   Patent: US 6136310-A 9 24-OCT-2000;
FEATURES   Location/Qualifiers
     source   1..1404
                     /organism="unknown"
BASE COUNT   313 a   446 c   379 g   266 t
ORIGIN

Query Match   81.5%;   Score 1166.6; DB 6; Length 1404;
Best Local Similarity   89.8%;   Pred. No. 1.9e-226;
Matches 1285; Conservative   0; Mismatches 119; Indels   27; Gaps   2;

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Qy    1  ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG  60
         |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    1  ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCTTGTCCCAG  60

Qy   61  GTGAAGCTGCAGTGGGGCGAAGGAGTCTTCGACCTTGCGACCCTGTCCGCACC  120
         |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   61  GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120

Qy  121  TGCGTTGTCTCTGGTGGCTCCATCAGCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCC  180
         ||||||||||||| ||| |||||  ||||||||||||||||||||||||||||||||||
Db  121  TGCAGTGTCTCTGGTGGCTCCATCAGCAGTGGTTATTATGGTGGATCCGCCAGTCC  180

Qy  181  CCAGGGAAGGGACTGGAGTGGATTGGGCGTATCTATACCAGTGGGAGCACCAACTAC  240
         ||||||||||||| |||||| ||||| |||| |||||||||| |||||||||||||||
Db  181  CCAGGGAAGGGACTGGAGTGGATTGGGCGTATCAGCTACAGCGGGAGCACCAACTAC  240
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Query Match          78.7%;  Score 1125.8;  DB 9;  Length 1633;
Best Local Similarity 88.1%;  Pred. No. 3.5e-218;
Matches 1249;  Conservative 0;  Mismatches 162;  Indels 6;  Gaps 2;

Qy     15 GTTCTTCCTCCTGTGCAGCTCCAGATGGTCCTGTCCCAGGTGAAGCTGCAGCA 74
          ||||| || |||| ||| ||||||||| ||||| |||||||||||||||
Db     98 GTGCTGGGTTTCCTGTTGTCTATTTAAAAGTGTCAGTGTGAGGTGCAGTGGTGA 157

Qy     75 GTGGGGCGAAGGACTTCTGGCACCTGTCCGACCTGTCCTGGTTGTCTCTGG 134
          ||  || ||||||||  ||| |||||||| |||||||| |||||||||| |
Db    158 GTCCGGGGAGGGCCTGGTACAGCCTGGGGGTCCTGACACTCTCCTGTGCAGTCTG- 216

Qy    135 TGGCTCCATCAGCGGTTACTACTACTGGAACTGGATCCGGCAGCCCCAGGAGGGGACT 194
          |  ||||| |||| |||||||| ||| ||  || || || ||||| |||||||||||
Db    217 --GCTTCACCTTCAGTCAGTAACTATATGAATTAAACTGGGTCCGGCCAGGCAGGGGGACT 274

Qy    195 GGAGTGGATTGGCCATATTTATGGTAATGGTGACCACAGTTCTTCCTGAACTCCCTCAA 254
          ||| || || |||| ||||| || ||  |||| ||||||| ||||| ||||||||| ||
Db    275 GGAGTGGCTTTCGTACATCAGTACTAGTGCGCTTCCAACTTTACGCAGACCCTGTGAA 334

Qy    255 GAGTGCAGTCACCATTTCAAAAGACACAGTCCAAGACAGTTCTTCCTGAACTGAATTC 314
          | | | ||| |||| ||| || ||  | |||| |||| ||| || ||| || |  |
Db    335 GGGCCGGTTCACCATCTCCAGAGACAGCCGCAAAAACTCACTGTTTCTGCATATGGGCAG 394

Qy    315 TGTGACCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCTGCCCTGATTGCAC 374
          | |||| ||||||| ||| ||||||||||||||||||||  | || |||||||
Db    395 CCTGAGAGCCGAGGACACGGCCGTGTCTATTACTGTGCGAGAGGGTACAGCAGCAGC 454

Qy    375 AACCATTTGTTATGGCGGTCGATGTCTGGGGCCCGGGAGACGTCCACCGTCTC 434
          |||| ||||| || |||| ||||| ||||||| ||||||| || || ||||||
Db    455 TGCCATAAAGTA---CAACTGGTTCGACTCCTGGGGCCAGGGAACCCTGGTCACCGTCTC 511

Qy    435 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTC 494
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    512 CTCAGCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTC 571

Qy    495 TGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACGGGTGACGGT 554
          |||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||
Db    572 TGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGGAACGGGTGACGGT 631

Qy    555 GTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC 614
          |||||||||||||||||||||||||||||||||||||| ||||| ||| |||||||||||
Db    632 GTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC 691

Qy    615 CTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA 674
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    692 CTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA 751

Qy    675 GACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGA 734
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 GACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGA 811

Qy    735 GCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGG 794
          ||||||||||||||||||||||||||| |||||||||||||||||||||| |||||||||
Db    812 GCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGG 871

Qy    795 GGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC 854
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    872 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC 931

Qy    855 CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAA 914
          |||||| ||||| || |||||||||||||||||||||||||||||||||||||||||||
Db    932 CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAA 991

Qy    915 CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTA 974
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    992 CTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTA 1051

Qy    975 CAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG 1034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1052 CAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG 1111

Qy   1035 CAAGGGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT 1094
          |||| | || ||| | ||| |||||||||||||||  | ||||||||||||||||||||
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Qy   1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
          ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db   1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
          |||||||||||||||||||||||||||||||||||||| |||||||||||
Db   1354 CTGCACAACCACTACACCAGAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1404
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RESULT 14
AK097859
LOCUS   AK097859   1633 bp   mRNA   linear   PRI 15-JUL-2002
DEFINITION   Homo sapiens cDNA FLJ40540 fis, clone THYMU1000554, highly similar
               to Homo sapiens mRNA for immunoglobulin lambda heavy chain.
ACCESSION   AK097859
VERSION   AK097859.1   GI:21757751
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens shymus cDNA to mRNA, clone_lib:THYMU1
               clone:THYMU1000554.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
               Kodaira,H., Furuya,T., Takahashi,T., Kikkawa,E., Omura,Y., Abe,K.,
               Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
               Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
               Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,D.,
               Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
               Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K.,
               Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
               Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE   2   (bases 1 to 1633)
AUTHORS   Isogai,T. and Yamamoto,J.
TITLE   Direct Submission
JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
               Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
               (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
               Economy, Trade and Industry of Japan; cDNA full insert sequencing:
               Research Association for Biotechnology (RAB); cDNA library
               construction: Helix Research Institute (HRI) (supported by Japan
               Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
               HRI, and Biotechnology Center, National Institute of Technology and
               Evaluation; clone selection for full insert sequencing: HRI and
               RAB; annotation: HRI and RAB.
FEATURES   Location/Qualifiers
     source   1..1633
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="THYMU1000554"
               /tissue_type="shymus"
               /clone_lib="THYMU1"
               /note="cloning vector: pME18SFL3"
     CDS   84..1508
               /note="unnamed protein product"
               /codon_start=1
               /protein_id="BAC05186.1"
               /db_xref="GI:21757752"
               /translation="MELGLCWVFLVAILKGVSQCEVQLVESGGGLVQPGGSLTLSCAVS
               GFFTFSNYELNWVRQAPGKGLEWLSYISTGSASQLYADPVKGRFTISRDSGKNSLFLHM
               GSLRAEDTAVYYCARGYSTAAAAIKYNWFDSWGQGTLVTVSSASTKGPSVFPLAPSSK
               STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
               SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD
               TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
               VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVVTLPPSREEMTKNQVSL
               TCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF
               SCSVMHEALHNHYTQKSLSLSPGK"
BASE COUNT   370 a   521 c   445 g   297 t
ORIGIN

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Db   1112  CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT  1171
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Qy   1095  CTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA  1154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1172  CTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA  1231

Qy   1155  TGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA  1214
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1232  GGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA  1291

Qy   1215  CATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCC  1274
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1292  CATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCC  1351

Qy   1275  CGTGCTGGACTCCGACGGCCTCCTTCTTCTTCTACAGCAAGCTCACCGTGGACAAGAGCAG  1334
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1352  CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAG  1411

Qy   1335  GTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGCATGAGGCTCTGCACAACCACTA  1394
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1412  GTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGCATGAGGCTCTGCACAACCACTA  1471

Qy   1395  CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
           ||||||||||||||||||||||||||||||||||||||
Db   1472  CACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAATGA  1508
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RESULT 15
BD000501
LOCUS       BD000501        1507 bp    DNA        linear      PAT 31-JAN-2002
DEFINITION  Process for producing monoclonal antibody.
ACCESSION   BD000501
VERSION     BD000501.1   GI:18623614
KEYWORDS    JP 2000342279-A/1.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1507)
  AUTHORS   Kusunoki,C. and Fukushima,A.
  TITLE     Process for producing monoclonal antibody
  JOURNAL   Patent: JP 2000342279-A 1 12-DEC-2000;
            JAPAN TOBACCO INC,ABGENIX INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000342279-A/1
            PD   12-DEC-2000
            PF   30-MAR-2000 JP 2000097874
            PR
            PI   CHIHIRO KUSUNOKI,ATSUSHI FUKUSHIMA
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/02, PC
            C12P21/08//
            PC   C07K16/18,C12N15/00,C12N5/00,C12N15/00
            CC
FEATURES             Location/Qualifiers
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  FT     CDS          (12)..(1400).
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                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
BASE COUNT      330 a    498 c    409 g    270 t
ORIGIN
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Query Match       78.6%;  Score 1124.2;  DB 6;  Length 1507;
Best Local Similarity  89.5%;  Pred. No. 7.4e-218;
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Qy    61  GTGAAGCTGCGCAGCAGTGCGCGAAGGACTTCGCAGCCTTCGGAGACCCCTGTCCGCACC  120
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Qy   1021  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC  1080
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Search completed: April 6, 2003, 01:56:00
Job time : 4496.25 secs

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OM protein - protein search, using sw model

Run on:        March 29, 2003, 09:06:24 ; Search time 8.31417 Seconds
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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and is derived by analysis of the total score distribution.
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SUMMARIES

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3	973	78.3	236	3	US-08-487-550-10	Sequence 10, Appl
4	880.5	70.8	236	4	US-09-049-672A-7	Sequence 7, Appli
5	867.5	69.8	235	4	US-09-049-672A-10	Sequence 10, Appl
6	861	69.3	235	2	US-08-378-939-12	Sequence 12, Appl
7	855.5	68.8	238	4	US-08-793-450-6	Sequence 6, Appli
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9	844	67.9	240	4	US-09-049-672A-11	Sequence 11, Appl
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16	548	44.1	105	1	US-08-422-101-9	Sequence 9, Appli
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19	548	44.1	105	2	US-08-788-800-6	Sequence 6, Appli
20	548	44.1	105	3	US-08-422-093-9	Sequence 9, Appli
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22	535	43.0	104	4	US-09-025-769B-170	Sequence 170, App
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24	502.5	40.4	235	3	US-08-812-586-16	Sequence 16, Appl
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35	467.5	37.6	128	1	US-08-478-039-110	Sequence 110, App
36	467.5	37.6	128	1	US-08-476-349A-110	Sequence 110, App
37	467.5	37.6	128	4	US-08-523-894-4	Sequence 4, Appli
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ALIGNMENTS

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; Sequence 2, Application US/08487550
; Patent No. 6113898
;- GENERAL INFORMATION:
;-  APPLICANT: Anderson, Darrell R.
;-  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;-  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;-  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;-  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;-  NUMBER OF SEQUENCES: 12
;-  CORRESPONDENCE ADDRESS:
;-   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;-   STREET: 699 Prince Street
;-   CITY: Alexandria
;-   STATE: VA
;-   COUNTRY: USA
;-   ZIP: 22314
;-  COMPUTER READABLE FORM:
;-   MEDIUM TYPE: Floppy disk
;-   COMPUTER: IBM PC compatible
;-   OPERATING SYSTEM: PC-DOS/MS-DOS
;-   SOFTWARE: PatentIn Release #1.0, Version #1.30
;-  CURRENT APPLICATION DATA:
;-   APPLICATION NUMBER: US/08/487,550
;-   FILING DATE: 07-JUN-1995
;-   CLASSIFICATION: 435
;-  ATTORNEY/AGENT INFORMATION:
;-   NAME: Teskin, Robin L.
;-   REGISTRATION NUMBER: 35,030
;-   REFERENCE/DOCKET NUMBER: 012712-131
;-  TELECOMMUNICATION INFORMATION:
;-   TELEPHONE: 703-836-6620
;-   TELEFAX: 703-836-2021
;-  INFORMATION FOR SEQ ID NO: 2:
;-   SEQUENCE CHARACTERISTICS:
;-    LENGTH: 234 amino acids
;-    TYPE: amino acid
;-    TOPOLOGY: linear
;-   MOLECULE TYPE: protein
US-08-487-550-2

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Best Local Similarity   100.0%;  Pred. No. 9.9e-103;
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RESULT 2
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; Sequence 6, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
;   APPLICANT: Hanna, Nabil
;   APPLICANT: Newman, Roland A.
;   APPLICANT: Reff, Mitchell E.
;   TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;   TITLE OF INVENTION: Therapy
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314-3187
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/523,894
;   FILING DATE: 06-SEP-1995
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-165
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 233 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-523-894-6

Query Match   81.7%; Score 1015.5; DB 4; Length 233;
Best Local Similarity   86.0%; Pred. No. 1.4e-82;
Matches 196; Conservative   10; Mismatches   21; Indels   1; Gaps   1;

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Qy 187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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Db 186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
US-08-487-550-10
; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 236 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-487-550-10

Query Match   78.3%; Score 973; DB 3; Length 236;
Best Local Similarity   80.1%; Pred. No. 8.3e-79;
Matches 189; Conservative   13; Mismatches   32; Indels   2; Gaps   1;

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Db 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy 179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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Db 181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4
US-09-049-672A-7
; Sequence 7, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Lal, Preeti

~ ; APPLICANT: Tang, Y. Tom
~ ; APPLICANT: Yue, Henry
~ ; APPLICANT: Au-Young, Janice
~ ; APPLICANT: Corley, Neil C.
~ ; APPLICANT: Guegler, Karl J.
~ ; APPLICANT: Baughn, Mariah R.
~ ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
~ ; NUMBER OF SEQUENCES: 28
~ ; CORRESPONDENCE ADDRESS:
~ ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
~ ; STREET: 3174 Porter Drive
~ ; CITY: Palo Alto
~ ; STATE: CA
~ ; COUNTRY: USA
~ ; ZIP: 94304
~ ; COMPUTER READABLE FORM:
~ ; MEDIUM TYPE: Diskette
~ ; COMPUTER: IBM Compatible
~ ; OPERATING SYSTEM: DOS
~ ; SOFTWARE: FastSEQ for Windows Version 2.0
~ ; CURRENT APPLICATION DATA:
~ ; APPLICATION NUMBER: US/09/049,672A
~ ; FILING DATE: HEREWITH
~ ; CLASSIFICATION: 536
~ ; PRIOR APPLICATION DATA:
~ ; APPLICATION NUMBER:
~ ; FILING DATE:
~ ; ATTORNEY/AGENT INFORMATION:
~ ; NAME: Cerrone, Michael C
~ ; REGISTRATION NUMBER: 39,132
~ ; REFERENCE/DOCKET NUMBER: PF-0497 US
~ ; TELECOMMUNICATION INFORMATION:
~ ; TELEPHONE: 650-855-0555
~ ; TELEFAX: 650-845-4166
~ ; TELEX:
~ ; INFORMATION FOR SEQ ID NO: 7:
~ ; SEQUENCE CHARACTERISTICS:
~ ; LENGTH: 236 amino acids
~ ; TYPE: amino acid
~ ; STRANDEDNESS: single
~ ; TOPOLOGY: linear
~ ; IMMEDIATE SOURCE:
~ ; LIBRARY: ADRETUT05
~ ; CLONE: 2492122
US-09-049-672A-7

Query Match 70.8%; Score 880.5; DB 4; Length 236;
Best Local Similarity 74.9%; Pred. No. 1.3e-70;
Matches 173; Conservative 17; Mismatches 38; Indels 3; Gaps 1;

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Qy   7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAP  63
         || ||  ||||||| ||||||||  ||  :|:|  ||||||||||
Db   6 LLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP  65

Qy  64 ILVIYDDSDRPSGIPERFSGGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGT 123
         |||||  ||:|::||||||||||||||||||||  ||||||
Db  66 KLLIYGSRNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSLSGVVFGGGT 125

Qy 124 RVTVLGQPKAAPSVLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 183
         :|||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db 126 KLTVLGQPKAAPSVLFPPSSEELQANRATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185

Qy 184 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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RESULT 5
US-09-049-672A-10
; Sequence 10, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

~ ; APPLICANT: Lal, Preeti
~ ; APPLICANT: Tang, Y. Tom
~ ; APPLICANT: Yue, Henry
~ ; APPLICANT: Au-Young, Janice
~ ; APPLICANT: Corley, Neil C.
~ ; APPLICANT: Guegler, Karl J.
~ ; APPLICANT: Baughn, Mariah R.
~ ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
~ ; NUMBER OF SEQUENCES: 28
~ ; CORRESPONDENCE ADDRESS:
~ ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
~ ; STREET: 3174 Porter Drive
~ ; CITY: Palo Alto
~ ; STATE: CA
~ ; COUNTRY: USA
~ ; ZIP: 94304
~ ; COMPUTER READABLE FORM:
~ ; MEDIUM TYPE: Diskette
~ ; COMPUTER: IBM Compatible
~ ; OPERATING SYSTEM: DOS
~ ; SOFTWARE: FastSEQ for Windows Version 2.0
~ ; CURRENT APPLICATION DATA:
~ ; APPLICATION NUMBER: US/09/049,672A
~ ; FILING DATE: HEREWITH
~ ; CLASSIFICATION: 536
~ ; PRIOR APPLICATION DATA:
~ ; APPLICATION NUMBER:
~ ; FILING DATE:
~ ; ATTORNEY/AGENT INFORMATION:
~ ; NAME: Cerrone, Michael C
~ ; REGISTRATION NUMBER: 39,132
~ ; REFERENCE/DOCKET NUMBER: PF-0497 US
~ ; TELECOMMUNICATION INFORMATION:
~ ; TELEPHONE: 650-855-0555
~ ; TELEFAX: 650-845-4166
~ ; TELEX:
~ ; INFORMATION FOR SEQ ID NO: 10:
~ ; SEQUENCE CHARACTERISTICS:
~ ; LENGTH: 235 amino acids
~ ; TYPE: amino acid
~ ; STRANDEDNESS: single
~ ; TOPOLOGY: linear
~ ; IMMEDIATE SOURCE:
~ ; LIBRARY: THYRNOT10
~ ; CLONE: 2872705
US-09-049-672A-10

Query Match 69.8%; Score 867.5; DB 4; Length 235;
Best Local Similarity 74.7%; Pred. No. 1.8e-69;
Matches 177; Conservative 16; Mismatches 29; Indels 15; Gaps 4;

```
Qy   7 LLGLLLL------WLPGARCAYELTQPPSVSVSPGQTARITCGGDNS--RNEYVHWYQQ  57
         || |||        ||| |||||||  ||||| : |  ||||||||
Db   5 LLFLTLLTQGTGSWAQSA----LTQPASVSGSPGQSITISCTGTSSDVGGGYNYVSWYQQ  59

Qy  58 KPARAPILVIYDDSDRPSGIPERFSGGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHP 117
         ||||| ||| :|:||||||||||||||||||||||||||  ::
Db  60 SPGTAPKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSY-VGNNIV 118

Qy 118 VFGGGTRVTVLGQPKAAPSVLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV 177
         ||||||  :|||||||||| ||||||||||||||||||||||||||||||||||||
Db 119 VFGGGTKLIVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV 178

Qy 178 KAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 179 KAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235
```

RESULT 6
US-08-378-939-12
; Sequence 12, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:

APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-939-12

Query Match   69.3%; Score 861; DB 2; Length 235;
Best Local Similarity 75.1%; Pred. No. 6.9e-69;
Matches 175; Conservative 16; Mismatches 38; Indels 4; Gaps 2;

Qy   5 AQLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNS--RNEYVHWYQQKPAR 61
         ||| | | ||||| |||||||||||||||||| |||| : || |||||
Db   4 ALLLTLLITQDTGSWAQSALTQPASVSGGSPGQSITISCTGTNNDVGSYNLVSWYQQHPGK 63

Qy 62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
         :: :: || : |||| |||||||:|| |||||| |||||||||||
Db 64 APKIMIYEVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCCSY-AGSYTVVFGG 122

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
        ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 123 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 182

Qy 182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 183 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 7
US-08-793-450-6
; Sequence 6, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-6

Query Match   68.8%; Score 855.5; DB 4; Length 238;
Best Local Similarity 73.2%; Pred. No. 2.2e-68;
Matches 167; Conservative 14; Mismatches 32; Indels 15; Gaps 2;

Qy 17 GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSG 76
         || | |:|||||||||||||||||||||||| :| ||||| || :: |||||
Db 16 GVHSDIELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLVIYGKNNRPSG 75

Qy 77 IPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPS 136
         |:|||||||||:|| ||||||| : ||| |||||||||||||||||||
Db 76 IPDRFSGSSSGNTASLTITGAQAEDEADYFCN-----SGGKVFGGGTKLTVLGQPKAAPS 130

Qy 137 VTLFPPS--------SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
        |||||| ||||||||||||||||||||||||||||||||||||||||
Db 131 VTLFPPSLEELQANKATLEELQANKATLVCLISDFYPGAVTVLAWKADGRPVKAGVETNKP 190

Qy 187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
        |||||||||||||||||||||||||||||||||||||||||| ||||
Db 191 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTAEKTVAPAECS 238

RESULT 8
US-09-049-672A-12
; Sequence 12, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTUT13
CLONE: 3116314
US-09-049-672A-12

Query Match   68.8%; Score 855; DB 4; Length 235;
Best Local Similarity 72.6%; Pred. No. 2.4e-68;
Matches 167; Conservative 17; Mismatches 44; Indels 2; Gaps 1;

Qy   7 LLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGG--DNSRNEVHWYQQKPARAPI 64
          | |: . |||||| ||||||||||||||||||: ||| ||||
Db   6 LLLALLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGTTSNIASNSVHWYQLVPGAAPK 65

Qy   65 LVIYDDSDRPSGIPERFSGSKSGNTALTINGVEAGDEADYCQVWDRASDHPVFGGGTR 124
          |||: .::|||:|||:|||||||:|:||| ::||| |:|||||||
Db   66 LLIYANDQRASGVPDRFSGSKSGTSASLAISGLRPEDETDYYCATWDDSVSGWMFGGGTK 125

Qy 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

Qy 185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||:|||:||||||||||||||||||||||||
Db 186 TPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 9
US-09-049-672A-11
; Sequence 11, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LNDNOT08
CLONE: 3056213
US-09-049-672A-11

Query Match   67.9%; Score 844; DB 4; Length 240;
Best Local Similarity 71.4%; Pred. No. 2.3e-67;
Matches 172; Conservative 16; Mismatches 45; Indels 8; Gaps 3;

Qy   1 MRVPAQLLGLLLWL----PGARCAYELTQPPSVSVSPGQTARITCG--GDNSRNEYVH 53
          :|| |||||| |:|||||||||||||||||||||| ::|
Db   1 MSVPTMAWMMLLGLLAYGSGVDSQTVVTQEPSFSVSPGGVTLTCGLSSGSVSTSNYPS 60

Qy   54 WYQQKPARAPILIVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRA 113
          |||| |:|| |::|||: .::|||:|||||:||||||:|:||| ::|||
Db   61 WYQQTPGQAPRTLIYGTSVRSSGVPDRFSGSILGNKAGLTITGAQADDESDYYCVLY-RR 119

Qy 114 SDHPVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD 173
          |||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db 120 SGSWVFGGGTKLSVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD 179

Qy 174 SSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db 180 SSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTEC 239

Qy 234 S 234
          |
Db 240 S 240

RESULT 10
US-09-152-060-70
; Sequence 70, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762

; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 70
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-70

Query Match   65.3%;   Score 812; DB 4; Length 235;
Best Local Similarity 74.6%;   Pred. No. 1.5e-64;
Matches 159; Conservative 19; Mismatches 33; Indels 2; Gaps 1;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
         ||||||| ||| |:|: : |:|: | : ::|||||| :: |||||||
Db   23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPPKLLSYRNNNRPSGISERL 82

Qy   82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
         | ||| ||:||| ||||||||| :: ||||||| : |||||||||||||||||||
Db   83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

Qy 142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

Qy 202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         ||||||||||||||||||||||||||| ||||
Db 203 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 11
US-09-152-060-88
; Sequence 88, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-88

Query Match   65.1%;   Score 809; DB 4; Length 235;
Best Local Similarity 74.2%;   Pred. No. 2.8e-64;
Matches 158; Conservative 20; Mismatches 33; Indels 2; Gaps 1;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
         ||||||| ||| |:|: : |:|: | : ::|||||| :: |||||||
Db   23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPPKLLSYRNNNRPSGISERL 82

Qy   82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
         | ||| ||:||| ||||||||| :: ||||||| : |||||||||||||||||||
Db   83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

Qy 142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

Qy 202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         |||||||||||||||||||||||||||||||||
Db 203 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 12
US-08-751-359-22
; Sequence 22, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB.504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-751-359-22

Db   4   APLLLAVLAHTSGSLVQAALTQPSSVSANPGETVKITCSGDRS---YYGWYQQKAPGSAP   60

Qy   64   ILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGT 123
              :||| .::;||||||||||||||||| :||:|||| :||||:||||||:: ||||||||
Db   61   VTVIYANTNRPSDIPSRFSGSKSGSTATLTITGVQADDEAVYYCGSADSSSTAGIFGAGT 120

Qy   124   RVTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
              :||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||:
Db   121   TLTVLGQPKVAPTITLFPPSKEELNEATKATLVCLINDFYPSPVTVDWVIDGS-TRSG-E 178

Qy   183   TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
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Db   179   TTAPQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNGTSITKTLKRSEC 229

RESULT 14
US-08-761-277A-51
; Sequence 51, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
;   APPLICANT: Denney Jr., Dan W.
;   TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
;   TITLE OF INVENTION: Leukemia
;   NUMBER OF SEQUENCES: 80
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Medlen & Carroll, LLP
;   STREET: 220 Montgomery Street, Suite 2200
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/761,277A
;   FILING DATE: 06-DEC-1996
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/644,664
;   FILING DATE: 01-MAY-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MacKnight, Kamrin T.
;   REGISTRATION NUMBER: 38,230
;   REFERENCE/DOCKET NUMBER: GENITOPE-02406
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 705-8410
;   TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 51:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 109 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-761-277A-51

Query Match   45.6%; Score 567; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   126   TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   186   PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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Db   61   PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 109

RESULT 15
5189147-10

Query Match   53.0%; Score 658.5; DB 4; Length 229;
Best Local Similarity 57.6%; Pred. No. 5.8e-51;
Matches 133; Conservative 32; Mismatches 59; Indels 7; Gaps 5;

Qy   5   AQLLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQK-PARAP   63
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Db   4   APLLLAVLAHTSGSLVQAALTQPSSVSANPGETVKITCSGDRS---YYGWYQQKAPGSAP   60

Qy   64   ILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGT 123
              :||| .::;||||||||||||||||| :||:|||| :||||:||||||:: ||||||||
Db   61   VTVIYANTNRPSDIPSRFSGSKSGSTATLTITGVQADDEAVYYCGSADSSSTAGIFGAGT 120

Qy   124   RVTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
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Db   121   TLTVLGQPKVAPTITLFPPSKEELNEATKATLVCLINDFYPSPVTVDWVIDGS-TRSG-E 178

Qy   183   TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
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Db   179   TTAPQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNGTSITKTLKRSEC 229

RESULT 13
US-08-907-146-22
; Sequence 22, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
;   APPLICANT: Michael, Nancy M
;   APPLICANT: Accavitti, Marianne
;   APPLICANT: Thompson, Craig B
;   TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES
;   NUMBER OF SEQUENCES: 25
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: USA
;   ZIP: 77210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/907,146
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/751,359
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Highlander, Steven L
;   REGISTRATION NUMBER: 37,642
;   REFERENCE/DOCKET NUMBER: ARSB:504
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 512/418-3000
;   TELEFAX: 512/474-7577
;   INFORMATION FOR SEQ ID NO: 22:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 229 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
US-08-907-146-22

Query Match   53.0%; Score 658.5; DB 4; Length 229;
Best Local Similarity 57.6%; Pred. No. 5.8e-51;
Matches 133; Conservative 32; Mismatches 59; Indels 7; Gaps 5;

Qy   5   AQLLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQK-PARAP   63
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;Patent No. 5189147
;    APPLICANT: SAITO, HARUO;KRANZ, DAVID M.;ELSEN, HERMAN N.;
;TONEGAWA, SUSUMU
;    TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR
;ANTIBODY
;    NUMBER OF SEQUENCES: 21
;    CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/07/271,216
;        FILING DATE: 14-NOV-1988
;    PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: 666,988
;        FILING DATE: 31-OCT-1984
;        APPLICATION NUMBER: 620,122
;        FILING DATE: 13-JUN-1984
;SEQ ID NO:10:
;    LENGTH: 200
5189147-10


Query Match            45.1%;     Score 560.5;  DB 6;   Length 200;
Best Local Similarity  53.3%;     Pred. No. 2.4e-42;
Matches  112; Conservative   28; Mismatches   51;  Indels   19;  Gaps   4;

Qy    24 LTQPPSVSVSPGQTARITC--GGDNSRNEYVHWYQQKPARAPIL-VIYDDSDRPSGIPE 79
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Db     4 VTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQQKPDHPLFTGLIGGTNNRAPGVPA 63

Qy    80 RFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDHPVFGGGTRVTVLGQPKAAPSVTL 139
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Qy   140 FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSY 199
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Db   109 FPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQSNNKYMASSY 168

Qy   200 LSLTPEQWKSHRSYSCQVTHEGSTVEKTVA 229
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Db   169 LTLTARAWERHSSYSCQVTHEGHTVEKSLS 198


Search completed: March 29, 2003, 09:17:39
Job time : 10.3142 secs
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                  GenCore version 5.1.4 p5.4578
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:            March 29, 2003, 09:06:23 ; Search time 24.0673 Seconds
                                              (without alignments)
                                              1295.559 Million cell updates/sec

Title:             US-09-758-173-2
Perfect score:     1243
Sequence:          1 MRVPAQLLGLLLWLPGARC........CQVTHEGSTVEKTVAPTECS 234

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5
Searched:          908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:    908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing:   Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :    A_Geneseq_101002:*
          1:  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a printed,
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1243	100.0	234	18	AAW01817	Primatised anti-hu
2	1243	100.0	234	19	AAW63760	Macaque primatized
3	1243	100.0	234	23	AAU11538	Protein sequence o
4	1015.5	81.7	233	18	AAW14924	Ant-CD4 monkey-hum
5	991.5	79.8	247	22	ABG19295	Novel human diagno
6	979	78.8	238	22	ABG19299	Novel human diagno
7	976.5	78.6	232	22	AAU14412	Human novel protei
8	973	78.3	236	19	AAW63764	Macaque primatized
9	973	78.3	236	23	AAU11645	Protein sequence o
10	973	78.3	269	23	ABP41361	Human ovarian anti
11	970	78.0	236	18	AAW01821	Primatised anti-hu
12	959	77.2	231	22	AAU14176	Human novel protei
13	959	77.2	234	22	ABG23084	Novel human diagno
14	958.5	77.1	232	22	AAU14236	Human novel protei
15	944	75.9	218	22	AAU08381	Anti-OPGbp antibod
16	944	75.9	233	23	AAU82012	Human secreted pro
17	939.5	75.6	236	22	AAU14472	Human novel protei
18	936.5	75.3	244	21	AAB43979	Human cancer assoc
19	936	75.3	226	22	ABG19294	Novel human diagno
20	925	74.4	233	9	AAP81260	VDJC regions of hu
21	912	73.4	231	23	AAU81991	Human secreted pro
22	906.5	72.9	232	22	AAM23527	Human EST encoded
23	905	72.8	238	22	ABG19297	Novel human diagno
24	898.5	72.3	246	22	ABB12413	Human bone marrow
25	884.5	71.2	217	14	AAR42163	Anti-HIV-1 recombi
26	881	70.9	236	22	ABG23083	Novel human diagno
27	880.5	70.8	236	22	AAB36209	Human immune syste
28	880	70.8	235	20	AAW88465	Monoclonal antibod
29	879.5	70.8	217	19	AAW40533	Antibody HB4C5 lig
30	870	70.0	249	22	ABG12886	Novel human diagno
31	867.5	69.8	235	22	ABG19290	Novel human diagno
32	867.5	69.8	235	22	AAB36212	Human immune syste
33	865.5	69.6	219	21	AAB30594	Variable and first
34	864.5	69.5	236	22	ABG19293	Novel human diagno
35	864	69.5	235	22	AAG64474	Human type antihum
36	864	69.5	244	22	ABG19296	Novel human diagno
37	864	69.5	251	22	ABG19291	Novel human diagno
38	863	69.4	235	22	AAG64472	Human type antihum
39	861	69.3	235	14	AAR31024	Antibody D light c
40	860	69.2	235	22	AAM38953	Human polypeptide
41	860	69.2	235	22	AAG64474	Human type antihum
42	855.5	68.8	238	17	AAR93165	Anti-rhesus D reco
43	855	68.8	235	22	AAB36214	Human immune syste
44	853	68.6	614	23	ABB06275	Plasmid scFv(CC046
45	849	68.3	240	21	AAY96306	Human IGFAM-18 imm

ALIGNMENTS

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RESULT 1
AAW01817
ID   AAW01817 standard; Protein; 234 AA.
XX
AC   AAW01817;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7C10 light chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca Cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US10053.
XX
PR   07-JUN-1995;  95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
```

DR   N-PSDB; AAT62509.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 6; Fig 8A; 81pp; English.
XX
CC   2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy
CC   variable genes (see also AAT62509 and AAT62510) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01819-22). The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   234 AA;

Query Match   100.0%; Score 1243; DB 18; Length 234;
Best Local Similarity   100.0%; Pred. No. 1e-70;
Matches   234; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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Qy   121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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Db   121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

Qy   181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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RESULT 2
AAW63760
ID   AAW63760 standard; Protein; 234 AA.
XX
AC   AAW63760;
XX
DT   29-SEP-1998 (first entry)
XX
DE   Macaque primatized 7C10 light chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.

DR   N-PSDB; AAV35484.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 3a; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7C10 light
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence   234 AA;

Query Match   100.0%; Score 1243; DB 19; Length 234;
Best Local Similarity   100.0%; Pred. No. 1e-70;
Matches   234; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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Qy   121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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Db   121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

Qy   181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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Db   181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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RESULT 3
AAU11538
ID   AAU11538 standard; Protein; 234 AA.
XX
AC   AAU11538;
XX
DT   12-MAR-2002 (first entry)
XX
DE   Protein sequence of primatised form of the light chain of 7C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
PN   WO200189567-A1.

```
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   N-PSDB; AAS17242.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 3a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present protein
CC   sequence represents the light chain of 7C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence   234 AA;

Query Match             100.0%;  Score 1243;  DB 23;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1e-70;
Matches  234;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA  60

Qy    61  RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120

Qy   121  GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180

Qy   181  VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 4
AAW14924
ID   AAW14924 standard; Protein; 233 AA.
XX
AC   AAW14924;
XX
DT   18-OCT-1997  (first entry)
XX
DE   Ant-CD4 monkey-human chimeric antibody CE9.1.
```

```
XX
KW   CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW   cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW   leukaemia; lymphoma; graft-versus-host disease; asthma;
KW   transplant rejection; HIV; therapy; CE9.1.
XX
OS   Chimaeric Macaca cynomolgus;
OS   Chimaeric Homo sapiens.
XX
PN   WO9709351-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996;  96WO-US14324.
XX
PR   06-SEP-1995;  95US-0523894.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Hanna N, Newman RA, Reff ME;
XX
DR   WPI; 1997-201913/18.
DR   N-PSDB; AAT62867.
XX
PT   Chimeric antibody comprising monkey variable domains and human
PT   constant domains - affects CD4-mediated immune functions, esp.
PT   useful for treatment of autoimmune disease, e.g. rheumatoid
PT   arthritis
XX
PS   Claim 6; Page 79-80; Page 79-80; 155pp; English.
XX
CC   A polypeptide (AAW14924) comprises the lambda variable and constant
CC   domains of anti-human CD4 monkey/human chimeric antibody CE9.1.
CC   This antibody contains the antigen binding domains (see also
CC   AAW14922-23) of a cynomolgus monkey anti-CD4 monoclonal antibody, a
CC   human heavy chain constant region of gamma 1 isotype and Gmla, Gm1z
CC   allotype, and a human lambda light constant region of the Oz minus,
CC   mcg minus genotype and Ke minus allotype. The immunoglobulin genes
CC   (see also AAT62867) were cloned into mammalian expression vector
CC   TCAE 6, and chimeric antibody was produced in CHO cells. CE9.1
CC   binds to domain 1 of human, but not macaque, CD4, a region involved
CC   in the interaction with MHC Class II molecules on antigen
CC   presenting cells. It shows potent immunomodulatory activity with
CC   low immunogenicity in humans, and can be used to treat autoimmune
CC   diseases such as rheumatoid arthritis.
XX
SQ   Sequence   233 AA;

Query Match             81.7%;    Score 1015.5;  DB 18;  Length 233;
Best Local Similarity   86.0%;    Pred. No. 1.8e-56;
Matches  196;  Conservative   10;  Mismatches   21;  Indels   1;  Gaps   1;

Qy     7  LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV  66
          ||||| :|||||||||||||||||||||||||||||||||||||||||:|::| |||||
Db     7  LLGLLAHFTDSA-ASYELSQPRSVSVSPGQTAGFTCGGDNVGRKSVQWYQQKPPQAPVLV  65

Qy    67  IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
          |||||||||||||||||||||||||||||::||||||||||| ||||||| :|||||||:
Db    66  IYADSERPSGIPARFSGSNSGNTATLTISGVEAGDEADYYCQVWDSTADHWVFGGGTRLT 125

Qy   127  VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   126  VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 185

Qy   187  SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   186  SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 5
ABG19295
ID   ABG19295 standard; Protein; 247 AA.
XX
```

```
Qy   183  TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   196  TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  247
```

```
RESULT 6
ABG19299
ID   ABG19299 standard; Protein; 238 AA.
XX
AC   ABG19299;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #19290.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS83486.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 49658; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   238 AA;

Query Match      78.8%;  Score 979;  DB 22;  Length 238;
Best Local Similarity   80.3%;  Pred. No. 3.7e-54;
Matches  187;  Conservative  13;  Mismatches  21;  Indels  12;  Gaps   2;

Qy    12  LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR  61
```

```
AC   ABG19295;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #19286.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS83482.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 49654; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   247 AA;

Query Match      79.8%;  Score 991.5;  DB 22;  Length 247;
Best Local Similarity   81.9%;  Pred. No. 6.3e-55;
Matches  190;  Conservative  14;  Mismatches  17;  Indels  11;  Gaps   2;

Qy     8  LGLLLWLPGARC----AYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARA  62
          |::||::| :|           :::|||||||||||||||||||||||||||||:|
Db    22  LGLL------SHCTASVTSFVLAQPPSVSVAPGETARITCGADNIGRRSVHWYQQRPGGA  75

Qy    63  PILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGG 122
          |::|||:||||||:||   | :::| :::|||||||||||||||||:: : :||||||||
Db    76  PVLVIYDSDRPSEIPQRFSGSNSGDTATLTISGVEAGDEADYYCQVWDDDNSHVVFGGG 135

Qy   123  TRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
          ::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   136  TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 195
```

```
Db    8 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCSGDTLGDKYACWYQQKPGH 67

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121

Db   68 SPVLVIFQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWD--SSTAVFGG 125

Qy  122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181

Db  126 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 185

Qy  182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

Db  186 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 238


RESULT 7
AAU14412
ID   AAU14412 standard; Protein; 232 AA.
XX
AC   AAU14412;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human novel protein #283.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02623.
XX
PR   25-JAN-2000; 2000US-0491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22717.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Example 4; Page 805-806; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human
CC   proteins or their active domains. The polypeptides, polynucleotides and
CC   antibodies raised against the polypeptides are used in a method of
CC   treatment of a mammal and prevention of disorders caused by the aberrant
CC   protein expression or activity. The polypeptides can be used as
CC   molecular weight markers, food supplements, and in antibody production.
CC   The polypeptides are used to identify compounds which bind to the
CC   polypeptides. Polynucleotides of the invention are used as probes and
CC   primers, for sequencing, for chromosome or gene mapping, in the
CC   production of recombinant proteins, and in generating anti-sense DNA or
CC   RNA and in gene therapy. Polypeptides of the invention can be used to
CC   target drugs to a tumour, in assays to determine biological activity, to
CC   raise antibodies/elicit an immune response, to determine quantitative
CC   protein levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
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CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   graft-versus-host disease, eczema, haemophilia, thrombosis,
CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence represents a protein of the invention.
XX
SQ   Sequence   232 AA;

Query Match             78.6%;  Score 976.5;  DB 22;  Length 232;
Best Local Similarity   80.3%;  Pred. No. 5.1e-54;
Matches 187;  Conservative  14;  Mismatches  21;  Indels  11;  Gaps   2;

Qy   12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSNEYVHWYQQKPAR 61
        :  :|:|          |: :||||||||||||||||||| |||  :|: |||||| :
Db    1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCSGDNLGNKYVAWYQQKAGQ 60

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
        :|:|||: |||||||||||||||||:||||||||||:|:: ||||||||||
Db   61 SPVLVIYQDDKRPSEIPERFSGSNGNTATLTISGTQAMDEADYYCQAWD -SSTAVMFGG 119

Qy  122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
        |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  120 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 179

Qy  182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  180 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 232


RESULT 8
AAW63764
ID   AAW63764 standard; Protein; 236 AA.
XX
AC   AAW63764;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 16C10 light chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO981970-6-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;  97WO-US19906.
XX
PR   08-NOV-1996;  96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35488.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28  useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 5a; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 16C10 light
```

```
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   MAb's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence   236 AA;

Query Match             78.3%;  Score 973;  DB 19;  Length 236;
Best Local Similarity   80.1%;  Pred. No. 8.6e-54;
  Matches  189;  Conservative  13;  Mismatches  32;  Indels   2;  Gaps   1;

Qy          1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58
              |||||||||||||||||||||  |||||||||||||||||| :  ||  :  |||||
Db          1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60

Qy         59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
              | | ||:||||  ||||| |||||||||| ::|  :| |  | :|||||||||:  : :
Db         61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy        119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy        179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 9
AAU11645
ID   AAU11645 standard; Protein; 236 AA.
XX
AC   AAU11645;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Protein sequence of primatised form of the light chain of 16C10 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   N-PSDB; AAS17246.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy
XX
PS   Example 8; Fig 5a; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present protein
CC   sequence represents the light chain of 16C10, a primatised antibody
CC   used in the invention to induce apoptosis and inhibit production of
CC   interleukin-2 (IL-2).
XX
SQ   Sequence   236 AA;

Query Match             78.3%;  Score 973;  DB 23;  Length 236;
Best Local Similarity   80.1%;  Pred. No. 8.6e-54;
  Matches  189;  Conservative  13;  Mismatches  32;  Indels   2;  Gaps   1;

Qy          1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58
              |||||||||||||||||||||  |||||||||||||||||| :  ||  :  |||||
Db          1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60

Qy         59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
              | | ||:||||  ||||| |||||||||| ::|  :| |  | :|||||||||:  : :
Db         61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy        119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180

Qy        179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 10
ABP41361
ID   ABP41361 standard; Protein; 269 AA.
XX
AC   ABP41361;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Human ovarian antigen HCNSF57, SEQ ID NO:2493.
XX
KW   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW   ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW   infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW   PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW   inflammatory condition; immune disorder; blood disorder;
KW   cardiovascular disorder; respiratory disorder; neurological disorder;
KW   gastrointestinal disorder; urinary system disorder; drug screening;
KW   gene therapy; chromosome mapping; forensic analysis;
KW   antibody preparation; cytostatic; immunomodulatory; neuroprotective;
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KW   antiinflammatory; gynaecological; reproductive.
XX
OS   Homo sapiens.
XX
PN   WO20020677-A1.
XX
PD   03-JAN-2002.
XX
PF   07-JUN-2001; 2001WO-US18569.
XX
PR   07-JUN-2000; 2000US-209467P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CE, Rosen CA;
XX
DR   WPI; 2002-147878/19.
DR   N-PSDB; ABQ54438.
XX
PT   Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT   useful in the prevention, treatment and diagnosis of cancer (e.g.
PT   ovarian cancer), immune disorders, cardiovascular disorders and
PT   neurological diseases -
XX
PS   Claim 11; SEQ ID No 2493; 2922pp; English.
XX
CC   The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC   ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC   encompasses polypeptides 90% identical and polynucleotides 95% identical
CC   to the sequences of the invention. The invention additionally relates to
CC   recombinant vectors and host cells comprising human ovarian antigen
CC   polynucleotides, antibodies against human ovarian antigens, and the use
CC   of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC   treating, prognosing or preventing various ovary and/or breast-related
CC   disorders. Such conditions include ovarian cancer and breast cancer, and
CC   metastatic tumours of ovarian or breast origin, reproductive system
CC   disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC   polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC   disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC   shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC   vaginitis), immune disorders (e.g., congenital and acquired
CC   immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC   blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC   respiratory disorders, neurological disorders, gastrointestinal disorders
CC   and urinary system disorders. Ovarian antigen polypeptides and
CC   polynucleotides may also be used in screening for compounds which
CC   modulate ovarian antigen expression or activity. The polynucleotides may
CC   further be used for gene therapy, chromosome mapping, in the
CC   identification of individuals and in forensic analysis, and the
CC   polypeptides may be used as food additives or to prepare antibodies
CC   useful in disease diagnosis, drug targeting and phenotyping. The present
CC   sequence represents a human ovarian antigen of the invention.
CC   Note:The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   269 AA;

Query Match             78.3%;  Score 973;  DB 23;  Length 269;
Best Local Similarity   79.8%;  Pred. No. 9.8e-54;
Matches  186;  Conservative  14;  Mismatches  21;  Indels  12;  Gaps  2;

Qy   12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
            :  |          ||||||||||||||||||||||| ||||  ||||| |||||||
Db   39 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQ 98

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
          :  ||||||||||||||||||||| ||||||||||||||||||||:||| | |||||
Db   99 SPVLVIYQDNXRPSGIPERFSGSNSGNTATLIISGTQAMDEADYYCQAWD--SXTXVFGG 156

Qy  122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  157 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 216
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Qy  182 ETTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
           ||||||||||||||||||| ||||||  ||||||||||||||||||||||
Db  217 ETTPSKQSNNKYAASSYLSLTPEQWKSHXSYSCQVTHEGSTVEKTVAPTECS 269

RESULT 11
AAW01821
ID   AAW01821 standard; Protein; 236 AA.
XX
AC   AAW01821;
XX
DT   25-MAY-1997  (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 16C10 light chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO964878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US10053.
XX
PR   07-JUN-1995;   95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Brams P,  Hanna N,  Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT62512.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 14; Fig 10A; 81pp; English.
XX
CC   2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 16C10.  Cloned 16C10 light and
CC   heavy variable genes (see also AAT62512 and AAT62513) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells.  Primatised 7C10 and 7B6 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-20).  The
CC   primatised antibodies inhibit the B7:CD28 pathway, making them
CC   useful immunosuppressants for the treatment of autoimmune disorders
CC   and graft-versus-host disease.
XX
SQ   Sequence   236 AA;

Query Match             78.0%;  Score 970;  DB 18;  Length 236;
Best Local Similarity   79.7%;  Pred. No. 1.3e-53;
Matches  188;  Conservative  14;  Mismatches  32;  Indels  2;  Gaps  1;

Qy    1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58
          |||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db    1 MRVPAQLGLGLLLLWLPGARCESVLTQPPSVSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60

Qy   59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
          |  |: ||||||||||||||||||||| |||||||||||||||||||||| : :  |||
Db   61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120

Qy  119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
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Db   121 FGGGTRLTVLGQPKAAPSVTLFPPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 12
AAU14176
ID   AAU14176 standard; Protein; 231 AA.
XX
AC   AAU14176;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human novel protein #47.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02623.
XX
PR   25-JAN-2000; 2000US-0491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22481.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Example 4; Page 553; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human
CC   proteins or their active domains. The polypeptides, polynucleotides and
CC   antibodies raised against the polypeptides are used in a method of
CC   treatment of a mammal and prevention of disorders caused by the aberrant
CC   protein expression or activity. The polypeptides can be used as
CC   molecular weight markers, food supplements, and in antibody production.
CC   The polypeptides are used to identify compounds which bind to the
CC   polypeptides. Polynucleotides of the invention are used as probes and
CC   primers, for sequencing, for chromosome or gene mapping, in the
CC   production of recombinant proteins, and in generating anti-sense DNA or
CC   RNA and in gene therapy. Polypeptides of the invention can be used to
CC   target drugs to a tumour, in assays to determine biological activity, to
CC   raise antibodies/elicit an immune response, to determine quantitative
CC   protein levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   graft-versus-host disease, eczema, haemophilia, thrombosis,
CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence represents a protein of the invention.
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XX
SQ   Sequence  231 AA;

Query Match            77.2%;    Score 959;  DB 22;  Length 231;
Best Local Similarity  79.0%;    Pred. No. 6.4e-53;
Matches  184; Conservative  14; Mismatches  23; Indels  12; Gaps  2;

Qy    12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
             :|:|         :||:||||||||||||||||||||:||||||||:||||||
Db     1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYASWYQQKAGQ 60

Qy    62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVMDRASDHPVFGG 121
             :|||||||||||||||||||||||||||||||||||| |||||| :|||  ||||||
Db    61 SPVLVIYRHSKRPSGIPERFSGSNSGNTATLTISGTQVMDEADYYCQAWD--SSIVVFGG 118

Qy   122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy   182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 13
ABG23084
ID   ABG23084 standard; Protein; 234 AA.
XX
AC   ABG23084;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #23075.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C,   Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS87271.
XX
PT   New isolated polynucleotide and encoded polypeptide, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 53443; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
```

CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence   234 AA;

Query Match   77.2%;   Score 959; DB 22; Length 234;
Best Local Similarity   78.5%;   Pred. No. 6.5e-53;
Matches 183; Conservative 17; Mismatches 21; Indels 12; Gaps 2;

Qy   12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
                 :|:| ||||||||||||||||||||:|||||| ::| ||||||
Db   4 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCFGDKLGDKYSSWYQQKPGQ 63

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
              :|:||::||:|||||||||||||||| ||||||| :| ||| |:|| |||
Db   64 SPLLVLYQDTNRPSGIPERFSGSNSGNTATLTISETQAMDEGDYYCQAWD--SNTVVFGG 121

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                 ||||||||||||||||||||||||||||||| :| |||||||||||||||||||
Db 122 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181

Qy 182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 14
AAU14236
ID   AAU14236 standard; Protein; 232 AA.
XX
AC   AAU14236;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human novel protein #107.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02623.
XX
PR   25-JAN-2000; 2000US-0491404.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22541.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Example 4; Page 582; 894pp; English.

XX
CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicit an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.
XX
SQ Sequence   232 AA;

Query Match   77.1%;   Score 958.5; DB 22; Length 232;
Best Local Similarity   78.5%;   Pred. No. 6.9e-53;
Matches 183; Conservative 16; Mismatches 23; Indels 23; Gaps 2;

Qy   12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
                 :|:| ||||||||||||||||||||:|||||| ::| ||||||
Db   1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQ 60

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
              :|:||::||:|||||||||||||||| ||||||| :| ||| :::|| |||
Db   61 SPVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTLY-VFGT 119

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                 ||::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 120 GTKVTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGV 179

Qy 182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
              ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db 180 ETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 232

RESULT 15
AAU08381
ID   AAU08381 standard; Peptide; 218 AA.
XX
AC   AAU08381;
XX
DT   17-DEC-2001 (first entry)
XX
DE   Anti-OPGbp antibody light chain, S.
XX
KW   Antibody; OPGbp; human; S light chain; osteopathic;
KW   osteoprotegrin binding protein; osteoclast formation; bone resorption;
KW   loss of bone mass; bone tumour; osteoporosis; bone cancer;
KW   rheumatoid arthritis; hypercalcaemia of malignancy; mutein; mutant;
KW   steroid-induced osteoporosis; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Region   5..26
FT   /label= FR1
FT   /note= "Framework region"

```
Query Match              75.9%;  Score 944;  DB 22;  Length 218;
Best Local Similarity    84.4%;  Pred. No. 5.2e-52;
Matches  178;  Conservative  14;  Mismatches  19;  Indels  0;  Gaps  0;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERFSG 83
        ||||||||||||||||||   :||:||||| :||:|||:||:|||:||||||||||||||
Db    8 LTQPPSVSVSPGQTATITCSGDALPKQYVWYRQKPGQAPLLVIYEDSERPSGIPERFSG 67

Qy   84 SKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFPPS 143
        |:|||:|||||| |||:|| : : |:||||||||| ||||||::|||||||||||||||
Db   68 SSSGTEVTLSISGVQAEDEADYCQSTDSSGTYVVFGGGTKLTVLSQPKAAPSVTLFPPS 127

Qy  144 SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLT 203
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Db  188 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 218

Search completed: March 29, 2003, 09:10:14
Job time : 26.0673 secs
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FT                     Gln-Ser-Val"
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FT                     /note= "Wild-type Met substituted by Thr"
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FT                     /note= "Complementarity determining region"
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FT                     /note= "Wild-type Ala substituted by Val"
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PR   23-FEB-2000; 2000US-0511139.
PR   22-FEB-2001; 2001US-0791153.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Deshpande RV, Hitz A, Boyle WJ, Sullivan JK;
XX
DR   WPI; 2001-557706/62.
DR   N-PSDB; AAS13364.
XX
PT   Antibodies that bind antagonistically to osteoprotegrin binding
PT   protein, useful for treating osteoporosis, metastasis of cancer to
PT   bone, rheumatoid arthritis, hypercalcaemia of malignancy and
PT   steroid-induced osteoporosis -
XX
PS   Claim 10; Fig 8; 239pp; English.
XX
CC   The invention relates to an antibody or antigen binding domain (or
CC   fragment, variant or derivative), which binds to an osteoprotegrin
CC   binding protein (OPGbp) and which is an antagonistic antibody.
CC   The antibody or antigen binding domain may be administered to inhibit
CC   osteoclast formation or activation, inhibit bone resorption in a mammal,
CC   prevent or treat loss of bone mass in a mammal and to prevent or treat
CC   tumour cell growth in bone. The loss of bone mass results from
CC   osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC   hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC   present sequence is a full length, cloned anti-OPGbp antibody light
CC   chain, S.
XX
SQ   Sequence  218 AA;
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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 8.97055 Seconds
(without alignments)
1531.829 Million cell updates/sec

Title: US-09-758-173-2
Perfect score: 1243
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	1243	100.0	234	9	US-09-948-429B-2	Sequence 2, Appli
3	973	78.3	236	9	US-10-124-905-10	Sequence 10, Appli
4	973	78.3	236	9	US-09-948-429B-10	Sequence 10, Appl
5	936.5	75.3	244	10	US-09-925-301-1424	Sequence 1424, Ap
6	880	70.8	235	10	US-09-747-669-6	Sequence 6, Appli
7	873.5	70.3	221	9	US-10-001-857-202	Sequence 202, App
8	865.5	69.6	219	10	US-09-974-449-38	Sequence 38, Appl
9	812	65.3	235	9	US-09-852-797-70	Sequence 70, Appl
10	812	65.3	235	10	US-09-853-161-70	Sequence 70, Appl
11	812	65.3	235	10	US-09-852-659A-70	Sequence 70, Appl
12	809	65.1	235	9	US-09-853-161-88	Sequence 88, Appl
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39	606	48.8	123	9	US-09-796-692-1095	Sequence 1095, Ap
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44	600	48.3	125	9	US-09-796-692-737	Sequence 737, App
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ALIGNMENTS

RESULT 1
US-10-124-905-2
; Sequence 2, Application US/10124905
; Patent No. US2002016613A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids

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;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-10-124-905-2

Query Match            100.0%;    Score 1243;  DB 9;  Length 234;
Best Local Similarity  100.0%;    Pred. No. 3.8e-56;
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RESULT 2
US-09-948-429B-2
; Sequence 2, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/948,429B
;    FILING DATE:
;    CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 09/383,916
;    FILING DATE:
;    APPLICATION NUMBER: US 08/487,550
;    FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
;   INFORMATION FOR SEQ ID NO: 2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 234 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-09-948-429B-2
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Query Match            100.0%;    Score 1243;  DB 9;  Length 234;
Best Local Similarity  100.0%;    Pred. No. 3.8e-56;
Matches  234;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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RESULT 3
US-10-124-905-10
; Sequence 10, Application US/10124905
; Patent No. US2002016136A1
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;    STREET: 699 Prince Street
;    CITY: Alexandria
;    STATE: VA
;    COUNTRY: USA
;    ZIP: 22314
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/10/124,905
;    FILING DATE:
;    CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 09/383,916
;    FILING DATE:
;    APPLICATION NUMBER: US 08/487,550
;    FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;    NAME: Teskin, Robin L.
;    REGISTRATION NUMBER: 35,030
;    REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 703-836-6620
;    TELEFAX: 703-836-2021
;   INFORMATION FOR SEQ ID NO: 10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 236 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-10-124-905-10


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RESULT 4
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; Sequence 10, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/948,429B
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 236 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-948-429B-10

Query Match   78.3%;   Score 973;   DB 9;   Length 236;
Best Local Similarity   80.1%;   Pred. No. 1.3e-42;
Matches 189;   Conservative 13;   Mismatches 32;   Indels 2;   Gaps 1;

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Db   61 PGTAPKLLIYDINKRPSGISDRFSGGSKSGTAASLAITGLQTEDEADYYCQSYDSLNAQV 120

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Qy  119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSHPV 178
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Db  121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSPVK 180

Qy  179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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RESULT 5
US-09-925-301-1424
; Sequence 1424, Application US/09925301
; Patent No. US2002052308A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;   FILE REFERENCE: PA106
;   CURRENT APPLICATION NUMBER: US/09/925,301
;   CURRENT FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: PCT/US00/05882
;   PRIOR FILING DATE: 2000-03-08
;   PRIOR APPLICATION NUMBER: 60/124,270
;   PRIOR FILING DATE: 1999-03-12
;   NUMBER OF SEQ ID NOS: 1694
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1424
;   LENGTH: 244
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (59)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (62)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (221)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1424

Query Match   75.3%;   Score 936.5;   DB 10;   Length 244;
Best Local Similarity   75.4%;   Pred. No. 9.2e-41;
Matches 184;   Conservative 15;   Mismatches 34;   Indels 11;   Gaps 2;

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Qy    2 RVPAQLLG-LLLLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNE  50
        : ||||||| :||||||    :|||||||||||:|| ||||||||||||
Db    1 RVRRQSSGNLTMAWTPLLLPLLLTFCTVSEASYELTQPPSVSVSPGQTARITCSGDALPXK  60
Qy   51 YVHWYQQKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVW 110
        |||:|||| :|:|||| :|:||||||||||||| : ||||||||||||| :|||||:
Db   61 YXTWYQQKSGQAPVLVIYEDTRRPSAIPERFSASSSGTMATLTISGAQVEDEADYYCYST 120
Qy  111 DRASDHPVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW 170
        |||  ||||||:|||||||||||||||||||||||||||||||||||||||||||
Db  121 DSSSYRVFGGGTKLITVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAW 180
Qy  171 KADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP 230
        ||||||||:||||||||||||||:||||||:|||||||||||||||||:|||||||||
Db  181 KADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHXSYSCQVTHEGSTVEKTVAP 240
Qy  231 TECS 234
        ||||
Db  241 TECS 244
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RESULT 6
US-09-747-669-6
; Sequence 6, Application US/09747669
; Patent No. US2002122807A1
; GENERAL INFORMATION:

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 ;   APPLICANT: Dan, Michael D.
 ;   APPLICANT: Saleh, Mansoor
 ;   TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
 ;   TITLE OF INVENTION:   4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
 ;   TITLE OF INVENTION:   ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
 ;   TITLE OF INVENTION:   AND DETECTION OF CANCERS
 ;   FILE REFERENCE: 31608200l001
 ;   CURRENT APPLICATION NUMBER: US/09/747,669
 ;   CURRENT FILING DATE:  2002-04-08
 ;   PRIOR APPLICATION NUMBER: US 09/111,286
 ;   PRIOR FILING DATE: 1998-07-07
 ;   NUMBER OF SEQ ID NOS: 7
 ;   SOFTWARE: FastSEQ for Windows Version 4.0
US-09-747-669-6
 ;   SEQ ID NO 6
 ;   LENGTH: 235
 ;   TYPE: PRT
 ;   ORGANISM: Artificial Sequence
 ;   FEATURE:
 ;   OTHER INFORMATION: Synthetic construct
US-09-747-669-6

Query Match             70.8%;      Score 880; DB 10;    Length 235;
Best Local Similarity   73.9%;      Pred. No. 6.1e-38;
Matches 170; Conservative  21; Mismatches  37; Indels   2; Gaps   1;

Qy        7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPI 64
            || ||||         ||||||| ||||:|  :||||||   :: ||||||||||||||
Db        6 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSNSNIGSKTVNWYQQLPGTAPK 65

Qy       65 LVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTR 124
            |||||||||||||     ||||||||||||| |:|:|:||||||| || |:|     ||
Db       66 FLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTK 125

Qy      125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
            :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      126 LTVLGQPKAAPSVTLFPPSSEELQANKPTLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

Qy      185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 7
US-10-001-857-202
 ;   Sequence 202, Application US/10001857
 ;   Publication No. US20020183500A1
 ;   GENERAL INFORMATION:
 ;   APPLICANT: Macina, Roberto
 ;   APPLICANT: Recipon, Herve
 ;   APPLICANT: Chen, Sei-Yu
 ;   APPLICANT: Sun, Yongming
 ;   APPLICANT: Liu, Chenghua
 ;   TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
 ;   FILE REFERENCE: DEX-0273
 ;   CURRENT APPLICATION NUMBER: US/10/001,857
 ;   CURRENT FILING DATE:  2001-11-20
 ;   PRIOR APPLICATION NUMBER: 60/252,054
 ;   PRIOR FILING DATE: 2000-11-20
 ;   NUMBER OF SEQ ID NOS: 208
 ;   SOFTWARE: PatentIn version 3.1
 ;   SEQ ID NO 202
 ;   LENGTH: 221
 ;   TYPE: PRT
 ;   ORGANISM: Homo sapien
US-10-001-857-202

Query Match             70.3%;      Score 873.5; DB 9;   Length 221;
Best Local Similarity   76.9%;      Pred. No. 1.2e-37;
Matches 170; Conservative  16; Mismatches  18; Indels  17; Gaps   3;

Qy       24 LTQPPSVSVSPGQTARITCGGDNSR---NEYVHWYQQKPARAPILVIYDDSDRPSGIPE 79
            |||||||  :    ||||||||||   :  ||||||||||| |:|  || ||:|||||
Db        8 LTQPPSVSGAPGQRVTISCTGSSSNIGAGYDYVHWYQQLPGTAPKLMIYEVAKRPSGVSD 67
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   ;   PRIOR APPLICATION NUMBER: PCT/US98/04858
   ;   PRIOR FILING DATE: 1998-03-12
   ;   PRIOR APPLICATION NUMBER: 60/040,762
   ;   PRIOR FILING DATE: 1997-03-14
   ;   PRIOR APPLICATION NUMBER: 60/040,710
   ;   PRIOR FILING DATE: 1997-03-14
   ;   PRIOR APPLICATION NUMBER: 60/050,934
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,100
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,357
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,189
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/057,765
   ;   PRIOR FILING DATE: 1997-09-05
   ;   PRIOR APPLICATION NUMBER: 60/048,970
   ;   PRIOR FILING DATE: 1997-06-06
   ;   PRIOR APPLICATION NUMBER: 60/068,368
   ;   PRIOR FILING DATE: 1997-12-19
   ;   NUMBER OF SEQ ID NOS: 118
   ;   SOFTWARE: PatentIn Ver. 2.0
   ;
   ;   SEQ ID NO 70
   ;     LENGTH: 235
   ;     TYPE: PRT
   ;     ORGANISM: Homo sapiens
   US-09-852-797-70

   Query Match             65.3%;  Score 812;  DB 9;  Length 235;
   Best Local Similarity   74.6%;  Pred. No. 1.6e-34;
   Matches 159;  Conservative 19;  Mismatches 33;  Indels 2;  Gaps 1;

   Qy    24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
             ||||||    |||||||||  :|:.        :: ||| |||
   Db    23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHGPPKLLSYRNNNRPSGISERL 82

   Qy    82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
             |||:  ||||   |:.::   |:||||   :          :|:|||||||||||||||
   Db    83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

   Qy   142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db   143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

   Qy   202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
             ||||||||||||||||||||||||||||||||
   Db   203 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235


   RESULT 10
   US-09-853-161-70
   ;  Sequence 70, Application US/09853161
   ;  Patent No. US20020076756A1
   ;  GENERAL INFORMATION:
   ;     APPLICANT: Rosen et al.
   ;     TITLE OF INVENTION: 28 Human Secreted Proteins
   ;     FILE REFERENCE: PZ003P3
   ;     CURRENT APPLICATION NUMBER: US/09/853,161
   ;     CURRENT FILING DATE: 2001-05-11
   ;   PRIOR APPLICATION NUMBER: 60/265,583
   ;   PRIOR FILING DATE: 2001-02-02
   ;   PRIOR APPLICATION NUMBER: 09/152,060
   ;   PRIOR FILING DATE: 1998-09-11
   ;   PRIOR APPLICATION NUMBER: PCT/US98/04858
   ;   PRIOR FILING DATE: 1998-03-12
   ;   PRIOR APPLICATION NUMBER: 60/040,762
   ;   PRIOR FILING DATE: 1997-03-14
   ;   PRIOR APPLICATION NUMBER: 60/040,710
   ;   PRIOR FILING DATE: 1997-03-14
   ;   PRIOR APPLICATION NUMBER: 60/050,934
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,100
   ;   PRIOR FILING DATE: 1997-05-30
```

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   ;   PRIOR APPLICATION NUMBER: 60/048,357
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,189
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/057,765
   ;   PRIOR FILING DATE: 1997-09-05
   ;   PRIOR APPLICATION NUMBER: 60/048,970
   ;   PRIOR FILING DATE: 1997-06-06
   ;   PRIOR APPLICATION NUMBER: 60/068,368
   ;   PRIOR FILING DATE: 1997-12-19
   ;   NUMBER OF SEQ ID NOS: 118
   ;   SOFTWARE: PatentIn Ver. 2.0
   ;
   ;   SEQ ID NO 70
   ;     LENGTH: 235
   ;     TYPE: PRT
   ;     ORGANISM: Homo sapiens
   US-09-853-161-70

   Query Match             65.3%;  Score 812;  DB 10;  Length 235;
   Best Local Similarity   74.6%;  Pred. No. 1.6e-34;
   Matches 159;  Conservative 19;  Mismatches 33;  Indels 2;  Gaps 1;

   Qy    24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
             ||||||    |||||||||  :|:.        :: ||| |||
   Db    23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHGPPKLLSYRNNNRPSGISERL 82

   Qy    82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
             |||:  ||||   |:.::   |:||||   :          :|:|||||||||||||||
   Db    83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

   Qy   142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   Db   143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

   Qy   202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
             ||||||||||||||||||||||||||||||||
   Db   203 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235


   RESULT 11
   US-09-852-659A-70
   ;  Sequence 70, Application US/09852659A
   ;  Patent No. US20020077287A1
   ;  GENERAL INFORMATION:
   ;     APPLICANT: Rosen et al.
   ;     TITLE OF INVENTION: 28 Human Secreted Proteins
   ;     FILE REFERENCE: PZ003P4
   ;     CURRENT APPLICATION NUMBER: US/09/852,659A
   ;     CURRENT FILING DATE: 2001-05-11
   ;   PRIOR APPLICATION NUMBER: 60/265,583
   ;   PRIOR FILING DATE: 2001-02-02
   ;   PRIOR APPLICATION NUMBER: 09/152,060
   ;   PRIOR FILING DATE: 1998-09-11
   ;   PRIOR APPLICATION NUMBER: PCT/US98/04858
   ;   PRIOR FILING DATE: 1998-03-12
   ;   PRIOR APPLICATION NUMBER: 60/040,762
   ;   PRIOR FILING DATE: 1997-03-14
   ;   PRIOR APPLICATION NUMBER: 60/040,710
   ;   PRIOR FILING DATE: 1997-03-14
   ;   PRIOR APPLICATION NUMBER: 60/050,934
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,100
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,357
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/048,189
   ;   PRIOR FILING DATE: 1997-05-30
   ;   PRIOR APPLICATION NUMBER: 60/057,765
   ;   PRIOR FILING DATE: 1997-09-05
   ;   PRIOR APPLICATION NUMBER: 60/048,970
   ;   PRIOR FILING DATE: 1997-06-06
   ;   PRIOR APPLICATION NUMBER: 60/068,368
   ;   PRIOR FILING DATE: 1997-12-19
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; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 70
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-70

Query Match   65.3%;   Score 812; DB 10; Length 235;
Best Local Similarity 74.6%;   Pred. No. 1.6e-34;
Matches 159; Conservative 19; Mismatches 33; Indels 2; Gaps 1;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
             |||||| |||:| :: :: || : ::||||||||
Db   23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHGHPPKLLSYRNNNRPSGISERL 82

Qy   82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
             |:|::|||:|| |||::: |||||||||:   :||||||:||||||||||||
Db   83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

Qy 142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

Qy 202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
             |||||||||||||||||||||||||||||||
Db 203 LTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 12
US-09-852-797-88
; Sequence 88, Application US/09852797
; Patent No. US2002017294A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERNCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-88

Query Match   65.1%;   Score 809; DB 9; Length 235;
Best Local Similarity 74.2%;   Pred. No. 2.2e-34;

Matches 158; Conservative 20; Mismatches 33; Indels 2; Gaps 1;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
             |||||| |||:| :: :: || : ::||||||||
Db   23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHGHPPKLLSYRNNNRPSGISERL 82

Qy   82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
             |:|::|||:|| |||::: |||||||||:   :||||||:||||||||||||
Db   83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

Qy 142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

Qy 202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
             |||||||||||||||||||||||||||||||
Db 203 LTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 13
US-09-853-161-88
; Sequence 88, Application US/09853161
; Patent No. US2002076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 88
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-88

Query Match   65.1%;   Score 809; DB 10; Length 235;
Best Local Similarity 74.2%;   Pred. No. 2.2e-34;
Matches 158; Conservative 20; Mismatches 33; Indels 2; Gaps 1;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
             |||||| |||:| :: :: || : ::||||||||
Db   23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHGHPPKLLSYRNNNRPSGISERL 82

Qy   82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
             |:|::|||:|| |||::: |||||||||:   :||||||:||||||||||||
Db   83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

Qy   142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

Qy   202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||
Db   203 LTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 14
US-09-852-659A-88
; Sequence 88, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen et al.
;   TITLE OF INVENTION: 28 Human Secreted Proteins
;   FILE REFERENCE: PZ003P4
;   CURRENT APPLICATION NUMBER: US/09/852,659A
;   CURRENT FILING DATE: 2001-05-11
;   PRIOR APPLICATION NUMBER: 60/265,583
;   PRIOR FILING DATE: 2001-02-02
;   PRIOR APPLICATION NUMBER: 09/152,060
;   PRIOR FILING DATE: 1998-09-11
;   PRIOR APPLICATION NUMBER: PCT/US98/04858
;   PRIOR FILING DATE: 1998-03-12
;   PRIOR APPLICATION NUMBER: 60/040,762
;   PRIOR FILING DATE: 1997-03-14
;   PRIOR APPLICATION NUMBER: 60/040,710
;   PRIOR FILING DATE: 1997-03-14
;   PRIOR APPLICATION NUMBER: 60/050,934
;   PRIOR FILING DATE: 1997-05-30
;   PRIOR APPLICATION NUMBER: 60/048,100
;   PRIOR FILING DATE: 1997-05-30
;   PRIOR APPLICATION NUMBER: 60/048,357
;   PRIOR FILING DATE: 1997-05-30
;   PRIOR APPLICATION NUMBER: 60/048,189
;   PRIOR FILING DATE: 1997-05-30
;   PRIOR APPLICATION NUMBER: 60/057,765
;   PRIOR FILING DATE: 1997-09-05
;   PRIOR APPLICATION NUMBER: 60/048,970
;   PRIOR FILING DATE: 1997-06-06
;   PRIOR APPLICATION NUMBER: 60/068,368
;   PRIOR FILING DATE: 1997-12-19
;   NUMBER OF SEQ ID NOS: 121
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-852-659A-88

Query Match   65.1%; Score 809; DB 10; Length 235;
Best Local Similarity   74.2%; Pred. No. 2.2e-34;
Matches 158; Conservative   20; Mismatches 33; Indels   2; Gaps   1;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
          |||||||||||||||||| ::||||||::||||||||
Db   23 LTQPPSVSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPPKLLSYRNNNRPSGISERL 82

Qy   82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
          |||| : |||||:||||||||||| : |||| :||||||||||||||||
Db   83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGTKLTVLGQPKAAPSVTLFP 142

Qy   142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202

Qy   202 LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||
Db   203 LTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 15
US-09-736-371B-19
; Sequence 19, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
;   APPLICANT: Waldmann, Herman
;   APPLICANT: Frewin, Mark
;   TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
;   FILE REFERENCE: Waldmann
;   CURRENT APPLICATION NUMBER: US/09/736,371B
;   CURRENT FILING DATE: 2002-04-25
;   PRIOR APPLICATION NUMBER: 9815909.8 °
;   PRIOR FILING DATE: 1998-07-21
;   PRIOR APPLICATION NUMBER: PCT/GB99/02380
;   PRIOR FILING DATE: 1999-07-21
;   NUMBER OF SEQ ID NOS: 30
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Rattus
US-09-736-371B-19

Query Match   64.7%; Score 804; DB 10; Length 216;
Best Local Similarity   74.0%; Pred. No. 3.7e-34;
Matches 159; Conservative   15; Mismatches 35; Indels   6; Gaps   3;

Qy   24 LTQPPSVSVSPGQTARITC--GGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
          :|||||||||||||||||| : ||||| :||||:::||||
Db   4 VTQANSVSTSLGSTVKLSCTLSSGNIENNYVHWYQLYEGRSPTTMIYDDDKRPDGVPDRF 63

Qy   82 SGS--KSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTL 139
          ||| :||||||||::|||| : |:: : |||||:::|||||||:||||||||||||||
Db   64 SGSIDRSSNSAFLTIHNVAIEDEAIYFCHSY--VSSFNVFGGGTKLTVLRQPKAAPSVTL 121

Qy   140 FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSY 199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSY 181

Qy   200 LSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          ||||||||||||||||||||||||||||||||||
Db   182 LSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 216

Search completed: March 29, 2003, 09:38:36
Job time : 10.9705 secs

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                    GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:      March 29, 2003, 09:06:23 ; Search time 5.57924 Seconds
                                         (without alignments)
                                  1739.566 Million cell updates/sec

Title:          US-09-758-173-2
Perfect score:  1243
Sequence:       1 MRVPAQLGLLLLWLPGARC..........CQVTHEGSTVEKTVAPTECS 234

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:      112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_40:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result        Query
 No.   Score  Match Length DB  ID             Description
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  1     548   44.1   105   1   LAC_HUMAN      P01842 homo sapien
  2     522   42.0   213   1   ILL1_HUMAN     P15814 homo sapien
  3     472   38.0   111   1   LV3B_HUMAN     P80748 homo sapien
  4     444   35.7   108   1   LV5A_HUMAN     P01719 homo sapien
  5     417   33.5   107   1   LV4C_HUMAN     P01717 homo sapien
  6     415   33.4   105   1   LAC_PIG        P01846 sus scrofa
  7     412   33.1   105   1   LAC1_MOUSE     P01843 mus musculu
  8     407   32.7   106   1   LV4A_HUMAN     P01715 homo sapien
  9     400   32.2   111   1   LV7A_HUMAN     P01720 homo sapien
 10     399   32.1   105   1   LAC_RABIT      P01847 oryctolagus
 11     399   32.1   106   1   LV4B_HUMAN     P01716 homo sapien
 12     397   31.9   106   1   LV4E_HUMAN     P06889 homo sapien
 13     385.5  31.0   104   1   LAC1_RAT       P20766 rattus norv
 14     380.5  30.6   104   1   LAC2_RAT       P20767 rattus norv
 15     378   30.4   106   1   LV4D_HUMAN     P01718 homo sapien
 16     377   30.3   105   1   LAC5_MUSSP     P20765 mus spretus
 17     374.5  30.1   104   1   LAC3_MOUSE     P01845 mus musculu
 18     369.5  29.7   104   1   LAC2_MOUSE     P01844 mus musculu
 19     368   29.6   130   1   LV1G_HUMAN     P06316 homo sapien
 20     360   29.0   108   1   LV3A_HUMAN     P01714 homo sapien
 21     357   28.7   111   1   LV1D_HUMAN     P01702 homo sapien
 22     347   27.9   105   1   LAC5_MOUSE     P20764 mus musculu
 23     342   27.5   111   1   LV1C_HUMAN     P01701 homo sapien
 24     331   26.6   111   1   LV6C_HUMAN     P06317 homo sapien
 25     328   26.4   109   1   LV1F_HUMAN     P06888 homo sapien
 26     327   26.3   111   1   LV2G_HUMAN     P01710 homo sapien
 27     326.5  26.3   103   1   LAC_CHICK      P20763 gallus gall
 28     326.5  26.3   112   1   LV1B_HUMAN     P01700 homo sapien
 29     325.5  26.2   112   1   LV2K_HUMAN     P04209 homo sapien
 30     325   26.1   111   1   LV1A_HUMAN     P01699 homo sapien
 31     322.5  25.9   112   1   LV6A_HUMAN     P01721 homo sapien
 32     320.5  25.8   117   1   KV1J_HUMAN     P01602 homo sapien
 33     318.5  25.6   129   1   KV1W_HUMAN     P04431 homo sapien
 34     318    25.6   111   1   LV2F_HUMAN     P01709 homo sapien
 35     314.5  25.3   131   1   LV6E_HUMAN     P06319 homo sapien
 36     313    25.2   109   1   LV1F_HUMAN     P04208 homo sapien
 37     313    25.2   111   1   LV2C_HUMAN     P01706 homo sapien
 38     310.5  25.0   112   1   LV1H_HUMAN     P06887 homo sapien
 39     310    24.9   109   1   LV2E_HUMAN     P01708 homo sapien
 40     310    24.9   111   1   LV2I_HUMAN     P01712 homo sapien
 41     303    24.4   111   1   LV2A_HUMAN     P01704 homo sapien
 42     302    24.3   111   1   LV2B_HUMAN     P01705 homo sapien
 43     298.5  24.0   129   1   KV1X_HUMAN     P04432 homo sapien
 44     298    24.0   111   1   LV2D_HUMAN     P01707 homo sapien
 45     298    24.0   113   1   LV1_CHICK      P04210 gallus gall

                           ALIGNMENTS

RESULT 1
LAC_HUMAN
ID   LAC_HUMAN      STANDARD;      PRT;      105 AA.
AC   P01842; P80423;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig lambda chain C regions.
GN   IGLC1 AND IGLC2 AND IGLC3.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (BENCE-JONES PROTEIN SH).
RX   MEDLINE=69088380; PubMed=4883841;
RA   Milstein C., Clegg J.B., Jarvis J.M.;
RT   "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT   Bence-Jones protein.";
RL   Biochem. J. 110:631-652(1968).
RN   [2]
RP   SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RX   MEDLINE=70166723; PubMed=4905564;
RA   Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT   complete amino acid sequence and the location of the disulfide
RT   bridges.";
RL   J. Biol. Chem. 245:2171-2176(1970).
RN   [3]
RP   SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RX   MEDLINE=83186114; PubMed=6404900;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. IV. Assignment of a subsubgroup.";
RL   J. Biochem. 93:421-429(1983).
RN   [4]
RP   SEQUENCE (BENCE-JONES PROTEIN KERN).
RX   MEDLINE=71150336; PubMed=5549568;
RA   Ponstingl H., Hess M., Hilschmann N.;
RT   "Structural rule of antibodies. Primary structure of a monoclonal
RT   immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones
RT   protein Kern). V. The complete amino acid sequence and its genetic
RT   interpretation."; 
RL   Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
RN   [5]
RP   PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RX   MEDLINE=74109253; PubMed=4814727;
RA   Chen B.L., Poljak R.J.;
RT   "Amino acid sequence of the (lambda) light chain of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 13:1295-1302(1974).
RN   [6]
RP   SEQUENCE (DOT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
```

RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
RX   MEDLINE=75046825; PubMed=4215080;
RA   Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
RA   Saul F.;
RT   "The three-dimensional structure of the fab' fragment of a human
RT   myeloma immunoglobulin at 2.0-A resolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
RN   [8]
RP   PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY OF MCG.
RX   MEDLINE=90133913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
RN   [11]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82080680; PubMed=6273747;
RA   Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
RT   "Clustered arrangement of immunoglobulin lambda constant region genes
RT   in man.";
RL   Nature 294:536-540(1981).
CC   -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN
CC   FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE
CC   KERN+ MARKER, AND THE MCG+ MARKER. THE NEWM PROTEIN HAS THE
CC   OZ+ MARKER, THE MCG PROTEIN
CC   HAS THE KERN+ MARKER, AND THE MCG+ MARKER.
CC   -!- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE
CC   3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE
CC   (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
CC   SEQUENCE (LAMBDA-3).
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---
DR   EMBL; J00253; AAA59107.1; -.
DR   EMBL; L38562; AAB36581.1; ALT_INIT.
DR   EMBL; X51754; CAB38569.1; ALT_INIT.
DR   EMBL; X51755; CAA36049.1; -.
DR   EMBL; X51755; CAA36051.1; -.
DR   PIR; A02125; L2HU.
DR   PDB; 2MCG; 15-JUL-92.
DR   PDB; 7FAB; 31-JAN-94.
DR   Genew; HGNC:5855; IGLC1.
DR   Genew; HGNC:5856; IGLC2.
DR   Genew; HGNC:5857; IGLC3.
DR   MIM; 147220; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_cl.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.

KW   Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT   NON_TER   1   1
FT   DISULFID   27   86
FT   DISULFID   104   104
FT   VARIANT   5   5   INTERCHAIN (WITH HEAVY CHAIN).
FT   /FTId=VAR_003898.
FT   VARIANT   7   7   A -> N (IN MCG+ MARKER).
FT   /FTId=VAR_003899.
FT   VARIANT   45   45   S -> T (IN MCG+ MARKER).
FT   /FTId=VAR_003900.
FT   VARIANT   56   56   S -> G (IN KERN+ MARKER).
FT   /FTId=VAR_003901.
FT   VARIANT   82   82   T -> K (IN MCG+ MARKER).
FT   /FTId=VAR_003902.
FT   R -> K (IN OZ+ MARKER).
FT   STRAND   4   4
FT   STRAND   7   11
FT   HELIX   15   19
FT   TURN   20   21
FT   STRAND   23   33
FT   STRAND   38   43
FT   TURN   44   45
FT   STRAND   46   48
FT   TURN   50   51
FT   STRAND   52   54
FT   STRAND   58   59
FT   TURN   61   62
FT   STRAND   65   73
FT   HELIX   75   79
FT   TURN   80   80
FT   STRAND   84   90
FT   TURN   91   92
FT   STRAND   93   99
SQ   SEQUENCE   105 AA;   11236 MW; DCD9C7C201C13CC2 CRC64;

Query Match   44.1%;
Best Local Similarity   100.0%; Score 548; DB 1; Length 105;
Matches 105; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
                                                          Pred. No. 9.6e-38;

Qy   130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 60

Qy   190 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
           |||||||||||||||||||||||||||||||||||||||||||||
Db   61 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 105

RESULT 2
ILL1_HUMAN
ID   ILL1_HUMAN   STANDARD;   PRT;   213 AA.
AC   P15814;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
DE   related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
DE   (CD179b antigen).
GN   IGLL1 OR IGL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89315835; PubMed=2501791;
RA   Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
RA   McKearn J.P.;
RT   "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
RT   expressed in pre-B cells and may encode the human immunoglobulin
RT   omega light-chain protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989).
RN   [2]
RP   SEQUENCE FROM N.A.

```
RC   TISSUE=Lymphoid;
RX   MEDLINE=91108327; PubMed=1703205;
RA   Evans R.J., Hollis G.F.;
RT   "Genomic structure of the human Ig lambda 1 gene suggests that it may
RT   be expressed as an Ig lambda 14.1-like protein or as a canonical B
RT   cell Ig lambda light chain: implications for Ig lambda gene
RT   evolution.";
RL   J. Exp. Med. 173:305-311(1991).
CC   -!- SUBUNIT: Associates non-covalently with VPREB1.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
CC       B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 1:64-67(2000);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/696419174_g.htm".
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; M27749; AAA36100.1; -.
DR   EMBL; M34513; AAA36096.1; -.
DR   EMBL; M34511; AAA36096.1; JOINED.
DR   EMBL; M34512; AAA36096.1; JOINED.
DR   PIR; A33911; A33911.
DR   HSSP; P01842; 7FAB.
DR   Genew; HGNC:5870; IGLL1.
DR   MIM; 146770; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; B-cell; Signal.
FT   SIGNAL        1     37       POTENTIAL.
FT   CHAIN        38    213       IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 1.
FT   DOMAIN       97    108       J REGION (BY SIMILARITY TO LAMBDA
FT                               LIGHT-CHAIN).
FT   DOMAIN      109    213       C REGION (BY SIMILARITY TO LAMBDA
FT                               LIGHT-CHAIN).
SQ   SEQUENCE   213 AA;  22963 MW;  9133A7742B943C79 CRC64;

Query Match             42.0%;  Score 522;  DB 1;  Length 213;
Best Local Similarity   77.1%;  Pred. No. 2.8e-35;
Matches  101;  Conservative    8;  Mismatches   16;  Indels    6;  Gaps    2;

Qy        110 WDRA--SDH---PVPGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYP 163
              |||   ||    :::||||||||||||||||||||||||||||||||||||::||||
Db         83 WPRGFGSKHNSVTHVFGSGTQLTVLSQPKATPSVTLFPPSSEELQANKATLVCLMNDFYP 142

Qy        164 GAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST 223
              ||||||||||| | ::| ||| ||:|||||||||||||||||||||:|| ||||| |||
Db        143 GILTVTWKADGTPITQGVEMTTPSKQSNNKYAASSYLSLTPEQWRSRRSYSCQVMHEGST 202

Qy        224 VEKTVAPTECS 234
              ||||||| ||
Db        203 VEKTVAPAECS 213

RESULT 3
LV3B_HUMAN
ID   LV3B_HUMAN     STANDARD;      PRT;   111 AA.
AC   P80748;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Ig lambda chain V-III region LOI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
RC   TISSUE=Urine;
RX   MEDLINE=99941384; PubMed=10510403;
RA   Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
RT   "Nephritogenic lambda light chain dimer: a unique human
RT   miniautoantibody against complement factor H.";
RL   J. Immunol. 163:4590-4596(1999).
CC   -!- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
CC       TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- DISEASE: THE BLOCKING OF FACTOR H BY LOI PROTEIN LEADS TO THE
CC       DEVELOPMENTAL OF MEMBRANOPROLIFERATIVE GLOMERULONEPHRITIS (MPGN).
DR   PDB; 2LOI; 29-DEC-99.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; 3D-structure.
FT   BINDING      15     15       SCR3.
FT   BINDING      25     25       SCR3.
FT   BINDING      29     29       SCR3.
FT   BINDING      48     51       SCR3.
FT   BINDING      94     94       SCR3.
FT   DISULFID     21     86       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11935 MW;  6949BEBFDE82053 CRC64;

Query Match             38.0%;  Score 472;  DB 1;  Length 111;
Best Local Similarity   76.6%;  Pred. No. 1.4e-31;
Matches   85;  Conservative   14;  Mismatches   12;  Indels    0;  Gaps    0;

Qy         22 YELTQPPSVSVSPGQTARITCGGDNSRNEVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
              ||||||||||| :::||||||||| |:|||||||:: ||| :|||||||||||||||
Db          1 YVLTQPPSVSVAPGETARLTCGGNDIGSESVHWYQQKPGQAPVLVIYFDRDRPSGIPERF 60

Qy         82 SGSKSGNTALTLTINGVEAGDEADYCQVWDRASDHPVFGGGTRVTVLGQPK 132
              |||.||||||| ||.|||||||||||||| ::|| ||||||||||:|||||
Db         61 SGSNSGNTATLTISRVEAGDEADYCQLWDSSSEHVFGGGTKLTVLSQPK 111

RESULT 4
LV5A_HUMAN
ID   LV5A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01719;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-V region DEL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75112179; PubMed=4452363;
RA   Eulitz M.;
RT   "A new subgroup of human L-chains of the lambda-type. Primary
RT   structure of Bence-Jones protein DEL.";
RL   Eur. J. Biochem. 50:49-69(1974).
CC   -!- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
CC       CHAIN SUBGROUP V.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01985; L5HUDL.
DR   HSSP; P80748; 2LOI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin v region; Bence-Jones protein.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11342 MW;  BE8ED9C09C9E451 CRC64;
```

Query Match   35.7%;   Score 444; DB 1; Length 108;
Best Local Similarity   73.1%;   Pred. No. 2.4e-29;
Matches   79;   Conservative   15;   Mismatches   14;   Indels   0;   Gaps   0;

Qy   22   YELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERF   81
               |:||||||||||||||||||||||||||: ||||||||||||:|:|::|:||||||||||
Db   1   YVLSQPPSVSVAPGQTARITCGGDGIGKSVHWYQQKPGQAPVLVVHEDNDRPAGIPERF   60

Qy   82   SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLG   129
               ||||||||||| ||||:|||:||||||||::||| : ||||||:||||
Db   61   SGSNSGNTAAITISRVEAGDEADYYCEVWDRTAHVVFGGGTKLTVLG   108

RESULT 5
LV4C_HUMAN
ID   LV4C_HUMAN   STANDARD;   PRT;   107 AA.
AC   P01717;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-IV region Hil.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=78187276; PubMed=418804;
RA   Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
RT   "Amino acid sequence of the variable region of the light (lambda)
RT   chain from human myeloma cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 17:1718-1723(1978).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
CC   IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
CC   155-ILE (HIL NUMBERING) INSTEAD OF VAL.
DR   PIR; A01983; L4HUHL.
DR   HSSP; P80748; 2LOI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig;1.
DR   SMART; SM00406; IGv;1.
KW   Immunoglobulin V region.
FT   NON TER   107   107
SQ   SEQUENCE   107 AA; 11517 MW; A5C8AFFE0C0C590A CRC64;

Query Match   33.5%;   Score 417; DB 1; Length 107;
Best Local Similarity   68.8%;   Pred. No. 3.5e-27;
Matches   75;   Conservative   15;   Mismatches   17;   Indels   2;   Gaps   1;

Qy   21   AYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPER   80
               :||||||||||||||||||||| :|:| |||||||||:|||||| |: ||||||||||:|
Db   1   SYELTQPPSVSVSPGQTARITCSANALPNQYAYWYQQKPGQAPVMVIYKDTQRPSGIPQR   60

Qy   81   FSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLG   129
               ||||||||||||||||||||||||||||:|||| : :||: ||||:||||
Db   61   FSSSTSGTTVTLTISGVQAEDEADYYCQAWDNSAS--IFGGGTKLTVLG   107

RESULT 6
LAC_PIG
ID   LAC_PIG   STANDARD;   PRT;   105 AA.
AC   P01846;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain C region.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=78000254; PubMed=409425;
RA   Novotny J., Franek F., Margolies M.N., Haber E.;
RT   "Amino acid sequence of normal (microheterogeneous) porcine
RT   immunoglobulin lambda chains.";
RL   Biochemistry 16:3765-3772(1977).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MIXTURE OF NORMAL
CC   IMMUNOGLOBULINS.
DR   PIR; A02129; L1PG.
DR   HSSP; P01842; 2MCG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_cl.
DR   Pfam; PF00047; ig;1.
DR   SMART; SM00407; IGcl;1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1   1
FT   DISULFID   27   86
FT   DISULFID   104   104   INTERCHAIN (WITH HEAVY CHAIN).
SQ   SEQUENCE   105 AA; 11003 MW; 3817AAEBD747C396 CRC64;

Query Match   33.4%;   Score 415; DB 1; Length 105;
Best Local Similarity   74.3%;   Pred. No. 4.9e-27;
Matches   78;   Conservative   9;   Mismatches   18;   Indels   0;   Gaps   0;

Qy 130   QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ   189
               |||||:|||||||||||||||:||||||||||||||||||||||||||||:||||||:::|
Db   1   QPKAAPTVNLFPPSSEELGTNKATLVCLISDFYPGAVTVTWKAGGTTVTQGVETTKPSKQ   60

Qy 190   SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS   234
               |||||||||||:|:||:||||:|||||:||||: :||||||:|:|:
Db   61   SNNKYAASSYLALSASDWKSSSGFTCQVTHEGTIVEKTVTPSECA   105

RESULT 7
LAC1_MOUSE
ID   LAC1_MOUSE   STANDARD;   PRT;   105 AA.
AC   P01843;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda-1 chain C region.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83014953; PubMed=6812053;
RA   Selsing E., Miller J., Wilson R., Storb U.;
RT   "Evolution of mouse immunoglobulin lambda genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
RN   [2]
RP   SEQUENCE FROM N.A. (MOPC 315).
RX   MEDLINE=81148806; PubMed=6259534;
RA   Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
RA   Gefter M.L., Baltimore D.;
RT   "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
RL   Nature 290:65-67(1981).
RN   [3]
RP   SEQUENCE FROM N.A. (S43).
RX   MEDLINE=82220143; PubMed=6283385;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Somatic variants of murine immunoglobulin lambda light chains.";
RL   Nature 298:380-382(1982).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX   MEDLINE=71107854; PubMed=5276767;
RA   Appella E.;
RT   "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
CC   -!- MISCELLANEOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1

```
CC      NORMAL LAMBDA-2 CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING
CC      A LARGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
CC      APPEARS COMPLETELY NORMAL.
CC      -----------------------------------------------------------------
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----------------------------------------------------------------
DR      EMBL; J00582; AAA51636.1; -.
DR      EMBL; J00587; AAB59672.1; -.
DR      PIR; A02126; LIMS.
DR      HSSP; P01842; 7FAB.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003597; Ig_c1.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00407; IGc1; 1.
DR      PROSITE; PS00290; IG_MHC; 1.
KW      Immunoglobulin domain; Immunoglobulin C region.
FT      NON_TER       1       1
FT      DISULFID     27      86
FT      DISULFID    104     104      INTERCHAIN (WITH HEAVY CHAIN).
FT      CONFLICT     19      20      ET -> TE (IN REF. 4).
FT      CONFLICT     56      56      Q -> E (IN REF. 4).
FT      CONFLICT     75      75      MISSING (IN REF. 4).
FT      CONFLICT     81      82      HS -> SH (IN REF. 4).
FT      CONFLICT     85      85      S -> SS (IN REF. 4).
FT      CONFLICT     96      96      E -> Q (IN REF. 4).
SQ      SEQUENCE    105 AA;  11575 MW;  A89F2B09BCFCA018 CRC64;

Query Match             33.1%;  Score 412;  DB 1;  Length 105;
Best Local Similarity   71.4%;  Pred. No. 8.6e-27;
Matches   75;  Conservative  12;  Mismatches  18;  Indels   0;  Gaps   0;

Qy   130  QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ  189
              :||::|||||||||||:| |||::| |||||: || || |  |:| |||||:||
Db     1  QPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQ   60

Qy   190  SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS  234
              |||||  ||| |:||:|| |:|:|||||||| |::::  :||
Db    61  SNNKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKSLSRADCS  105


RESULT 8
LV4A_HUMAN
ID      LV4A_HUMAN     STANDARD;      PRT;    106 AA.
AC      P01715;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig lambda chain V-IV region Bau.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=75059189; PubMed=4435717;
RA      Baczko K., Braun D., Hilschmann N.;
RT      "Pattern of antibody structure, the primary structure of monoclonal
RT      immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
RT      protein Bau).";
RL      Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).
CC      -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR      PIR; A01981; L4HUBU.
DR      HSSP; P80748; 2LOI.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.


KW      Immunoglobulin V region; Bence-Jones protein.
FT      NON_TER      106     106
SQ      SEQUENCE    106 AA;  11305 MW;  4B6A68BE0EC46571 CRC64;

Query Match             32.7%;  Score 407;  DB 1;  Length 106;
Best Local Similarity   71.3%;  Pred. No. 2.2e-26;
Matches   77;  Conservative  10;  Mismatches  19;  Indels   2;  Gaps   1;

Qy    22  YELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERF   81
              |||:||||| ||||| :|:|||||:|  || ||| ::||:| ||||||||||||||
Db     1  YGLTQPPSLSVSPGQTASITCSGDKLGEQYCVWYQQKPGQSPVLVIYHDSKRPSGIPERF   60

Qy    82  SGSKSGNTALTLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLG  129
              |||:||||||:|| :|:||||||||||:|| ||  : :||||:|:||
Db    61  SGSNSGTTATLTISGTQAMDEADYYCQAWD--SYTVIFGGGTKLTVLG  106


RESULT 9
LV7A_HUMAN
ID      LV7A_HUMAN     STANDARD;      PRT;    111 AA.
AC      P01720;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig lambda chain V-VII region MOT.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=81122740; PubMed=6780787;
RA      Kojima M., Odani S., Ikenaka T.;
RT      "Amino acid sequence of the lambda type light chain of a human IgG1
RT      myeloma protein (MOT) with unusual antigenicity; a possible new
RT      subgroup of lambda chain having a unique N-terminal sequence.";
RL      Mol. Immunol. 17:1407-1414(1980).
CC      -!- MISCELLANEOUS: THIS SEQUENCE REPRESENTS A NEW LAMBDA CHAIN
CC          SUBGROUP. IT HAS AN AMINO-TERMINAL EXTENSION OF THREE RESIDUES
CC          COMPARED WITH OTHER HUMAN LAMBDA CHAINS.
CC      -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC          MARKERS.
CC      -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR      PIR; A01986; L7HUMT.
DR      HSSP; P80748; 2LOI.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v;
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
KW      Immunoglobulin V region.
FT      NON_TER      111     111
SQ      SEQUENCE    111 AA;  11942 MW;  140A28A2F86A6911 CRC64;

Query Match             32.2%;  Score 400;  DB 1;  Length 111;
Best Local Similarity   69.4%;  Pred. No. 8.5e-26;
Matches   75;  Conservative  10;  Mismatches  23;  Indels   0;  Gaps   0;

Qy    22  YELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERF   81
              |||:|||| ||||||:| |||:|| :|  ||||||||||||:|||||||||||||
Db     4  YELTQPPSVSLAAGQTAMITCEGNDIGERSVHWYQQKPGQAPVPVIYDDADRPSGVPARF   63

Qy    82  SGSKSGNTALTLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLG  129
              |||:||||||:|| :|:||||||||||:|| ||   ::|||||:|:||
Db    64  SGYNSGNSAILTINRVEAGDEADYFCQSWDNGSYEVVFGTGMVTVLG  111


RESULT 10
LAC_RABIT
ID      LAC_RABIT      STANDARD;      PRT;    105 AA.
AC      P01847;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
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```
DE   Ig lambda chain C region.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82091105; PubMed=6797414;
RA   Garcia I., Jaton J.-C.;
RT   "The primary structure of the constant region of Basilea-rabbit
RT   immunoglobulin lambda-chains.";
RL   Biochem. J. 197:177-183(1981).
CC   -!- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC
CC       SPECIFICITY.
DR   PIR; A02130; L7RB.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_cl.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER       1      1
FT   DISULFID     27     86
FT   DISULFID    104    104       INTERCHAIN (WITH HEAVY CHAIN).
SQ   SEQUENCE   105 AA;  11484 MW;  B4275I3272E8663D CRC64;

     Query Match             32.1%;  Score 399;  DB 1;  Length 105;
     Best Local Similarity   72.4%;  Pred. No. 9.6e-26;
     Matches   76;  Conservative    9;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
                 ||| :|||||||||||||||      |||||||||||  |||   ||  :    |||||
Db           1 QPAVTPSVILFPPSSEELKDNKATLVCLISDFYPRTVKVNWKADGNSVTQGVDTTQPSKQ  60

Qy         190 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
               ||||||||:|  |:|||  ::| |||||| :|||:||||:|:||
Db          61 SNNKYAASSFLHLTANQWKSYQSVTCQVTHEGHTVEKSLAPAECS 105


RESULT 11
LV4B_HUMAN
ID   LV4B_HUMAN      STANDARD;      PRT;   106 AA.
AC   P01716;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-IV region X.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69088380; PubMed=4883841;
RA   Milstein C., Clegg J.B., Jarvis J.M.;
RT   "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT   Bence-Jones protein.";
RL   Biochem. J. 110:631-652(1968).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01982; L4HUX.
DR   HSSP; P80748; 2LOI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   NON_TER     106    106
SQ   SEQUENCE   106 AA;  11334 MW;  24D0434AA812855 CRC64;

     Query Match             32.1%;  Score 399;  DB 1;  Length 106;
     Best Local Similarity   71.0%;  Pred. No. 9.7e-26;
     Matches   76;  Conservative   11;  Mismatches   18;  Indels    2;  Gaps    1;
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Qy          22 YELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
                :||:||||||||||||||    ||  :::|:|  ::||::|  |||||::|||||
Db           1 YDLTQPPSVSVSPGQTASITCSGDKLGDKDVCWYQQRPGQSPVLVIYQDNQRSSGIPERF 60

Qy          82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVL 128
               ||||||||||||   ||||||||  :.| ||:|||    |||||
Db          61 SGSNSGNTATLTISGTQAMDEADYYCQAWDSMS--VVFGGGTRLJTVL 105


RESULT 12
LV4E_HUMAN
ID   LV4E_HUMAN      STANDARD;      PRT;   106 AA.
AC   P06889;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-IV region MOL.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=87156515; PubMed=3103603;
RA   Holm E., Sletten K., Husby G.;
RT   "Structural studies of a carbohydrate-containing
RT   immunoglobulin-lambda-light-chain amyloid-fibril protein (AL) of
RT   variable subgroup III.";
RL   Biochem. J. 239:545-551(1986).
CC   -!- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
CC       HOMOLOGY.
DR   PIR; A26019; L4HUML.
DR   HSSP; P80748; 2LOI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Amyloid; Glycoprotein.
FT   DISULFID     21     86                   BY SIMILARITY.
FT   CARBOHYD     90     90                   N-LINKED (GLCNAC...) (PROBABLE).
FT   NON_TER     106    106
SQ   SEQUENCE   106 AA;  11272 MW;  D9BB77D4797D2123 CRC64;

     Query Match             31.9%;  Score 397;  DB 1;  Length 106;
     Best Local Similarity   67.6%;  Pred. No. 1.4e-25;
     Matches   73;  Conservative   13;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          22 YELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
                :||:||||||||||||||    ||  :::|:|  ::||::|  |||||::|||||
Db           1 YELTQPPSVSVSPGQTATISCSGDKLGESYYDWYQQSPGQSPLLVIYEGDKRPSGIPZRF 60

Qy          82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLG 129
               ||||||||||||   |||||||     ::|     |||||||||
Db          61 SGSNSGNTATLTISGTESMDEADYYCQAWNSSS--VLFGGGTKLJTVLG 106


RESULT 13
LAC1_RAT
ID   LAC1_RAT        STANDARD;      PRT;   104 AA.
AC   P20766;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda-1 chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87305594; PubMed=3114047;
RA   Steen M.L., Hellman L., Pettersson U.;
```

RT "The immunoglobulin lambda locus in rat consists of two C lambda
RT genes and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M22520; AAA41419.1; ALT_INIT.
DR PIR; A27390; A27390.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER   1
FT DISULFID   27   85
FT DISULFID   103   103
SQ SEQUENCE   104 AA; 11565 MW; CBF7181F4BC878A CRC64;

Query Match   31.0%; Score 385.5; DB 1; Length 104;
Best Local Similarity   66.7%; Pred. No. 1.2e-24;
Matches   70; Conservative   17; Mismatches   17; Indels   1; Gaps   1;

Qy   130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ 189
              ||||||||||||||||||||:|||||||||||| :|: ||||| :||||||||
Db   1 QPKATPSVTLFPPSSEELKTDKATLVCMVTDFYPGVMTVVWKADGTPITQGVETTQPFKQ 60

Qy   190 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
              ||||| |||:|||||||||:| ||||||||||| |||:|||:||
Db   61 -NNKYMATSYLLTAKAWETHSNYSCQVTHEENTVEKSLSRAECS 104

RESULT 14
LAC2_RAT
ID LAC2_RAT   STANDARD;   PRT;   104 AA.
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda-2 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda
RT genes and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M22521; AAA41420.1; ALT_INIT.
DR PIR; B27390; B27390.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 1.

DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER   1   85
FT DISULFID   27   103
FT DISULFID   103   103   INTERCHAIN (WITH HEAVY CHAIN).
SQ SEQUENCE   104 AA; 11318 MW; F08790GDE43F7276 CRC64;

Query Match   30.6%; Score 380.5; DB 1; Length 104;
Best Local Similarity   65.4%; Pred. No. 2.9e-24;
Matches   68; Conservative   18; Mismatches   17; Indels   1; Gaps   1;

Qy   130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ 189
              ||| :|:|:||||||||||||||||||||| :|: :|:||||:|||||||
Db   1 QPKSTPTLTVFPPSTEELQGNKATLVCLISDFYPSDVEVAWKANGAPISQGVDTANPTKQ 60

Qy   190 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
              ||||| |||||||||||||||::|:|||||||||||||:::|
Db   61 -GNKYIASSFLRLTAEQWRSRNSFTCQVTHEGNTVEKSLSPAEC 103

RESULT 15
LV4D_HUMAN
ID LV4D_HUMAN   STANDARD;   PRT;   106 AA.
AC P01718;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-IV region Kern.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=7150336; PubMed=5549568;
RA Ponstingl H., Hess M., Hilschmann N.;
RT "Structural rule of antibodies. Primary structure of a monoclonal
RT immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
RT protein Kern). V. The complete amino acid sequence and its genetic
RT interpretation.";
RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01984; L4HUKN.
DR HSSP; P80748; 2LOI.
DR InterPro; IPR003006; Ig_MHC;
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID   21   86   BY SIMILARITY.
FT NON_TER   106   106
SQ SEQUENCE   106 AA; 11277 MW; C8B4A05B9CB43CBE CRC64;

Query Match   30.4%; Score 378; DB 1; Length 106;
Best Local Similarity   65.4%; Pred. No. 4.8e-24;
Matches   70; Conservative   15; Mismatches   20; Indels   2; Gaps   1;

Qy   22 YELTQPPSVSVSPGQTARITCGGDNREYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
             | ||||||||||||||||| ||:||||| |:||:||| |:::||||||||||
Db   1 YALTQPPSVSVSPGQTAVITCGGDNLEKTFVSWFQQRPGQSPLLVIYHTSERPSEIPERF 60

Qy   82 SGGKSGNTATLTITNGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVL 128
             ||||| |||| || ::| ||||||| || |||||| :||:||
Db   61 SGSSGATATLTISGAQSVEDEADYFCQTWDTIT--AIFGGGTKLTVL 105

Search completed: March 29, 2003, 09:11:11
Job time : 6.57924 secs

```
              GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:    March 29, 2003, 09:06:23 ; Search time 21.223 Seconds
                                       (without alignments)
                                       2271.829 Million cell updates/sec

Title:            US-09-758-173-2
Perfect score:    1243
Sequence:         1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 234

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:       671580

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   SPTREMBL_21:*
        1:  sp_archea:*
        2:  sp_bacteria:*
        3:  sp_fungi:*
        4:  sp_human:*
        5:  sp_invertebrate:*
        6:  sp_mammal:*
        7:  sp_mhc:*
        8:  sp_organelle:*
        9:  sp_phage:*
       10:  sp_plant:*
       11:  sp_rodent:*
       12:  sp_virus:*
       13:  sp_vertebrate:*
       14:  sp_unclassified:*
       15:  sp_rvirus:*
       16:  sp_bacteriap:*
       17:  sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	981	78.9	233	4	Q8TBC9	Q8tbc9 homo sapien
2	917.5	73.8	233	4	Q96I69	Q96I69 homo sapien
3	885	71.2	237	4	Q8WUK4	Q8wuk4 homo sapien
4	883	71.0	237	4	Q8WTU6	Q8wtu6 homo sapien
5	856.5	68.9	236	4	Q96E61	Q96e61 homo sapien
6	763	61.4	240	4	Q8WUK3	Q8wuk3 homo sapien
7	700	56.3	235	11	Q99M11	Q99m11 mus musculu
8	551	44.3	106	4	Q8TCJ5	Q8tcj5 homo sapien
9	479.5	38.6	234	11	Q8VCP0	Q8vcp0 mus musculu
10	468.5	37.7	130	11	Q9D8W4	Q9d8w4 mus musculu
11	464	37.3	239	4	Q8TCD0	Q8tcd0 homo sapien
12	462.5	37.2	238	11	Q8VCI6	Q8vci6 mus musculu
13	449.5	36.2	234	11	Q8R062	Q8r062 mus musculu
14	444	35.7	235	11	Q91W12	Q91w12 mus musculu
15	441.5	35.5	238	11	Q99M37	Q99m37 mus musculu
16	432.5	34.8	234	11	Q91WF8	Q91wf8 mus musculu
17	431.5	34.7	233	11	Q91WS9	Q91ws9 mus musculu
18	423	34.0	239	11	Q8VC55	Q8vc55 mus musculu
19	398.5	32.1	214	11	Q9RIA5	Q9ria5 mus musculu
20	395.5	31.8	234	11	Q8R028	Q8r028 mus musculu
21	382	30.7	107	4	Q9NSD6	Q9nsd6 homo sapien
22	376.5	30.3	107	4	Q9UL82	Q9ul82 homo sapien
23	375.5	30.2	105	11	Q99JC1	Q99jc1 mus musculu
24	347	27.9	110	4	Q8TE63	Q8te63 homo sapien
25	338	27.2	116	4	Q96JD0	Q96jd0 homo sapien
26	315.5	25.4	112	4	Q96JD1	Q96jd1 homo sapien
27	314	25.3	112	4	Q96JD2	Q96jd2 homo sapien
28	289	23.3	108	4	Q96B0	Q96b0 homo sapien
29	273.5	22.0	684	13	Q90544	Q90544 ginglymosto
30	264.5	21.3	127	11	Q92S9	Q92s89 mus musculu
31	252	20.3	257	13	Q90536	Q90536 ginglymosto
32	250	20.1	268	13	Q90524	Q90524 ginglymosto
33	250	20.1	471	4	Q8TC77	Q8tc77 homo sapien
34	245	19.7	106	5	Q9U410	Q9u410 schistosoma
35	244.5	19.7	134	11	Q8VDD0	Q8vdd0 mus musculu
36	243	19.5	109	4	Q9UL78	Q9ul78 homo sapien
37	241.5	19.4	267	13	Q90529	Q90529 ginglymosto
38	241.5	19.4	473	11	Q91205	Q91205 ginglymosto
39	241	19.4	107	4	Q9UL81	Q9ul81 homo sapien
40	238	19.1	107	4	Q96SA9	Q96sa9 homo sapien
41	237	19.1	481	11	Q91WT1	Q91wt1 mus musculu
42	235.5	18.9	259	13	Q90530	Q90530 ginglymosto
43	234.5	18.9	469	11	Q8R3V9	Q8r3v9 mus musculu
44	234	18.8	109	4	Q9UL85	Q9ul85 homo sapien
45	234	18.8	468	11	Q99L31	Q99l31 mus musculu

ALIGNMENTS

```
RESULT 1
Q8TBC9
ID   Q8TBC9                  PRELIMINARY;    PRT;    233 AA.
AC   Q8TBC9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 24.9 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC02823; AAH22823.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;   24867 MW;   367411BFD6F4DF92 CRC64;
```

Query Match   78.9%;   Score 981;   DB 4;   Length 233;
Best Local Similarity   79.4%;   Pred. No. 1.7e-80;
  Matches 185; Conservative 17; Mismatches 21; Indels 10; Gaps 1;

```
Qy      12 LLWLP------------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
              :  :        ||||||||||||||||||||:||::|||||| |: ||||
Db       1 MAWIPLLLPLLTLCTGSEASYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQ 60

Qy      62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
           |||:||| | ||:::||||||||||||:|:|: :||:||||||::|| : |: ||||
Db      61 APVLVIYKDNERRSGIPERFSGSSGTTVTLTISGVQAEDEADYYCQSADSSGTYWVFGG 120

Qy     122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 180

Qy     182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
```

Db 181 ETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 2
Q96I69
ID   Q96I69
AC   Q96I69;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:12849).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-CELL;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC007782; AAH07782.1; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;

Query Match   73.8%; Score 917.5; DB 4; Pred. No. 9.1e-75;
Best Local Similarity   78.1%;
Matches 178; Conservative   17; Mismatches   32; Indels   1; Gaps   1;

Qy   7 LLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDSRNEYVHWYQQKPARAPILV 66
          |||||||:|||||:||||||||||||||||||||||| ||| ::||||||||||
Db   7 LLG-LLSHCTGSGTSVVLTQPASVSVAPGQTARITCGGSNLGSKSVNWYQLRPGQAPILV 65

Qy   67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCCQVWDRASDHPVFGGGTRVT 126
          :::|||||||||||| ||||| |||||| |:|| ||:||
Db   66 VYENKERPAGIPERLSALTSEETATLTISSVVAGDEADYFCQVWDTTSQQYVFGTGTQVT 125

Qy 127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
          |||||| :|||||||||||||||||||||||||||||||||||| |||||||||||||
Db 126 VLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKP 185

Qy 187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||||||||||||||||
Db 186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
Q8WUK4
ID   Q8WUK4;
AC   Q8WUK4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 24.9 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020233; AAH20233.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 237 AA; 24897 MW; 73C7D7D8B039D186 CRC64;

Query Match   71.2%; Score 885; DB 4; Length 237;
Best Local Similarity   75.9%; Pred. No. 7.9e-72;
Matches 176; Conservative   17; Mismatches   35; Indels   4; Gaps   2;

Qy   7 LLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR---NEYVHWYQQKPARAP 63
          ||| | |:   : | :|| ::||| | : ||||| ||| || |||| | |
Db   6 LLLTLLAHCTGSWAQSVLTQPPSVSVSGAPGQRVTISCTGSSNIGAGYDVHWYQQLPGTAP 65

Qy   64 ILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRA-SDHPVFGGG 122
          :|| : |||||||||||||||||||||||| |||| : :|||| : ||| |||||||
Db   66 KLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGFVVFGGG 125

Qy 123 TRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
          |:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185

Qy 183 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237

RESULT 4
Q8WTU6
ID   Q8WTU6;
AC   Q8WTU6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 24.9 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022098; AAH22098.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;

Query Match   71.0%; Score 883; DB 4; Length 237;
Best Local Similarity   75.9%; Pred. No. 1.2e-71;
Matches 176; Conservative   17; Mismatches   35; Indels   4; Gaps   2;

Qy   7 LLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAP 63
          ||| | |:   : | :|| ::||| | : ||||| ||| || |||| | |
Db   6 LLLTLLAHCTGSWAQSVLTQPPSVSVSGAPGQRVTISCTGSSNIGAGYDVHWYQQLPGTAP 65

Qy   64 ILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRA-SDHPVFGGG 122
          :|| : |||||||||||||||||||||||| |||| : :|||| : ||| |||||||
Db   66 KLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDYSLSASGVFGGG 125

Qy 123 TRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182

```
Db    126 TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185
          |:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    183 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    186 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237
```

RESULT 5
```
Q96E61
ID   Q96E61            PRELIMINARY;       PRT;     236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:17259).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match             68.9%;  Score 856.5;  DB 4;  Pred. No. 2.9e-69;
Best Local Similarity   72.7%;  Pred. No. 2.9e-69;
Matches 168; Conservative 19; Mismatches 41; Indels 3; Gaps 1;

Qy      7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR---NEYVHWYQQKPARAP 63
          ||    || ||         |||||||:::   ||  ||||:  ::::   |||||:
Db      6 LLLTLLAHCTGSWAQSVLAQPPSVSGAPGQTVTISCTGSSNIGAGYAVHWYQQFPGAAP 65

Qy     64 ILVIYDDSDRPSGIPERFSGGKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGT 123
          |||||||||  |:|||||||||::||:||||||||:|::||||||:||||||| |||
Db     66 KVLIYGNYNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGAGT 125

Qy    124 RVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 183
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 KVTVLGQPKANPTVLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVET 185

Qy    184 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
```

RESULT 6
```
Q8WUK3
ID   Q8WUK3            PRELIMINARY;       PRT;     240 AA.
AC   Q8WUK3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.0 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020236; AAH20236.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
```

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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;

Query Match             61.4%;  Score 763;  DB 4;  Length 240;
Best Local Similarity   67.4%;  Pred. No. 7.8e-61;
Matches 155; Conservative 20; Mismatches 33; Indels 22; Gaps 6;

Qy     20 CAYE-LTQPPSVSVSPGQTARITCGGDNSRNEY-VHWYQQKPARAPILVIYDDSD----R 73
          ||::  |||||||   ||||||||||||:  |:  |:|||||:  :||:|   ::    :
Db     18 CALPVLTQPPSASAFLGASIKLTCLSREHSSYTIEWYQQRPGRSPQYIMKVKSDGSHNK 77

Qy     74 PSGIPERFSGSKSGNTATLTINGVEAGDEADYYC-------QV-WDRASDHPVFGGGTR 124
          |:::|||||||||||:|:||||:::    ::::|       ||     ||||||||||:
Db     78 GDGIPDRFMGSSSGADRYLTLSNIQSDDEAEYHCGESHTIDGQVGW------VFGGGTK 130

Qy    125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 LTVLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 190

Qy    185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 240
```

RESULT 7
```
Q99M11
ID   Q99M11            PRELIMINARY;       PRT;     235 AA.
AC   Q99M11;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 25.4 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002129; AAH02129.1; -.
HSSP; P01703; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match             56.3%;  Score 700;  DB 11;  Length 235;
Best Local Similarity   60.7%;  Pred. No. 3.6e-55;
Matches 142; Conservative 28; Mismatches 58; Indels 6; Gaps 3;

Qy      5 AQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGD--NSRNEVHWYQQKPARA 62
          | |||    :|     |         ||||||||    |:  : ::||  |||||||||
Db      4 APLLLVFLHHLTGSCAQLVLTQPSSVSTSLGSTAKLPCKASTCNIGDSYVNWYQQMGRS 63

Qy     63 PILVIYDDSDRPSGIPERFSGS--KSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
          ||||||||||:||||||:|||   |:|:||||||||:::  :||||||:|||||||| ||
Db     64 PTNMIYGDDLRPSGVSDRFSGSIDSSSNSAFLTIQNVQADDEADYYCQSY--SSGIRVFG 121
```

```
Qy    121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
          ||||: |||:|||| ||:||||||||||||||||||||||||||||| ||||:||| |
Db    122 GGTKLITVLSQPKTSPSVTLFPPSSEELETNKATLVCLISDFYPGAVTVDWKADGTPVTQG 181

Qy    181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          ||:|:|||||||||||||:||||||||||||||:|||||||||||||:::: ||
Db    182 VETTQPSKQSNNKYMASSYLTLTAKAWETHSSYSCQVTHEGHTVEKSLSRADCS 235
```

RESULT 8
```
Q8TCJ5
ID   Q8TCJ5;                     PRELIMINARY;         PRT;    106 AA.
AC   Q8TCJ5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 11.3 kDa protein (Fragment).
GN   DKFZp667J0810.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH NODE;
RA   Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL713800; CAD28551.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   106 AA;  11265 MW;  145272BBE65F4565 CRC64;
```

```
Query Match             44.3%;  Score 551; DB 4;  Length 106;
Best Local Similarity   99.1%;  Pred. No. 3.1e-42;
Matches  105;  Conservative   1;  Mismatches    0;  Indels     0;  Gaps     0;
```

```
Qy    129 GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK 188
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK 60
```

```
Qy    189 QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
          ||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 106
```

RESULT 9
```
Q8VCP0
ID   Q8VCP0;                     PRELIMINARY;         PRT;    234 AA.
AC   Q8VCP0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 25.7 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019474; AAH19474.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003599; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
```

KW   Hypothetical protein.
```
SQ   SEQUENCE   234 AA;  25702 MW;  102551C58AC2FA9F CRC64;
```

```
Query Match             38.6%;  Score 479.5; DB 11;  Length 234;
Best Local Similarity   42.4%;  Pred. No. 2.6e-35;
Matches  101;  Conservative   46;  Mismatches  82;  Indels     9;  Gaps     6;
```

```
Qy      1 MRVPAQLGLLLWLPGARCAYELTQ-PPSVSVSPGQTARITCGGDNSRNEYVHWYQQKP 59
          : ||: | |: : |||||| || ||  : |: ||:: :|||||:: :|:|
Db      1 MSVPTQVLGLLLLCLTGARCDIQLTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQ 60
```

```
Qy     60 ARAPILIVIYDDSDRPSGIPERFSGSGSGNTATLTINGVEAGDEADYCCQVWDRASDHP-V 118
          :: |: :| : |: || || |: |: :| ||: |||:| |:| || :|
Db     61 GKSPQLLVYNAKTLADGVPSRFSGSGSRSGTQFSLKINSLQPEDFGSYYCQ--HHSGIPFT 117
```

```
Qy    119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
          |:||: | ||||:|||||||||||||||||| ||||||||||||||||:|||||:||
Db    118 FGSGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176
```

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Qy    179 AGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 233
          ||  :|: : :|||||| | :|: |:| | ||| : |:|| :|| | : ||:||||||
Db    177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
```

RESULT 10
```
Q9D8W4
ID   Q9D8W4;                     PRELIMINARY;         PRT;    130 AA.
AC   Q9D8W4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810027O01Rik protein.
GN   1810027O01RIK.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007622; BAB25142.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:1916426; 1810027O01Rik.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   130 AA;  14253 MW;  4381979755E766E54 CRC64;
```

```
Query Match             37.7%;  Score 468.5; DB 11;  Length 130;
Best Local Similarity   68.5%;  Pred. No. 1.1e-34;
```

Matches   47; Conservative   14; Mismatches   19; Indels   7; Gaps   1;

```
Qy   108  QVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVT  167
          |___|         |||||::||||||||||||||||||||||||||::|||||| |||||
Db    11  QCW------VFGGGTKLTVLGQPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVT   63

Qy   168  VAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT  227
          |:::||||||||||:||||||||||||||||||||||||||::|::|||||||||||:||||
Db    64  VDWKVDGTPVTQGMETTVQPSKQSNNKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKS  123

Qy   228  VAPTECS  234
          :: |||
Db   124  LSRADCS  130
```

RESULT 11
Q8TCD0
ID   Q8TCD0;
AC   Q8TCD0;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.2 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022362; AAH22362.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match   37.3%; Score 464; DB 4; Length 239;
Best Local Similarity   41.8%; Pred. No. 6.6e-34;
Matches   102; Conservative   52; Mismatches   74; Indels   16; Gaps   8;

```
Qy     1  MRVPAQLLGLLLLWLPGARCAYELTQPP-SVSVSPGQTARITCGGDNS-----RNEYVHW   54
          |:||:||||||||||||:||:   |:| ||:|||||||||||||||||      ||||||
Db     1  MRLPAQLLGLLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNW   60

Qy    55  YQQKPARAPILVIVIYDDSDRPSGIPERFSGSGSKSGNTATLTINGVEAGDEADYYCQVWDRAS  114
          |||||||||||||||||:  |||:| ||||||||:||||||||||| |||||||  :||
Db    61  FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCM---QGT  117

Qy   115  DHP-VFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD  173
          ||| |||||||:||| |:|:|||:|||||||:| ||:|||||| ||:::||
Db   118  HWPSTFGQGTKLEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD  176

Qy   174  SSPVKAG--VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVA  229
          |: ::||   |||:|||||||||||:|: |:|: |||||:|||||||||||:
Db   177  NA-LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN  235

Qy   230  PTEC  233
          ||||
Db   236  RGEC  239
```

RESULT 12
Q8VCI6
ID   Q8VCI6;
AC   Q8VCI6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.2 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019760; AAH19760.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match   37.2%; Score 462.5; DB 11; Length 238;
Best Local Similarity   41.4%; Pred. No. 9e-34;
Matches   101; Conservative   49; Mismatches   77; Indels   17; Gaps   8;

```
Qy     1  MRVPAQLLGLLLLWLPGARCAYELTQPP-SVSVSPGQTARITCGGDNS-----RNEYVHW   54
          ||:||||||||:||||:  ||:|   :| ||:||||||||||||||||      ||||||
Db     1  MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHW   59

Qy    55  YQQKPARAPILVIVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRAS  114
          |||| |||||||||||:  |||:| ||||||:||||||||||| |||||||  :||
Db    60  YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS----QS  115

Qy   115  DH--PVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA  172
          ||   ||:|||:||| |:|:|||:|||||||:| ||:|||||| ||:::||
Db   116  THVPTFGGGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKI  174

Qy   173  DSSPVKAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVA  229
          |: ::||   |||:|||||||||||:|: |:|: |||||:||||||||||:||
Db   175  DGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN  234

Qy   230  PTEC  233
          ||||
Db   235  RNEC  238
```

RESULT 13
Q8R062
ID   Q8R062;
AC   Q8R062;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 25.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027418; AAH27418.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match   36.2%; Score 449.5; DB 11; Length 234;
Best Local Similarity   41.6%; Pred. No. 1.3e-32;
Matches   99; Conservative   43; Mismatches   87; Indels   9; Gaps   6;

```
Qy     1  MRVPAQLLGLLLLWLPGARCAYELTQ-PPSVSVSPGQTARITCGGDNSRNEYVHWYQQKP   59
          ||:|| |||||||||:  ||:||| |||:||||||||||||||||||||:||:|||||||
Db     1  MMSSAQFIGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKP   60

Qy    60  ARAPILVIVIYDDSDRPSGIPERFSGSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHP-V  118
```

```
Db   61 DGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYYCQQY---SQFPFT 117
          ||||  ||||||||||     ||||||   ||:||||||||||||| :  ||||
Qy  119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
          || ||| :| ||||  :|||||||||::::|||||:  ||||||||||||||| | |
Db  118 FGSGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176

Qy  179 AGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 233
          ||  ||| ||:|||:| :  ||| |||||||||||:|  || : :  |||||||| |:
Db  177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
```

RESULT 14
Q91W12
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ID   Q91W12         PRELIMINARY;      PRT;    235 AA.
AC   Q91W12;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:6582).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST TUMOR;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006643; AAH06643.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match    35.7%;  Score 444; DB 11; Length 235;
Best Local Similarity  43.0%;  Pred. No. 4.1e-32;
Matches  92;  Conservative  45;  Mismatches  69;  Indels  8;  Gaps  6;

Qy   24 LTQPPSV-SVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERFS  82
          |||| |  ||  ||| :||| :: :|| ::|| |||| | :||||||| ::|||||||
Db   26 LTQSPAIMSASPGERVTMTCSASSVS-HMHWYQQKSGTSPKRWIYDTFKLTSGVPDRFS  84

Qy   83 GSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFPP 142
          |||| |||  |||| | || |||||    ||:::| :||||:||| |||:|| |:|||
Db   85 GSGSGTSYSLTIISMEAEDVATYYCQQWSR--NPPTFGVGTKLE-LKRADAAPTVSIFPP 141

Qy  143 SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV-ETTTPSKQSNNKYAASSYLS 201
          ||| ||||||| ||||||||||| ||||    ||| ||  ||||||:|||:|  :||||
Db  142 SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 201

Qy  202 LTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 233
          ||:|||||||||||||:|| : |||||||| |:|
Db  202 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235
```

RESULT 15
Q99M37
```
ID   Q99M37         PRELIMINARY;      PRT;    238 AA.
AC   Q99M37;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 26.3 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002055; AAH02035.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match    35.5%;  Score 441.5; DB 11; Length 238;
Best Local Similarity  40.7%;  Pred. No. 7e-32;
Matches  99;  Conservative  49;  Mismatches  80;  Indels  15;  Gaps  8;

Qy    1 MRVPAQLLGLLLLWLPGARCAYELTQPP-SVSVSPGQTARITCGGDNS----RNEYVHW  54
          |::|:::||| |:| ::: |  |    || ::: ||||:||| ||||
Db    1 MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEW  59

Qy   55 YQQKPARAPILVIYDDSDRPSGIPERFSGSGSGNTATLTINGVEAGDEADYYCQVWDRAS 114
          |||| |||||||||:|| :||||||||||||||:| |||:|| :|: || :  :
Db   60 YLQKPGQSPKLLIYKVSNRFSGVEDRFSGSGSGTDFTLKISRVEAEDLGVYYC---FQGS 116

Qy  115 DHP-VFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD 173
          :|   ||||::|| ||| :|  |||||||||| :|||||||:|||||||||| ||||
Db  117 HVPYTFGSGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKID 175

Qy  174 SSPVKAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAP 230
          |||: || :||||||||||||||||||| |||:|||||||||||||:|| : |||||||
Db  176 GSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR 235

Qy  231 TEC 233
          |:|
Db  236 NEC 238

Search completed: March 29, 2003, 09:14:34
Job time : 24.223 secs
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                        GenCore version 5.1.4_p5_4578
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     March 29, 2003, 09:06:24 ; Search time 10.5021 Seconds
                                        (without alignments)
                                        2141.995 Million cell updates/sec

Title:      US-09-758-173-2
Perfect score: 1243
Sequence:   1 MRVPAQLLGLLLLWLPGARC.........CQVTHEGSTVEKTVAPTECS 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:   283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:      283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_73:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1016	81.7	232	2	S25756	Ig lambda chain -
2	1012.5	81.5	233	2	S25747	Ig lambda chain -
3	979	78.8	231	2	S25738	Ig lambda chain -
4	959	77.2	231	2	S25751	Ig lambda chain -
5	959	77.2	231	2	S25753	Ig lambda chain -
6	936	75.3	226	2	S25745	Ig lambda chain -
7	923	74.3	213	2	JE0247	Ig lambda chain NI
8	920	74.0	233	2	S25748	Ig lambda chain NI
9	920	74.0	235	2	S05270	Ig lambda chain pr
10	910	73.2	232	2	S25742	Ig lambda chain -
11	905	72.8	233	2	S25741	Ig lambda chain -
12	883	71.0	233	2	S25752	Ig lambda chain -
13	881	70.9	235	2	S25750	Ig lambda chain -
14	873	70.2	234	2	S25757	Ig lambda chain -
15	871.5	70.1	213	2	S21066	Ig lambda chain V
16	871.5	70.1	236	2	S25746	Ig lambda chain -
17	870	70.0	233	2	S25744	Ig lambda chain -
18	870	70.0	235	2	S14675	Ig lambda chain -
19	869.8	69.8	235	2	S25759	Ig lambda chain -
20	867.5	69.8	216	2	A42193	Ig lambda chain (B
21	862.5	69.4	217	2	JE0246	Ig lambda chain NI
22	859	69.1	216	2	S29258	Ig lambda chain V
23	850.5	68.4	235	2	S25754	Ig lambda chain -
24	846	68.1	216	2	S03401	Ig lambda chain (K
25	840.5	67.6	235	2	S25758	Ig lambda chain -
26	835	67.2	190	2	S25740	Ig lambda chain -
27	833.5	67.1	212	2	S70431	Ig lambda chain -
28	822	66.1	216	2	JE0245	Ig lambda chain NI
29	820.5	66.0	235	2	S25749	Ig lambda chain -
30	818	65.8	216	2	S69130	Ig lambda chain (D
31	799	64.3	208	2	B49444	Ig lambda chain (N
32	785	63.2	243	2	S25755	Ig lambda chain -
33	639.5	51.4	181	2	PT0220	Ig lambda chain v-
34	639.5	51.4	232	2	S17399	Ig lambda chain pr
35	635.5	51.1	214	2	PC4156	Ig lambda chain V
36	632	50.8	230	2	S49449	Ig lambda chain -
37	622.5	50.1	213	2	A21177	Ig light chain pre
38	603	48.5	118	2	S12441	Ig lambda chain (K
39	600	48.3	118	2	S12442	Ig lambda chain (K
40	579	46.6	118	2	S12440	Ig lambda chain (M
41	578	46.5	118	2	S12443	Ig lambda chain (K
42	576	46.3	118	2	A39949	Ig lambda chain J-
43	559	45.0	234	2	A39956	Ig lambda chain pr
44	548	44.1	105	1	L2HU	Ig lambda chain C
45	542.5	43.6	146	2	S02083	Ig lambda chain V-

ALIGNMENTS

```
RESULT 1
S25756
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25756
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25756
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COM>
A;Cross-references: EMBL:X57821; NID:g33741; PIDN:CAA40958.1; PID:g33742
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

Query Match      81.7%;  Score 1016;  DB 2;  Length 232;
Best Local Similarity  86.0%;  Pred. No. 9.4e-61;
Matches 196;  Conservative 14;  Mismatches 16;  Indels 2;  Gaps 2;

Qy       7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
           ||: ||| : :||  ||||||||| :  :||||||||:  ||||||||||||: ::
Db       7 LLG-LLSHCTGSVTSYVLTQPPSVSVAPGKTASITCGGNNIGSKSVHWYQQKPGQAPVLV 65

Qy      67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
           :|||||||||||||||||::|| ||||||: ||||||||||||||:  :|| ||||| ::
Db      66 VYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSD-VVFGGGTKLT 124

Qy     127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 184

Qy     187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 232

RESULT 2
S25747
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25747
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25747
A;Status: preliminary; translation not shown
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A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57812; NID:g33723; PIDN:CAA40949.1; PID:g33724
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match   81.5%; Score 1012.5; DB 2; Length 233;
Best Local Similarity   85.1%; Pred. No. 1.6e-60;
Matches 194; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

Qy   7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
Db   7 LLG-LLSHCTGSVTSYVLTQPPSVSVAPGKAARITCGGINIASKSVHWYQQKPGQAPVLV 65

Qy   67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
Db   66 VYGDSDRPSGIPERFSGSGNSGNTATLNISRVEAGDEAAYYCQVWDSSSDHVVFGGGTKLT 125

Qy 127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
Db 126 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 185

Qy 187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 3
S25738
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25738
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Molecule type: mRNA
A;Cross-references: EMBL:X57802; NID:g33701; PIDN:CAA40940.1; PID:g33702
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;146-214/Domain: immunoglobulin homology <IMM>

Query Match   78.8%; Score 979; DB 2; Length 231;
Best Local Similarity   80.3%; Pred. No. 2.7e-58;
Matches 187; Conservative 13; Mismatches 21; Indels 12; Gaps 2;

Qy   12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
Db   1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYACWYQQKPGH 60

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
Db   61 SPVLVIFQDSKRPSGIPERFSGSGNSGNTATLTISTQAMDEADYYCQAWD--SSTAVFGG 118

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy 182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 4
S25751
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25751
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25751
A;Molecule type: mRNA
A;Residues: 1-231 <COM>
A;Cross-references: EMBL:X57816; NID:g33731; PIDN:CAA40953.1; PID:g33732
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match   77.2%; Score 959; DB 2; Length 231;
Best Local Similarity   79.0%; Pred. No. 5.7e-57;
Matches 184; Conservative 14; Mismatches 23; Indels 12; Gaps 2;

Qy   12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
Db   1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYASWYQQKAGQ 60

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
Db   61 SPVLVIYRHSKRPSGIPERFSGSGNSGNTATLTISGTQVMDEADYYCQAWD--SSIVVFGG 118

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy 182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVAPTECS 234
Db 179 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVAPTECS 231

RESULT 5
S25753
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25753
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25753
A;Molecule type: mRNA
A;Residues: 1-231 <COM>
A;Cross-references: EMBL:X57818; NID:g33735; PIDN:CAA40955.1; PID:g33736
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;146-214/Domain: immunoglobulin homology <IMM>

Query Match   77.2%; Score 959; DB 2; Length 231;
Best Local Similarity   78.5%; Pred. No. 5.7e-57;
Matches 183; Conservative 17; Mismatches 21; Indels 12; Gaps 2;

Qy   12 LLWLP--------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
Db   1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGKTASITCFGDKLGDKYSSWYQQKPGQ 60

Qy   62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
Db   61 SPLLVLYQDTNRPSGIPERFSGSGNSGNTATLTISETQAMDEGDYYCQAWD--SNTVVFGG 118

Qy 122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
Db 119 GTKLTVLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178

Qy 182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
Db 179 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 231

RESULT 6
S25745
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25745
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25745
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-226 <COM>
A;Cross-references: EMBL:X57810; NID:g33717; PIDN:CAA40947.1; PID:g33718
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;141-209/Domain: immunoglobulin homology <IMM>

Query Match   75.3%; Score 936; DB 2; Length 226;
Best Local Similarity   79.0%; Pred. No. 1.9e-55;
Matches 177; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Qy   11 LLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDD 70
         || :|:||||||||||||||||||||||||||||::   :|:||||
Db   3 LLTFCTVSEASYELTQPPSGGSVSPGKTARITCSGDALPKKYAYWYQQKSGQSPVLVIYED 62

Qy   71 SDRPSGIPERFSGSSKSGNTATLTINGVEAGDEADYYCQWDRASDHPVFGGGTRVTVLGQ 130
         |||||||||||||||| : :| |||||||||::||||:||
Db   63 TKRPSGIPERFSFSSSGTMSTLTIISGAQVEDEADYYCYSTDRRGMHRVFGGGTKLTVLGQ 122

Qy   131 PKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQS 190
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 PKAAPSVLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQS 182

Qy   191 NNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         |||||||||||||||||||||||||||||||||||||||||||
Db   183 NNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 226

RESULT 7
JE0247
Ig lambda chain NIG250 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0247
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Takashi, I.; Shinoda,
submitted to JIPID, November 1998
A;Description: Structural relationship of lambda type light chains with AL amyloidosis.
A;Reference number: JE0245
A;Accession: JE0247
A;Molecule type: protein
A;Residues: 1-213 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;128-196/Domain: immunoglobulin homology <IMM>

Query Match   74.3%; Score 923; DB 2; Length 213;
Best Local Similarity   82.9%; Pred. No. 1.3e-54;
Matches 175; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERFSG 83
         ||||||||:||| ||||||||||::| |||||||||||||:|||| :|:|||||||||
Db   3 LTQPPSVSVAPGETATITCEGDNLGTRNVHWYQQKPGQAPVLVLYYDNVRPSGIPERFSG 62

Qy   84 SKSGNTATLTINGVEAGDEADYYCQWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFPPPS 143
         |:||||||||||||||||||||||||||||||:|||||||||||| |||||||||||||
Db   63 SNSVTAATLAISEVEAGDEADFYCWVWDRAANHFVFGPGTKVTALSQPKANPTVTLFPPPS 122

Qy   144 SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLT 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTKPSKQSNNKYAASSYLSLT 182

Qy   204 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         |||||||||||||||||||||||||||||||
Db   183 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 213

RESULT 8
S25748
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25748
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin laml
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25748
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match   74.0%; Score 920; DB 2; Length 233;
Best Local Similarity   77.6%; Pred. No. 2.2e-54;
Matches 177; Conservative 16; Mismatches 29; Indels 6; Gaps 1;

Qy   13 LWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
         ||| |||||||||||||||||||||||||||||||::   :|:|||||||||
Db   6 LWLTLTLTLCIGSVVSSELTQDDPAVSVALGQTVRITCQGDSLRAYYASWYQHKPGQAPILV 65

Qy   67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQWDRASDHPVFGGGTRVT 126
         || :::|||||||||| | | |||||||||||||:::||||||:::|
Db   66 IYGENNRPSGIPDRFSGSSSGNTASFAITGAQAEDEADYYCNSRDSSGDQVLFGGGTKLT 125

Qy   127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 185

Qy   187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 9
S05270
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S05270; S04601
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05270
A;Molecule type: mRNA
A;Residues: 1-235 <KIS1>
A;Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA3725.1; PID:g33395
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of c
A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04601
A;Molecule type: mRNA
A;Residues: 1-130 <KIS2>
A;Cross-references: EMBL:X14583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-235/Product: Ig lambda chain #status predicted <MAT>
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match   74.0%; Score 920; DB 2; Length 235;
Best Local Similarity 77.4%; Pred. No. 2.3e-54;
Matches 178; Conservative 15; Mismatches 35; Indels 2; Gaps 1;

Qy   7 LLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPI 64
       |||||||| || :| :|| || | || ||||| |||||
Db   6 LLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPK 65

Qy   65 LVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFGGGTR 124
      |:|:: |||||||| ||||:|:||||:| || | ||||||
Db   66 LLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLLSAGVFGGGTK 125

Qy 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
      :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

Qy 185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 10
S25742
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25742
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25742
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COM>
A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

Query Match   73.2%; Score 910; DB 2; Length 232;
Best Local Similarity 76.5%; Pred. No. 1e-53;
Matches 176; Conservative 17; Mismatches 35; Indels 2; Gaps 1;

Qy   7 LLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPI 64
       |||||||| |: :|: :|| || | || ||||| ||||
Db   3 LLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGRAPK 62

Qy   65 LVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFGGGTR 124
      |:|:: |||||||| ||||:|:||||:| || | ||||||
Db   63 LLIFENNKRPSAIPDRFSGSKSGTSATLGIAGLQTGDEADYYCGTWDSSLTDVVFGGGTK 122

Qy 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
      :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 123 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 182

Qy 185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 183 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 232

RESULT 11
S25741
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25741
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25741
A;Status: preliminary; translation not shown

A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57805; NID:g33707; PIDN:CAA40943.1; PID:g33708
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match   72.8%; Score 905; DB 2; Length 233;
Best Local Similarity 77.2%; Pred. No. 2.2e-53;
Matches 176; Conservative 15; Mismatches 31; Indels 6; Gaps 1;

Qy   13 LWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
      |||| : : ||||||||||||| || ||||||||||||:|
Db   6 LWLTLLTLCIGSVVSSLTQDPTVSVALGQTLRIKCQGDTIRSYYASWYQQKPGQAPTLL 65

Qy   67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFGGGTRVT 126
      |||||||| ||||:|:||||:| || | |||||| |:
Db   66 INGKDNRPSGIPDRFSGSTGNTASLTITGTQAEDEADYYCNSRDSSAAHLVFGGGTKLT 125

Qy 127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 VLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 185

Qy 187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
      ||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 12
S25752
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25752
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25752
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match   71.0%; Score 883; DB 2; Length 233;
Best Local Similarity 74.3%; Pred. No. 6.4e-52;
Matches 171; Conservative 21; Mismatches 36; Indels 2; Gaps 1;

Qy   7 LLGLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPI 64
       ||| ||:| |: : :|| || | || ||||| ||||
Db   4 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPK 63

Qy   65 LVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYCQVWDRASDHPVFGGGTR 124
      :|:|:: ||||||:||| |: : :|:|: ||| : |||||
Db   64 LLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGVVFGGGTK 123

Qy 125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
      :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 183

Qy 185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 184 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233

RESULT 13
S25750
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accesion: S25750
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) and -C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25750
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: EMBL:X57815; NID:g33729; PIDN:CAA40952.1; PID:g33730
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match   70.9%; Score 881; DB 2; Length 235;
Best Local Similarity   74.3%; Pred. No. 8.8e-52;
Matches 171; Conservative   20; Mismatches   37; Indels   2; Gaps   1;

Qy   7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPI 64
            :||| |: ::||||| ||: |::|||| |||| |:| |||
Db   6 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGASSNIGTNDVYWYQQLTGAPK 65

Qy   65 LVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTR 124
            |:|| ::| ||||||||||| ||:|| |||||| |||:|||||||| |||:||||||
Db   66 LLIYRNNQRPSGVPDRFSGSKSGSSASLAISGLQSEDEADYYCAAWDDSLSGPVFGGGTK 125

Qy   125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185

Qy   185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235

RESULT 14
S25757
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25757
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) and -C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-234 <COM>
A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;149-217/Domain: immunoglobulin homology <IMM>

Query Match   70.2%; Score 873; DB 2; Length 234;
Best Local Similarity   72.6%; Pred. No. 3e-51;
Matches 167; Conservative   25; Mismatches   36; Indels   2; Gaps   1;

Qy   7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPI 64
            :||| |: :::||||| ||: |::|||| |||| |:| |||
Db   5 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSTSNIGSNTVNWYQQLPGTAPK 64

Qy   65 LVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTR 124
            |:|| ::|| |||||||||| ||:|| |||||| |||:|||||||| |:||||||||
Db   65 VLIYNNERPSGVPDRFSGSKSGTSASLAISGLQSDDEADYYCAAWDDSLNGRLLGGGTK 124

Qy   125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
            :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184

Qy   185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db   185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 15
S21066
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S21066
R;Dlouha, A.; Lecroisey, A.; Henschen, A.; Ruttyn, Y.; Rouger, P.; Keil, B.
Protein Seq. Data Anal. 4, 319-324, 1991
A;Title: Partial amino acid sequence of the light chain of human anti-Rh(D) monoclonal ar
A;Reference number: S21066; MUID:92253545; PMID:1812484
A;Accession: S21066
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-213 <DLO>
A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 74-Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;128-196/Domain: immunoglobulin homology <IMM>

Query Match   70.1%; Score 871.5; DB 2; Length 213;
Best Local Similarity   78.5%; Pred. No. 3.4e-51;
Matches 168; Conservative   16; Mismatches   23; Indels   7; Gaps   2;

Qy   24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPER 80
            :|||||||||||||| |||| :||| || ::| |: |||| |:
Db   4 LTQPPSVSGAPGQRVTISCTGSSSNIGARYDVNWYQQLPGTAPKLLIYGNTIRPSGVPDR 63

Qy   81 FSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLF 140
            |||||||:|| | :|::|| :| ||||| |:|||| |||||||||||||||
Db   64 FSGSKSGTSASLAITGLQAEDEGDYYCQTW----DYVVFGGGTKLTVLGQPKAAPSVTLF 119

Qy   141 PPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYL 200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 PPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYL 179

Qy   201 SLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
            |||||||||||||||||||||||||||||||||
Db   180 SLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 213

Search completed: March 29, 2003, 09:16:15
Job time : 11.5021 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 16.9836 Seconds
                                           (without alignments)
                                           828.100 Million cell updates/sec

Title: US-09-758-173-8
Perfect score: 2561
Sequence: 1 MGWSLILLFLVAVATRVQCE.........MHEALHNHYTQKSLSLSPGK 478

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2561	100.0	478	3	US-08-487-550-8	Sequence 8, Appli
2	2184.5	85.3	452	3	US-09-027-449-71	Sequence 71, Appl
3	2184.5	85.3	452	4	US-09-026-985-71	Sequence 71, Appl
4	2184.5	85.3	452	4	US-09-121-952A-71	Sequence 71, Appl
5	2184.5	85.3	452	4	US-09-234-340A-71	Sequence 71, Appl
6	2146.5	83.8	449	4	US-09-679-397-2	Sequence 2, Appli
7	2146.5	83.8	449	4	US-09-680-148-2	Sequence 2, Appli
8	2138.5	83.5	459	1	US-08-157-101A-7	Sequence 7, Appli
9	2135	83.4	451	2	US-08-887-352B-18	Sequence 18, Appl
10	2135	83.4	451	4	US-09-109-207C-18	Sequence 18, Appl
11	2135	83.4	451	4	US-09-282-505-2	Sequence 2, Appli
12	2135	83.4	451	4	US-09-054-255-2	Sequence 2, Appli
13	2135	83.4	451	4	US-09-296-005-18	Sequence 18, Appl
14	2132	83.2	451	2	US-08-887-352B-14	Sequence 14, Appl
15	2132	83.2	451	2	US-08-887-352B-16	Sequence 16, Appl
16	2132	83.2	451	4	US-08-466-151-65	Sequence 65, Appl
17	2132	83.2	451	4	US-09-109-207C-14	Sequence 14, Appl
18	2132	83.2	451	4	US-09-109-207C-16	Sequence 16, Appl
19	2132	83.2	451	4	US-09-296-005-14	Sequence 14, Appl
20	2132	83.2	451	4	US-09-296-005-16	Sequence 16, Appl
21	2132	83.2	453	3	US-08-466-151-8	Sequence 8, Appli
22	2132	83.2	453	4	US-08-466-163B-8	Sequence 8, Appli
23	2100	82.0	476	2	US-08-378-939-10	Sequence 10, Appl
24	2089.5	81.6	467	4	US-09-049-672A-8	Sequence 8, Appli
25	2078	81.1	472	4	US-08-793-450-8	Sequence 8, Appli
26	2073	80.9	476	3	US-08-487-550-4	Sequence 4, Appli
27	2069	80.8	449	1	US-08-458-516-13	Sequence 13, Appl
28	2064	80.6	472	4	US-09-301-593-43	Sequence 43, Appl
29	2058.5	80.4	467	4	US-08-704-744-81	Sequence 81, Appl
30	2056.5	80.3	446	3	US-08-397-411-7	Sequence 7, Appl
31	2054	80.2	468	4	US-09-485-737B-67	Sequence 67, Appl
32	2054	80.2	472	4	US-09-301-593-30	Sequence 30, Appl
33	2054	80.2	711	4	US-09-485-737B-90	Sequence 90, Appl
34	2053	80.2	476	3	US-08-487-550-12	Sequence 12, Appl
35	2046.5	79.9	473	4	US-09-049-672A-4	Sequence 4, Appli
36	2040.5	79.7	552	5	PCT-US93-07832-23	Sequence 23, Appl
37	2037.5	79.6	469	2	US-07-934-373C-23	Sequence 23, Appl
38	2037.5	79.6	469	3	US-08-437-642B-23	Sequence 23, Appl
39	2037.5	79.6	469	4	US-08-146-206C-23	Sequence 23, Appl
40	2030	79.3	451	4	US-09-247-352-3	Sequence 3, Appli
41	2030	79.3	451	4	US-09-466-635-3	Sequence 3, Appli
42	2024.5	79.1	453	4	US-09-301-593-18	Sequence 18, Appl
43	2023.5	79.0	454	2	US-07-934-373C-22	Sequence 22, Appl
44	2023.5	79.0	454	3	US-08-437-642B-22	Sequence 22, Appl
45	2023.5	79.0	454	4	US-08-146-206C-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-8
; Sequence 8, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
;   APPLICANT: Anderson, Darrell R.
;   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/487,550
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
;   INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 478 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-487-550-8

Query Match   100.0%; Score 2561; DB 3; Length 478;
Best Local Similarity   100.0%; Pred. No. 9.7e-199;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
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Db   1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60

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Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
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Db   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120

Qy  121 YISHCRGRGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 YISHCRGRGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240

Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300

Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360

Qy  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
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Db  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420

Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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Db  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 2
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
GENERAL INFORMATION:
..   APPLICANT: Gonzalez, Tania R.
..   APPLICANT: Leong, Steven R.
..   APPLICANT: Presta, Leonard G.
..   TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
..   TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
..   NUMBER OF SEQUENCES: 72
..   CORRESPONDENCE ADDRESS:
..   ADDRESSEE: Genentech, Inc.
..   STREET: 1 DNA Way
..   CITY: South San Francisco
..   STATE: California
..   COUNTRY: USA
..   ZIP: 94080
..   COMPUTER READABLE FORM:
..   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
..   COMPUTER: IBM PC compatible
..   OPERATING SYSTEM: PC-DOS/MS-DOS
..   SOFTWARE: WinPatin (Genentech)
..   CURRENT APPLICATION DATA:
..   APPLICATION NUMBER: US/09/027,449
..   FILING DATE: 20-Feb-1998
..   CLASSIFICATION: 435
..   PRIOR APPLICATION DATA:
..   APPLICATION NUMBER: 60/074,330
..   FILING DATE: 22-Jan-1998
..   PRIOR APPLICATION DATA:
..   APPLICATION NUMBER: 60/038,664
..   FILING DATE: 21-Feb-1997
..   ATTORNEY/AGENT INFORMATION:
..   NAME: Love, Richard B.
..   REGISTRATION NUMBER: 34,659
..   REFERENCE/DOCKET NUMBER: P1085R3-2
..   TELECOMMUNICATION INFORMATION:
..   TELEPHONE: 650/225-5530
..   TELEFAX: 650/952-9881
..   INFORMATION FOR SEQ ID NO: 71:
..   SEQUENCE CHARACTERISTICS:
..   LENGTH: 452 amino acids
..   TYPE: Amino Acid

; TOPOLOGY: Linear
US-09-027-449-71

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Query Match            85.3%;  Score 2184.5;  DB 3;  Length 452;
Best Local Similarity  89.2%;  Pred. No. 2.1e-168;
Matches   411;  Conservative  16;  Mismatches 23;  Indels 11;  Gaps  3;

Qy   20 EVQLVESGGGLVQPCGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
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Db    1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYI--DPSNGET 58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
        ...::|:|||||||.|||...||||.||:.||||||||       .:.::|:: .:.:
Db   59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC------ARGDYRYNGDWFFDV 111

Qy  138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 171

Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
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Db  172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 231

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  232 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
        |||||||||:.|||||||||||||||||||||||||||||||||||||||||||||||||
Db  352 QVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411

Qy  438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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Db  412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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RESULT 3
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
GENERAL INFORMATION:
..   APPLICANT: Gonzalez, Tania R.
..   APPLICANT: Leong, Steven R.
..   APPLICANT: Presta, Leonard G.
..   TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
..   TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
..   NUMBER OF SEQUENCES: 72
..   CORRESPONDENCE ADDRESS:
..   ADDRESSEE: Genentech, Inc.
..   STREET: 1 DNA Way
..   CITY: South San Francisco
..   STATE: California
..   COUNTRY: USA
..   ZIP: 94080
..   COMPUTER READABLE FORM:
..   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
..   COMPUTER: IBM PC compatible
..   OPERATING SYSTEM: PC-DOS/MS-DOS
..   SOFTWARE: WinPatin (Genentech)
..   CURRENT APPLICATION DATA:
..   APPLICATION NUMBER: US/09/026,985
..   FILING DATE: 20-Feb-1998
..   CLASSIFICATION:
..   ATTORNEY/AGENT INFORMATION:
..   NAME: Love, Richard B.
..   REGISTRATION NUMBER: 34,659
..   REFERENCE/DOCKET NUMBER: P1085R3-1
..   TELECOMMUNICATION INFORMATION:
..   TELEPHONE: 650/225-5530

Right column

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;    TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 452 amino acids
;      TYPE: Amino Acid
;      TOPOLOGY: Linear
; US-09-026-985-71
;
; Query Match         85.3%;  Score 2184.5;  DB 4;  Length 452;
; Best Local Similarity   89.2%;  Pred. No. 2.1e-168;
; Matches  411;  Conservative  16;  Mismatches  23;  Indels  11;  Gaps  3;
;
Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
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Db    1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWRQAPGKGLEWVGYI--DPSNGET 58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YPEF 137
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Db   59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC------ARGDYRYNGDWFFDV 111

Qy  138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 171

Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
         |||||||||||||||||||||||||||||||||||||||||||||:| ||||||||||
Db  172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 231

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  232 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
         ||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db  352 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411

Qy  438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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Db  412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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; INFORMATION FOR SEQ ID NO: 71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 452 amino acids
;      TYPE: Amino Acid
;      TOPOLOGY: Linear
; US-09-121-952A-71
;
; Query Match         85.3%;  Score 2184.5;  DB 4;  Length 452;
; Best Local Similarity   89.2%;  Pred. No. 2.1e-168;
; Matches  411;  Conservative  16;  Mismatches  23;  Indels  11;  Gaps  3;
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RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
;    APPLICANT: Genentech, Inc., Hsei, Vanessa
;    APPLICANT: Koumenis, Iphigenia
;    APPLICANT: Leong, Steven R.
;    APPLICANT: Presta, Leonard G.
;    APPLICANT: Shahrokh, Zahra
;    APPLICANT: Zapata, Gerardo A.
;    TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES: 72
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Left column

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;    TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 452 amino acids
;      TYPE: Amino Acid
;      TOPOLOGY: Linear
; US-09-026-985-71
;
; Query Match         85.3%;  Score 2184.5;  DB 4;  Length 452;
; Best Local Similarity   89.2%;  Pred. No. 2.1e-168;
; Matches  411;  Conservative  16;  Mismatches  23;  Indels  11;  Gaps  3;
;
Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
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Db    1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWRQAPGKGLEWVGYI--DPSNGET 58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YPEF 137
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Db   59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC------ARGDYRYNGDWFFDV 111

Qy  138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 171

Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
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Db  172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 231

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  232 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
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Db  292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
         ||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db  352 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411

Qy  438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
         |||||||||||||||||||||||||||||||||||||||||
Db  412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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RESULT 4
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
;    APPLICANT: Genentech, Inc., Hsei, Vanessa
;    APPLICANT: Koumenis, Iphigenia
;    APPLICANT: Leong, Steven R.
;    APPLICANT: Presta, Leonard G.
;    APPLICANT: Shahrokh, Zahra
;    APPLICANT: Zapata, Gerardo A.
;    TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES: 72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Genentech, Inc.
;      STREET: 1 DNA Way
;      CITY: South San Francisco
;      STATE: California
;      COUNTRY: USA
;      ZIP: 94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/121,952A
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CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-234-340A-71

Query Match   85.3%; Score 2184.5; DB 4; Length 452;
Best Local Similarity   89.2%; Pred. No. 2.1e-168;
Matches   411; Conservative   16; Mismatches   23; Indels   11; Gaps   3;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT   79
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Db   1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYI--DPSNGET   58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF   137
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Db   59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC------ARGDYRYNGDWFFDV   111

Qy   138 WGGGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG   197
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Db   112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG   171

Qy   198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC   257
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC   231

Qy   258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN   317
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   232 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN   291

Qy   318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP   377
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP   351

Qy   378 QVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL   437
         |||||||||::|:|||||||||||||||||||||||||||||||||||||||||||||||
Db   352 QVVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL   411

Qy   438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   478
         |||||||||||||||||||||||||||||||||||||||||
Db   412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   452

RESULT 6
US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D2
; CURRENT APPLICATION NUMBER: US/09/679,397
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

Query Match   83.8%; Score 2146.5; DB 4; Length 449;
Best Local Similarity   88.3%; Pred. No. 2.5e-165;
Matches   408; Conservative   12; Mismatches   25; Indels   17; Gaps   3;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT   79
         |||||||||||||||||||||||| |||: |||:|||||||||:|||||: | |:|
Db   1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVA--RIYPTNGYT   58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG---YF   135
         .||:||| ||||| | ||:|||||:|||::|||||||||: |:
Db   59 RYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSR---------WGGDGFYAM   107

Qy   136 EFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT   195
         ::||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT   167

Qy   196 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTH   255
         ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db   168 SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH   227

Qy   256 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV   315
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   228 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV   287

Qy   316 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR   375
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   288 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR   347

Qy   376 EPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF   435
         ||||||||||::|:||||||||||||||||||||||||||||||||||||||||||||||
Db   348 EPQVVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF   407

Qy   436 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG   477
         ||||||||||||||||||||||||||||||||||||||||||
Db   408 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG   449

RESULT 7
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1D1
; CURRENT APPLICATION NUMBER: US/09/680,148

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; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
US-09-680-148-2
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Query Match             83.8%;   Score 2146.5; DB 4; Length 449;
Best Local Similarity   88.3%;   Pred. No. 2.5e-165;
Matches  408;  Conservative  12; Mismatches  25; Indels  17; Gaps   3;

Qy   20  EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT   79
         ||||||||||||||||||||||||||| |||||| ||||||| |
Db    1  EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVA--RIYPTNGYT   58

Qy   80  EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG----YF  135
         ||    ||||||| ||::| |||||:|| :|||||||||:            ||
Db   59  RYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSR---------WGGDGFYAM   107

Qy  136  EFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT  195
         ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  108  DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT  167

Qy  196  SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTH  255
         |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  168  SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH  227

Qy  256  TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV  315
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  228  TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV  287

Qy  316  HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR  375
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  288  HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR  347

Qy  376  EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF  435
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  348  EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF  407

Qy  436  FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG  477
         ||||||||||||||||||||||||||||||||||||||||||
Db  408  FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG  449
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RESULT 8
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-157-101A-7
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Query Match             83.5%;   Score 2138.5; DB 1; Length 459;
Best Local Similarity   87.2%;   Pred. No. 1.1e-164;
Matches  409;  Conservative  14; Mismatches  35; Indels  11; Gaps   3;

Qy   11  VAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFI   70
         :  ||||||||||||||||||||||| |||||| ||||||| :
Db    1  VGLLRGVCQCQVQLVESGGGVVQPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVI   60

Qy   71  RNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVC  130
         :  ||:||  | |||||||| ||::| |||||||:|| :| :||||
Db   61  LY--DGNHKFYADSVKGRFTISRDNSKNTLYLEVKSLQTEDTGVYYCIRDQ-------T  110

Qy  131  YGGY-FEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW  189
         ||||  |||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  111  YGVHRFDSWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW  170

Qy  190  NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK  249
         |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db  171  NSGALASGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK  230

Qy  250  SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY  309
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  231  SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY  290

Qy  310  VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK  369
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  291  VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK  350

Qy  370  AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  429
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  351  AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL  410

Qy  430  DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  411  DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  459
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RESULT 9
US-08-887-352B-18
; Sequence 18, Application US/08887352B
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
```

```
                    STREET:  1 DNA Way
                    CITY:  South San Francisco
                    STATE:  California
                    COUNTRY:  USA
                    ZIP:  94080
           COMPUTER READABLE FORM:
                    MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
                    COMPUTER:  IBM PC compatible
                    OPERATING SYSTEM:  PC-DOS/MS-DOS
                    SOFTWARE:  WinPatin (Genentech)
           CURRENT APPLICATION DATA:
                    APPLICATION NUMBER:  US/08/887,352B
                    FILING DATE:  03-Jul-1997
                    CLASSIFICATION:  530
           ATTORNEY/AGENT INFORMATION:
                    NAME:  Svoboda, Craig G.
                    REGISTRATION NUMBER:  39,044
                    REFERENCE/DOCKET NUMBER:  P1123
           TELECOMMUNICATION INFORMATION:
                    TELEPHONE:  650/225-1489
                    TELEFAX:  650/952-9881
           INFORMATION FOR SEQ ID NO:  18:
                    SEQUENCE CHARACTERISTICS:
                    LENGTH:  451 amino acids
                    TYPE:  Amino Acid
                    TOPOLOGY:  Linear
US-08-887-352B-18
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Query Match        83.4%;  Score 2135;  DB 2;  Length 451;
Best Local Similarity  88.5%;  Pred. No. 2.1e-164;
Matches 408;  Conservative  14;  Mismatches  27;  Indels  12;  Gaps  4;

Qy    20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT  78
            ||||||||||||||||||||:||||||: :  |||||||||||||:  : |||| ||
Db     1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIK---YSGE  57

Qy    79 TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF  137
           |:| |||||||:|||||||  |||:|:| ||||||||  || |   :|:
Db    58 TKYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGWHFAV  110

Qy   138 WGGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  197
           ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111 WGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  170

Qy   198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC  257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC  230

Qy   258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN  317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN  290

Qy   318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  350

Qy   378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  410

Qy   438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
           |||||||||||||||||||||||||||||||||||||||||
Db   411 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  451
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```
RESULT 10
US-09-109-207C-18
; Sequence 18, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE:  P1123R1
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                    CURRENT APPLICATION NUMBER: US/09/109,207C
                    CURRENT FILING DATE:  1998-06-30
                    PRIOR APPLICATION NUMBER:  US 60/051,554
                    PRIOR FILING DATE:  1997-07-03
                    NUMBER OF SEQ ID NOS:  44
           SEQ ID NO 18
                    LENGTH:  451
                    TYPE:  PRT
                    ORGANISM:  Artificial
                    FEATURE:
                    NAME/KEY:  Artificial
                    LOCATION:  1-451
                    OTHER INFORMATION:  Heavy chain sequence derived from MAE11
US-09-109-207C-18
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Query Match        83.4%;  Score 2135;  DB 4;  Length 451;
Best Local Similarity  88.5%;  Pred. No. 2.1e-164;
Matches 408;  Conservative  14;  Mismatches  27;  Indels  12;  Gaps  4;

Qy    20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT  78
            ||||||||||||||||||||:||||||: :  |||||||||||||:  : |||| ||
Db     1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIK---YSGE  57

Qy    79 TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF  137
           |:| |||||||:|||||||  |||:|:| ||||||||  || |   :|:
Db    58 TKYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGWHFAV  110

Qy   138 WGGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  197
           ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111 WGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  170

Qy   198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC  257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC  230

Qy   258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN  317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN  290

Qy   318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  350

Qy   378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  410

Qy   438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
           |||||||||||||||||||||||||||||||||||||||||
Db   411 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  451
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```
RESULT 11
US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT:  Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION:  Polypeptide variants
; FILE REFERENCE:  P1266R1
                    CURRENT APPLICATION NUMBER:  US/09/282,505A
                    CURRENT FILING DATE:  1999-03-31
                    NUMBER OF SEQ ID NOS:  2
           SEQ ID NO 2
                    LENGTH:  451
                    TYPE:  PRT
                    ORGANISM:  Artificial Sequence
                    FEATURE:
                    NAME/KEY:  Artificial Sequence
                    LOCATION:  1-451
                    OTHER INFORMATION:  Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2
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Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
        ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db  171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
        |||||||||:|| :||||||||||||||||||||||||||||||||||||||||||||||
Db  351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410

Qy  438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
        |||||||||||||||||||||||||||||||||||||||||
Db  411 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 13
US-09-296-005-18
; Sequence 18, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-18

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Query Match      83.4%;  Score 2135;  DB 4;   Length 451;
Best Local Similarity  88.5%;  Pred. No. 2.1e-164;
Matches  408;  Conservative 14;  Mismatches 27;  Indels 12;  Gaps  4;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
        ||||||||||||||||||||:||||| ||:  : : |||||||| ||||| ||   ||| |
Db    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIK---YSGE 57

Qy   79 TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
        |:| ||||:| |||||||||:| |||:||: |||||||||      :|:  |:|| |||
Db   58 TKYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGHWHFAV 110

Qy  138 WGGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  111 WGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
        ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db  171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
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Query Match      83.4%;  Score 2135;  DB 4;   Length 451;
Best Local Similarity  88.5%;  Pred. No. 2.1e-164;
Matches  408;  Conservative 14;  Mismatches 27;  Indels 12;  Gaps  4;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
        ||||||||||||||||||||:||||| ||:  : : |||||||| ||||| ||   ||| |
Db    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIK---YSGE 57

Qy   79 TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
        |:| ||||:| |||||||||:| |||:||: |||||||||      :|:  |:|| |||
Db   58 TKYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGHWHFAV 110

Qy  138 WGGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  111 WGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170
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RESULT 12
US-09-054-255-2
; Sequence 2, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody heavy chain
US-09-054-255-2

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Query Match      83.4%;  Score 2135;  DB 4;   Length 451;
Best Local Similarity  88.5%;  Pred. No. 2.1e-164;
Matches  408;  Conservative 14;  Mismatches 27;  Indels 12;  Gaps  4;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
        ||||||||||||||||||||:||||| ||:  : : |||||||| ||||| ||   ||| |
Db    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIK---YSGE 57

Qy   79 TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
        |:| ||||:| |||||||||:| |||:||: |||||||||      :|:  |:|| |||
Db   58 TKYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGHWHFAV 110

Qy  138 WGGQALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  111 WGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170
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Db   291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
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Db   378 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
                ||||||||:|:||||||||||||||||||||||||||||||||||||||||||

Qy   351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410

Qy   438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                ||||||||||||||||||||||||||||||||||||||||

Db   411 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
GENERAL INFORMATION:
  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
  TITLE OF INVENTION: Improving Polypeptides
  NUMBER OF SEQUENCES: 26
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 1 DNA Way
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94080
  COMPUTER READABLE FORM:
    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: WinPatin (Genentech)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/887,352B
    FILING DATE: 03-Jul-1997
    CLASSIFICATION: 530
  ATTORNEY/AGENT INFORMATION:
    NAME: Svoboda, Craig G.
    REGISTRATION NUMBER: 39,044
    REFERENCE/DOCKET NUMBER: P1123
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650/225-1489
    TELEFAX: 650/952-9881
  INFORMATION FOR SEQ ID NO: 16:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 451 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
US-08-887-352B-16

Query Match   83.2%; Score 2132; DB 2; Length 451;
Best Local Similarity   88.5%; Pred. No. 3.7e-164;
Matches   408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
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Db   1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLEWVASI---TYDGS 57

Qy   79 TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
              |||||||||| ||||||||||: |||| :|||||||||: :::------ ||||||
Db   58 TNYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGHWHFAV 110

Qy   138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy   198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
              |||||||||||||||||||||||||||||||||||||||||||||:||| ||||||||
Db   171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230

Qy   258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Db   291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
                ||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db   351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410
                ||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
Qy   438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                ||||||||||||||||||||||||||||||||||||||||
Db   411 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 14
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
GENERAL INFORMATION:
  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
  TITLE OF INVENTION: Improving Polypeptides
  NUMBER OF SEQUENCES: 26
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 1 DNA Way
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94080
  COMPUTER READABLE FORM:
    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: WinPatin (Genentech)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/887,352B
    FILING DATE: 03-Jul-1997
    CLASSIFICATION: 530
  ATTORNEY/AGENT INFORMATION:
    NAME: Svoboda, Craig G.
    REGISTRATION NUMBER: 39,044
    REFERENCE/DOCKET NUMBER: P1123
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650/225-1489
    TELEFAX: 650/952-9881
  INFORMATION FOR SEQ ID NO: 14:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 451 amino acids
    TYPE: Amino Acid
    TOPOLOGY: Linear
US-08-887-352B-14

Query Match   83.2%; Score 2132; DB 2; Length 451;
Best Local Similarity   88.5%; Pred. No. 3.7e-164;
Matches   408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
              ||||||||||||||||:||: :|: |||||||| |: |||:| ||||| ||||:---- :
Db   1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLEWVASI---TYDGS 57

Qy   79 TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
              |||||||||| ||||||||||: |||| :|||||||||: :::------ ||||||
Db   58 TNYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGHWHFAV 110

Qy   138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy   198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
              |||||||||||||||||||||||||||||||||||||||||||||:||| ||||||||
Db   171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230

Qy   258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy   318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
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Qy   318  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  377
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Db   291  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  350

Qy   378  QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  437
          ||||||||||: :|: :||||||||||||||||||||||||||||||||||||||||||
Db   351  QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  410

Qy   438  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
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Db   411  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  451
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Job time : 18.9836 secs

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            GenCore version 5.1.4 p5.4578
       Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    March 29, 2003, 09:14:52 ; Search time 18.3244 Seconds
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Title:           US-09-758-173-8
Perfect score:   2561
Sequence:        1 MGWSLILLFLVAVATRVQCE.........MHEALHNHYTQKSLSLSPGK 478

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters:   237916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Published Applications AA:*
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    8: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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   10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
   11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
   12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
   13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
   14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	2561	100.0	478	9	US-10-124-905-8	Sequence 8, Appli
2	2561	100.0	478	9	US-09-948-429B-8	Sequence 8, Appli
3	2184.5	85.3	452	9	US-09-726-258-71	Sequence 71, Appl
4	2160	84.3	451	10	US-09-822-698A-26	Sequence 26, Appl
5	2154	84.1	449	10	US-09-736-371B-21	Sequence 21, Appl
6	2149.5	83.9	731	10	US-09-825-012-46	Sequence 46, Appl
7	2149.5	83.9	741	10	US-09-825-012-55	Sequence 55, Appl
8	2144.5	83.7	729	10	US-09-825-012-52	Sequence 52, Appl
9	2144.5	83.7	739	10	US-09-825-012-61	Sequence 61, Appl
10	2138.5	83.5	730	10	US-09-825-012-49	Sequence 49, Appl
11	2138.5	83.5	740	10	US-09-825-012-58	Sequence 58, Appl
12	2135	83.4	451	10	US-09-920-171-18	Sequence 18, Appl
13	2132	83.2	451	9	US-09-925-179-65	Sequence 65, Appl
14	2132	83.2	451	10	US-09-920-171-14	Sequence 14, Appl
15	2132	83.2	451	10	US-09-920-171-16	Sequence 16, Appl
16	2132	83.2	453	9	US-09-925-179-8	Sequence 8, Appli
17	2132	83.2	453	10	US-09-802-077-8	Sequence 8, Appli
18	2132	83.2	453	10	US-09-802-096-8	Sequence 8, Appli
19	2129	83.1	451	9	US-09-925-179-66	Sequence 66, Appl
20	2122	82.9	451	9	US-09-925-179-68	Sequence 68, Appl
21	2091	81.6	476	10	US-09-747-669-3	Sequence 3, Appli
22	2073.5	81.0	475	10	US-09-740-002-25	Sequence 25, Appli
23	2073	80.9	476	9	US-10-124-905-4	Sequence 4, Appli
24	2073	80.9	476	10	US-09-948-429B-4	Sequence 4, Appli
25	2071.5	80.9	475	10	US-09-740-002-27	Sequence 27, Appl
26	2053	80.2	476	9	US-10-124-905-12	Sequence 12, Appl
27	2053	80.2	476	9	US-09-948-429B-12	Sequence 12, Appl
28	2004	78.3	443	10	US-09-917-410-4	Sequence 4, Appli
29	1997	78.0	470	10	US-09-859-053-36	Sequence 36, Appl
30	1996	77.9	470	10	US-09-859-053-32	Sequence 32, Appl
31	1992	77.8	451	9	US-09-996-288-230	Sequence 230, App
32	1989.5	77.7	450	9	US-09-996-288-220	Sequence 220, App
33	1989.5	77.7	450	10	US-09-796-848A-37	Sequence 37, Appl
34	1988.5	77.6	450	9	US-09-996-288-216	Sequence 216, App
35	1988.5	77.6	450	9	US-09-996-288-218	Sequence 218, App
36	1988.5	77.6	450	9	US-09-996-288-250	Sequence 250, App
37	1988.5	77.6	450	9	US-09-796-848A-43	Sequence 43, Appl
38	1988.5	77.6	450	10	US-09-796-848A-49	Sequence 49, Appl
39	1987.5	77.6	450	9	US-09-996-288-222	Sequence 222, App
40	1987.5	77.6	450	9	US-09-996-288-224	Sequence 224, App
41	1987.5	77.6	450	9	US-09-996-288-248	Sequence 248, App
42	1987.5	77.6	450	10	US-09-796-848A-39	Sequence 39, Appl
43	1987.5	77.6	450	10	US-09-796-848A-41	Sequence 41, Appl
44	1984.5	77.5	450	9	US-09-996-288-228	Sequence 228, App
45	1984.5	77.5	450	10	US-09-796-848A-47	Sequence 47, Appl

ALIGNMENTS

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RESULT 1
US-10-124-905-8
; Sequence 8, Application US/10124905
; Patent No. US2002016613A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, Darrell R.
;  TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;  TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;  TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;  TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;   STREET: 699 Prince Street
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22314
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/124,905
;   FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/383,916
;   FILING DATE:
;   APPLICATION NUMBER: US 08/487,550
;   FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-131
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-836-6620
;   TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 478 amino acids
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;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-10-124-905-8

Query Match        100.0%;   Score 2561;  DB 9;  Length 478;
Best Local Similarity   100.0%;  Pred. No. 1.4e-129;  Indels  0;  Gaps  0;
Matches  478;  Conservative  0;  Mismatches  0;

Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60

Qy   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120

Qy  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180

Qy  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240

Qy  241  KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300

Qy  301  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360

Qy  361  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420

Qy  421  NYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  NYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478


RESULT 2
US-09-948-429B-8
; Sequence 8, Application US/09948429B
; Patent No. US2002017769BA1
; GENERAL INFORMATION:
APPLICANT:  Anderson, Darrell R.
TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION:  PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES:  12
CORRESPONDENCE ADDRESS:
   ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
   STREET:  699 Prince Street
   CITY:  Alexandria
   STATE:  VA
   COUNTRY:  USA
   ZIP:  22314
COMPUTER READABLE FORM:
   MEDIUM TYPE:  Floppy disk
   COMPUTER:  IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:  PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:  US/09/948,429B
   FILING DATE:
   CLASSIFICATION:
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:  09/383,916
   FILING DATE:
   APPLICATION NUMBER:  US 08/487,550
```

```
;   FILING DATE:  07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Teskin, Robin L.
;   REGISTRATION NUMBER:  35,030
;   REFERENCE/DOCKET NUMBER:  012712-131
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  703-836-6620
;   TELEFAX:  703-836-2021
; INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  478 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-09-948-429B-8

Query Match        100.0%;   Score 2561;  DB 9;  Length 478;
Best Local Similarity   100.0%;  Pred. No. 1.4e-129;  Indels  0;  Gaps  0;
Matches  478;  Conservative  0;  Mismatches  0;

Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60

Qy   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120

Qy  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180

Qy  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240

Qy  241  KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300

Qy  301  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360

Qy  361  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420

Qy  421  NYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  NYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478


RESULT 3
US-09-726-258-71
; Sequence 71, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
APPLICANT:  Genentech, Inc., Hsei, Vanessa
APPLICANT:  Koumenis, Iphigenia
APPLICANT:  Leong, Steven R.
APPLICANT:  Presta, Leonard G.
APPLICANT:  Shahrokh, Zahra
APPLICANT:  Zapata, Gerardo A.
TITLE OF INVENTION:  ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION:  HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES:  72
CORRESPONDENCE ADDRESS:
   ADDRESSEE:  Genentech, Inc.
   STREET:  1 DNA Way
   CITY:  South San Francisco
   STATE:  California
   COUNTRY:  USA
```

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        ZIP:  94080
   COMPUTER READABLE FORM:
        MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
        COMPUTER:  IBM PC compatible
        OPERATING SYSTEM:  PC-DOS/MS-DOS
        SOFTWARE:  WinPatin (Genentech)
   CURRENT APPLICATION DATA:
        APPLICATION NUMBER:  US/09/726,258
        FILING DATE:
        CLASSIFICATION:
   PRIOR APPLICATION DATA:
        APPLICATION NUMBER:  09/234,182
        FILING DATE:
   PRIOR APPLICATION DATA:
        APPLICATION NUMBER:  60/094003
        FILING DATE:  24-JUL-1998
   ATTORNEY/AGENT INFORMATION:
        NAME:  Love, Richard B.
        REGISTRATION NUMBER:  34,659
        REFERENCE/DOCKET NUMBER:  P1085R4-1A
   TELECOMMUNICATION INFORMATION:
        TELEPHONE:  650/225-5530
        TELEFAX:  650/952-9881
   INFORMATION FOR SEQ ID NO:  71:
        SEQUENCE CHARACTERISTICS:
        LENGTH:  452 amino acids
        TYPE:  Amino Acid
        TOPOLOGY:  Linear
   US-09-726-258-71

Query Match     85.3%;  Score 2184.5;  DB 9;  Length 452;
Best Local Similarity   89.2%;  Pred. No. 1.5e-109;
Matches   411;  Conservative   16;  Mismatches   23;  Indels   11;  Gaps    3;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTESDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
         |||||| ||||||||||| |||||    ||:-||     ||:||    ||||||||||||
Db    1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMWVRQAPGKGLEWVGYI--DPSNGET 58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
         |  |||:||     |||||||       |:|:|||||
Db   59 TYNQFKGRFTLSRDNSKNTAYLQMNSLRAEDTAYYC------ARGDYRYNGDWFFDV 111

Qy  138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 171

Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
         ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 231

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  232 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
         ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  352 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411

Qy  438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
         |||||||||||||||||||||||||||||||||||||||||
Db  412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452

RESULT 4
US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US2002014 6750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
```

```
;   APPLICANT:  Henderikx, Maria P.G.
;   TITLE OF INVENTION:  MUCIN-1 Specific Binding Members and Methods of Use Thereof
;   FILE REFERENCE:  DYX-015.1 US
;   CURRENT APPLICATION NUMBER:  US/09/822,698A
;   CURRENT FILING DATE:  2001-03-30
;   PRIOR APPLICATION NUMBER:  US 09/538,913
;   PRIOR FILING DATE:  2000-03-30
;   NUMBER OF SEQ ID NOS:  112
;   SOFTWARE:  Microsoft Word
;   SEQ ID NO 26
;   LENGTH:  451
;   TYPE:  PRT
;   ORGANISM:  artificial sequence
;   FEATURE:
;   OTHER INFORMATION:  immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26

Query Match     84.3%;  Score 2160;  DB 10;  Length 451;
Best Local Similarity   89.8%;  Pred. No. 3e-108;
Matches   412;  Conservative   12;  Mismatches   27;  Indels    8;  Gaps    3;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
         :|||||||||||||||||||||||||    ||||    :||| ||| ||:|:|
Db    1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISG--SGGST 58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGGYFEFWG 139
         :||| ||||||||     || :|:|||     :||
Db   59 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA---KHTGGGV--WDPIDYWG 112

Qy  140 QGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  113 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 172

Qy  200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP 259
         ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  173 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 232

Qy  260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  233 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 292

Qy  320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  293 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 352

Qy  380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  353 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 412

Qy  440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
         |||||||||||||||||||||||||||||||||||||||
Db  413 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 5
US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
;   APPLICANT:  Waldmann, Herman
;   APPLICANT:  Frewin, Mark
;   TITLE OF INVENTION:  AGLYCOSYLATED ANTIBODIES
;   FILE REFERENCE:  Waldmann
;   CURRENT APPLICATION NUMBER:  US/09/736,371B
;   CURRENT FILING DATE:  2002-04-25
;   PRIOR APPLICATION NUMBER:  PCT/GB99/02380
;   PRIOR FILING DATE:  1998-07-21
;   PRIOR APPLICATION NUMBER:  9815909.8
;   PRIOR FILING DATE:  1999-07-21
;   NUMBER OF SEQ ID NOS:  30
;   SOFTWARE:  PatentIn Ver. 2.1
;   SEQ ID NO 21
;   LENGTH:  449
```

;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-736-371B-21

Query Match   84.1%;   Score 2154;   DB 10;   Length 449;
Best Local Similarity   89.5%;   Pred. No. 6.1e-108;
Matches   411;   Conservative   9;   Mismatches   29;   Indels   10;   Gaps   2;

```
Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGT  79
           ||||||||||||||||||||||| ||:||:|||:|||  ||| :||| || |||
Db    1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFPMAWVRQAPGKGLEWVSTI--STSGGRT  58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGYFEFWG 139
          ||| :|||||||||||:| | |||||||:||||||||||    |::||
Db   59 YYRDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFR------QYSGGFDYWG 110

Qy  140 QGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  111 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170

Qy  200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP 259
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db  171 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230

Qy  260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAK 319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHNAK 290

Qy  320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
          |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  291 TKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350

Qy  380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410

Qy  440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
          |||||||||||||||||||||||||||||||||||||||
Db  411 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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RESULT 6
US-09-825-012-46
;   Sequence 46, Application US/0982S012
;   Patent No. US20020122798A1
;   GENERAL INFORMATION:
;   APPLICANT: Young, Robert
;   TITLE OF INVENTION: Compounds for Targeting
;   FILE REFERENCE: 43191-256808
;   CURRENT APPLICATION NUMBER: US/09/825,012
;   CURRENT FILING DATE: 2001-04-03
;   PRIOR APPLICATION NUMBER: US 60/237,159
;   PRIOR FILING DATE: 2000-10-02
;   PRIOR APPLICATION NUMBER: GB 0008049.9
;   PRIOR FILING DATE: 2000-04-03
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 46
;   LENGTH: 731
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-46

Query Match   83.9%;   Score 2149.5;   DB 10;   Length 731;
Best Local Similarity   84.9%;   Pred. No. 1.7e-107;
Matches   406;   Conservative   21;   Mismatches   40;   Indels   11;   Gaps   2;

```
Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
          ||||  |||:|||:| | ::|| :||| : |||| ::||| ::||||:::||::||||||
Db    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP  60
```

RESULT 7
US-09-825-012-55
;   Sequence 55, Application US/09825012
;   Patent No. US2002012798A1
;   GENERAL INFORMATION:
;   APPLICANT: Young, Robert
;   TITLE OF INVENTION: Compounds for Targeting
;   FILE REFERENCE: 43191-256808
;   CURRENT APPLICATION NUMBER: US/09/825,012
;   CURRENT FILING DATE: 2001-04-03
;   PRIOR APPLICATION NUMBER: US 60/237,159
;   PRIOR FILING DATE: 2000-10-02
;   PRIOR APPLICATION NUMBER: GB 0008049.9
;   PRIOR FILING DATE: 2000-04-03
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 55
;   LENGTH: 741
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-55

Query Match   83.9%;   Score 2149.5;   DB 10;   Length 741;
Best Local Similarity   84.9%;   Pred. No. 1.7e-107;
Matches   406;   Conservative   21;   Mismatches   40;   Indels   11;   Gaps   2;

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Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
          ||||  |||:|||:| | ::|| :||| : |||| ::||| ::||||:::||::||||||
Db    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP  60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
          |||  || |  |:  :   |  | |:||||||||:|||||| |||:|| ||||||||  |
Db   61 GKGLEWVGEI--LPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSLRSEDTAVYYCARS 118

Qy  121 YISHCRGGVCYGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
           | :|     |  :|  |:| |:||||||||||||||||||||||||||||||||||||
Db  119 YDF-------AWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 169

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  170 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 229
```

```
Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
        ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  230 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 289

Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  290 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349

Qy  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409

Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  410 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
```

RESULT 8
US-09-825-012-52
; Sequence 52, Application US/09825012
; Patent No. US2002012279BA1
; GENERAL INFORMATION:
;   APPLICANT: Young, Robert
;   TITLE OF INVENTION: Compounds for Targeting
;   FILE REFERENCE: 43191-256808
;   CURRENT APPLICATION NUMBER: US/09/825,012
;   CURRENT FILING DATE: 2001-04-03
;   PRIOR APPLICATION NUMBER: US 60/237,159
;   PRIOR FILING DATE: 2000-10-02
;   PRIOR APPLICATION NUMBER: GB 0008049.9
;   PRIOR FILING DATE: 2000-04-03
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 729
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-52

  Query Match   83.7%; Score 2144.5; DB 10; Length 729;
  Best Local Similarity   84.9%; Pred. No. 3.1e-107;
  Matches   405; Conservative   21; Mismatches   40; Indels   11; Gaps   2;

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Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
        ||||  |||||| ||     :|||||  : ||:||| |   ||  |||   ::| | ||||
Db    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
        ||| |||| |     :   : :  |:  || |:|: : ||:|| :::: :|||||||  :
Db   61 GKGLEWVGEI--LPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSSLRSEDTAVYYCARS 118

Qy  121 YISHCRGGVCYGGYFEFWGQGALTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
                     :||  ::  |:|| |: |||||||||||||||||||||||||||||||
Db  119 YDF-------AWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 169

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  170 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 229

Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  230 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 289

Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  290 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349

Qy  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409

Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  410 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
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Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 477
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  410 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 466
```

RESULT 9
US-09-825-012-61
; Sequence 61, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
;   APPLICANT: Young, Robert
;   TITLE OF INVENTION: Compounds for Targeting
;   FILE REFERENCE: 43191-256808
;   CURRENT APPLICATION NUMBER: US/09/825,012
;   CURRENT FILING DATE: 2001-04-03
;   PRIOR APPLICATION NUMBER: US 60/237,159
;   PRIOR FILING DATE: 2000-10-02
;   PRIOR APPLICATION NUMBER: GB 0008049.9
;   PRIOR FILING DATE: 2000-04-03
;   NUMBER OF SEQ ID NOS: 102
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 739
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-61

  Query Match   83.7%; Score 2144.5; DB 10; Length 739;
  Best Local Similarity   84.9%; Pred. No. 3.1e-107;
  Matches   405; Conservative   21; Mismatches   40; Indels   11; Gaps   2;

```
Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
        ||||  |||||| ||     :|||||  : ||:||| |   ||  |||   ::| | ||||
Db    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
        ||| |||| |     :   : :  |:  || |:|: : ||:|| :::: :|||||||  :
Db   61 GKGLEWVGEI--LPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSSLRSEDTAVYYCARS 118

Qy  121 YISHCRGGVCYGGYFEFWGQGALTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
                     :||  ::  |:|| |: |||||||||||||||||||||||||||||||
Db  119 YDF-------AWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 169

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  170 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 229

Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  230 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 289

Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  290 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349

Qy  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409

Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 477
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  410 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 466
```

RESULT 10
US-09-825-012-49
; Sequence 49, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
;   APPLICANT: Young, Robert
;   TITLE OF INVENTION: Compounds for Targeting

; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-49

Query Match   83.5%; Score 2138.5; DB 10; Length 730;
Best Local Similarity   84.9%; Pred. No. 6.4e-107;
Matches 404; Conservative 21; Mismatches 40; Indels 11; Gaps   2;

Qy   1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
          ||||::||||||:||| | |:::||||||||||:|||::||||| :||::|| | |||||
Db   1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
          |||:|||||||||| | ||:||:|||||||||||::| ||||||:||||||||||||| :
Db   61 GKGLEWVGEI--LPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSSLRSEDTAVYYCARS 118

Qy   121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
          :|:|||||||||| |||||| | |:||:: ::|||||||||||||||||||||||||||
Db   119 YDF-------AWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 169

Qy   181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   170 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 229

Qy   241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 289

Qy   301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349

Qy   361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409

Qy   421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 465

RESULT 11
US-09-825-012-58
; Sequence 58, Application US/0982501   2
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 740
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-58

Query Match   83.5%; Score 2138.5; DB 10; Length 740;
Best Local Similarity   84.9%; Pred. No. 6.5e-107;
Matches 404; Conservative 21; Mismatches 40; Indels 11; Gaps   2;

Qy   1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
          ||||::||||||:||| | |:::||||||||||:|||::||||| :||::|| | |||||
Db   1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
          |||:|||||||||| | ||:||:|||||||||||::| ||||||:||||||||||||| :
Db   61 GKGLEWVGEI--LPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSSLRSEDTAVYYCARS 118

Qy   121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
          :|:|||||||||| |||||| | |:||:: ::|||||||||||||||||||||||||||
Db   119 YDF-------AWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 169

Qy   181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   170 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 229

Qy   241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   230 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 289

Qy   301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   290 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 349

Qy   361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   350 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 409

Qy   421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   410 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 465

RESULT 12
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. US2002005 4878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

Query Match   83.4%; Score 2135;   DB 10; Length 451;
Best Local Similarity   88.5%; Pred. No. 6.3e-107;
Matches 408; Conservative 14; Mismatches 27; Indels 12; Gaps   4;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78

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Db        ||||||||||||||||||||||||||||||:::  |:: |||||||| ||| |:
       1  EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIK---YSGE  57

Qy    79  TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
          ||:| ||||||||||||||:|: ||:: ||||||||
Db    58  TKYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYC------ARGSHYFGHWHFAV 110

Qy   138  WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111  WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy   198  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   171  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230

Qy   258  PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231  PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy   318  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   291  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350

Qy   378  QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
          ||||||||:: |||||||||||||||||||||||||||||||||||||||||||||||||
Db   351  QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410

Qy   438  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
          ||||||||||||||||||||||||||||||||||||||||
Db   411  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
```

RESULT 13
US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US2003004858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Tabl
US-09-925-179-65

Query Match   83.2%; Score 2132; DB 9; Pred. No. 9.2e-107;
Best Local Similarity   88.5%;
Matches 408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

```
Qy    20  EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
          | |||||||||||||||||||||:|::  ||:|||| :|
Db     1  EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI---TYDGS 57

Qy    79  TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
          ||| ||||||||||||:|: ||:: ||||||||
Db    58  TNYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYC------ARGSHYFGHWHFAV 110

Qy   138  WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111  WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy   198  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   171  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230
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RESULT 14
US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US2002054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match   83.2%; Score 2132; DB 10; Pred. No. 9.2e-107; Length 451;
Best Local Similarity   88.5%;
Matches 408; Conservative 13; Mismatches 28; Indels 12; Gaps 4;

```
Qy    20  EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
          | |||||||||||||||||||||:|::  ||:|||| :|
Db     1  EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI---TYDGS 57

Qy    79  TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
          ||| ||||||||||||:|: ||:: ||||||||
Db    58  TNYNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYC------ARGSHYFGHWHFAV 110

Qy   138  WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111  WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy   198  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   171  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230
```

```
Qy   258  PPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231  PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy   318  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   291  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350

Qy   378  QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
          |||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||
Db   351  QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410

Qy   438  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
          |||||||||||||||||||||||||||||||||||||||||
Db   411  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
```

```
Db   351  QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410
          |||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   438  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
          |||||||||||||||||||||||||||||||||||||||||
Db   411  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
```

Search completed: March 29, 2003, 09:38:42
Job time : 21.3244 secs

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RESULT 15
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US2002005487 8A1
; GENERAL INFORMATION:
;   APPLICANT: Lowman, Henry B.
;   APPLICANT: Presta, Leonard G.
;   APPLICANT: Jardieu, Paula M.
;   APPLICANT: Lowe, John
;   TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
;   FILE REFERENCE: P1123C2US
;   CURRENT APPLICATION NUMBER: US/09/920,171
;   CURRENT FILING DATE: 2001-08-01
;   PRIOR APPLICATION NUMBER: US 08/887,352
;   PRIOR FILING DATE: 1997-07-02
;   PRIOR APPLICATION NUMBER: US 09/296,005
;   PRIOR FILING DATE: 1999-04-21
;   NUMBER OF SEQ ID NOS: 44
;   SEQ ID NO 16
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

  Query Match             83.2%;  Score 2132;  DB 10;  Length 451;
  Best Local Similarity   88.5%;  Pred. No. 9.2e-107;
  Matches  408;  Conservative   13;  Mismatches   28;  Indels   12;  Gaps    4;

Qy    20  EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMY-WFRQAPGKGPEWVGFIRNKPNGGT 78
          |||||||||||||||||||||:::  ||||:  | :|::||||||||||| |:
Db     1  EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI---TYDGS 57

Qy    79  TEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
          |||| :|||||||||| |||:|||||:||| | ::      |: | :|
Db    58  TNYNPSVKGRITIISRDDSKNTFYLQMNSLRAEDTAVYYC------ARGSHYFGHWHFAV 110

Qy   138  WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   111  WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy   198  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   171  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230

Qy   258  PPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231  PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy   318  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   291  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350

Qy   378  QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
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                GenCore version 5.1.4_p5_4578
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      March 29, 2003, 09:06:23 ; Search time 49.1632 Seconds
                                         (without alignments)
                                         1295.559 Million cell updates/sec

Title:           US-09-758-173-8
Perfect score:   2561
Sequence:      1 MGWSLILLFLVAVATRVQCE.........MHEALHNHYTQKSLSLSPGK 478

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        908470 seqs, 13250620 residues

Total number of hits satisfying chosen parameters:      908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2561	100.0	478	19	AAW63763	Macaque primatized
2	2561	100.0	478	23	AAU11644	Protein sequence o
3	2555	99.8	478	18	AAW01820	Primatised anti-hu
4	2197	85.8	461	14	AAR42162	Anti-HIV-1 recombi
5	2184.5	85.3	452	20	AAY29458	Recombinant immuno
6	2184.5	85.3	452	21	AAB30322	Humanised anti-IL-
7	2184.5	85.3	452	21	AAY77766	Humanised anti-IL-
8	2183	85.2	474	23	AAO14065	Heavy chain protei
9	2177.5	85.0	477	22	AAU14288	Human novel protei
10	2175.5	84.9	452	19	AAW69316	Anti-IL-8 humanise
11	2172.5	84.8	475	13	AAR20057	Heavy chain of 3D6
12	2169.5	84.7	461	22	AAU07745	Humanised monoclon
13	2162	84.4	462	13	AAR22757	Reshaped CAMPATH-1
14	2161.5	84.4	444	21	AAY32263	Humanised anti-CD2
15	2160	84.3	451	22	AAE12715	Human recombinant
16	2156.5	84.2	481	13	AAR24442	Sequence of antibo
17	2154	84.1	449	21	AAY68810	A rat heavy chain
18	2151	84.0	477	15	AAR47453	chiT84.12 H3 heavy
19	2149.5	83.9	731	22	AAM52156	Humanised HMFG-1 h
20	2149.5	83.9	741	22	AAM52159	Humanised HMFG-1 h
21	2144.5	83.7	729	22	AAM52158	Humanised HMFG-1 h
22	2144.5	83.7	739	22	AAM52161	Humanised HMFG-1 h
23	2140	83.6	582	22	AAB81987	Humanised HMFG-1 h
24	2139	83.6	470	21	AAB08026	Ganglioside GD3 sp
25	2138.5	83.5	459	14	AAR42066	A dimeric anti-CD2
26	2138.5	83.5	730	22	AAM52157	Human anti-HBs hea
27	2138.5	83.5	740	22	AAM52160	Humanised HMFG-1 h
28	2137.5	83.5	465	22	AAB72228	Humanised HMFG-1 h
29	2137	83.4	466	13	AAR24812	Humanised 323/A3 (
30	2135	83.4	451	20	AAY50031	Sequence encoded b
31	2135	83.4	451	20	AAW95663	Human E27 anti-IgE
32	2135	83.4	451	21	AAB07473	Mus musculus anti-
33	2135	83.4	451	22	AAB74212	Amino acid sequenc
34	2135	83.4	451	22	AAB76952	E27 anti-IgE antib
35	2135	83.4	470	21	AAW90936	Full length heavy
36	2135	83.3	470	23	AAB74945	Humanised HFE7A de
37	2132.5	83.3	464	22	AAB72232	Humanised anti-Fas
38	2132	83.2	451	20	AAW95659	Humanised 323/A3 (
39	2132	83.2	451	20	AAW55661	Mus musculus anti-
40	2132	83.2	451	21	AAY85201	Mus musculus anti-
41	2132	83.2	451	22	AAB47088	Light chain anti-
42	2132	83.2	451	22	AAB76948	Anti-IgE antibody,
43	2132	83.2	451	22	AAB76950	Full length heavy
44	2132	83.2	453	14	AAR33311	Full length heavy
45	2132	83.2	453	21	AAY85199	Humanised MaE11 Ve
						Heavy chain amino

ALIGNMENTS

```
RESULT 1
AAW63763
ID   AAW63763 standard; Protein; 478 AA.
XX
AC   AAW63763;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7B6 heavy chain protein.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation.
XX
OS   Macaca fascicularis.
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997; 97WO-US19906.
XX
PR   08-NOV-1996; 96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P,  Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   N-PSDB; AAV35487.
XX
```

Left column:

```
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 4b; 87pp; English.
XX
CC   This sequence represents a primatized form of the antibody 7B6 heavy
CC   chain from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   MAb's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, Particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence   478 AA;

Query Match         100.0%;   Score 2561;  DB 19;  Length 478;
Best Local Similarity   100.0%;   Pred. No. 4.7e-152;
Matches  478;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120

Qy  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240

Qy  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300

Qy  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360

Qy  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420

Qy  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478

RESULT 2
AAU11644
ID   AAU11644 standard; Protein; 478 AA.
XX
AC   AAU11644;
XX
DT   12-MAR-2002  (first entry)
XX
```

Right column:

```
DE   Protein sequence of primatised form of the heavy chain of 7B6 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; mutein.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Hanna N,  Brams P;
XX
PI   2002-089895/12.
DR   N-PSDB; AAS17245.
XX
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 4b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present protein
CC   sequence represents the heavy chain of 7B6, a primatised antibody
CC   used in the invention to induce apoptosis.
XX
SQ   Sequence   478 AA;

Query Match         100.0%;   Score 2561;  DB 23;  Length 478;
Best Local Similarity   100.0%;   Pred. No. 4.7e-152;
Matches  478;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120

Qy  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180

Qy  181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
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Query Match   99.8%;   Score 2555;   DB 18;   Length 478;
Best Local Similarity 99.8%;   Pred. No. 1.1e-151;
Matches 477; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60

Qy    61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120

Qy   121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180

Qy   181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240

Qy   241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300

Qy   301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360

Qy   361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420

Qy   421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
```

RESULT 4
AAR42162
ID   AAR42162 standard; Protein; 461 AA.
XX
AC   AAR42162;
XX
DT   27-APR-1994 (first entry)
XX
DE   Anti-HIV-1 recombinant antibody 447-52D heavy chain.
XX
KW   Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW   HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW   acquired immune deficiency syndrome; chimeric antibody;
KW   surface glycoprotein gp120; V3 loop.
XX
OS   Homo sapiens.
XX
PN   WO9319785-A.
XX
PD   14-OCT-1993.
XX
PF   23-MAR-1993;   93WO-US02629.
XX
PR   01-APR-1992;   92US-0861701.
XX
PA   (MERI) MERCK & CO INC.
PA   (JOHN/) JOHNSON L S.
PA   (PFAR/) PFARR D S.
XX
PI   Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;
XX
DR   WPI; 1993-336600/42.
DR   N-PSDB; AAQ49834.
XX
PT   New recombinant human antibody - with HIV neutralising activity

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Db   181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300

Qy   301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360

Qy   361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420

Qy   421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
```

RESULT 3
AAW01820
ID   AAW01820 standard; Protein; 478 AA.
XX
AC   AAW01820;
XX
DT   25-MAY-1997 (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7B6 heavy chain.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7B6;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US10053.
XX
PR   07-JUN-1995;   95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   N-PSDB; AAT13847.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 8; Fig 9B; 81pp; English.
XX
CC   2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised
CC   forms of the light and heavy chains of cynomolgus monkey anti-human
CC   B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy
CC   variable genes (see also AAT62511 and AAT13847) are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of the primatised
CC   antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-19 and
CC   AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway,
CC   making them useful immunosuppressants for the treatment of
CC   autoimmune disorders and graft-versus-host disease.
XX
SQ   Sequence   478 AA;
```

```
PT  against at least two isolates, useful for preventing or treating
PT  infection in diagnosis, etc.
XX
PS  Example 9; Fig 2A; 154pp; English.
XX
CC  EBV-transformed cell lines and mouse-human heterohybridomas
CC  producing human MAbs specific for the gp120 V3 loop of HIV-1 MN
CC  isolate were obtained. MAb 447-52D was found to recognise the
CC  tetrapeptide motif GPGR, i.e. the Principal Neutralising
CC  Determinant common to the V3 loop of different HIV isolates.
CC  A recombinant Ab was produced in which the H chain V region was
CC  derived from 447-52D and to which a signal sequence and a H chain
CC  intronic sequence are appended, fused to a fragment contg. a short
CC  intronic segment of the human gamma 1 C region and the human gamma
CC  1 encoding domain in its genomic form.
XX
SQ  Sequence   461 AA;

Query Match             85.8%;  Score 2197;  DB 14;  Length 461;
Best Local Similarity   90.2%;  Pred. No. 2.4e-129;
Matches  416;  Conservative  14;  Mismatches  14;  Indels  29;  Gaps  1;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
            |||||:||||||| ||||||: ::|||:|||  ::|
Db    1 EVQLVESGGGLVKPGGSLRLTCVASGFTFSDVWLNMVRQAPGKGLEWVGRIKSRTDGGTT 60

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTSYISHCRG--GVCYGGYFEF 137
            :|||:|||||||||||:|||||||  ||:|||||||| ::  |  ||   ||  |
Db   61 DYAASVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCCTTDGFIMRGVSEDYYYYMDV 120

Qy  138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 WGKGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 180

Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db  181 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 240

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 300

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 360

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 420

Qy  438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
            |||||||||||||||||||||||||||||||||||||||||
Db  421 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 461


RESULT 5
AAY29458
ID  AAY29458 standard; Protein; 452 AA.
XX
AC  AAY29458;
XX
DT  05-OCT-1999  (first entry)
XX
DE  Recombinant immunoglobulin SEQ ID NO:71.
XX
KW  Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
KW  diagnosis; inflammatory disorder; conjugate; immunoglobulin;
KW  fusion protein.
XX
OS  Synthetic.
XX
PN  WO9937779-A1.
XX
```

```
PD  29-JUL-1999.
XX
PF  19-JAN-1999;  99WO-US01081.
XX
PR  24-JUL-1998;  98US-0122513.
PR  22-JAN-1998;  98US-0012116.
PR  20-FEB-1998;  98WO-US03337.
PR  24-JUL-1998;  98US-0121952.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;
PI  Zapata GA;
XX
DR  WPI; 1999-469134/39.
XX
PT  New conjugates of nonproteinaceous polymers with antibody fragments,
PT  used for treating inflammatory disorders
XX
PS  Disclosure; Page 354-355; 360pp; English.
XX
CC  The present invention describes a novel conjugate having one or more
CC  antibody fragments covalently attached to one or more nonproteinaceous
CC  polymer molecules, where the apparent size of the conjugate is at least
CC  about 500 kDa. Conjugates of antibody fragments which bind the human
CC  interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC  treating inflammatory disorders e.g. acute lung injury, ischaemic
CC  reperfusion disorder, and autoimmune diseases. They can also be used
CC  for treating e.g. inflammatory skin diseases including psoriasis and
CC  atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
CC  diseases. The conjugates can also be used as reagents in an animal
CC  model system for in vivo study of the biological functions of the
CC  antigen recognised by the conjugate. The present sequence represents
CC  a recombinant immunoglobulin protein from the present invention.
XX
SQ  Sequence   452 AA;

Query Match             85.3%;  Score 2184.5;  DB 20;  Length 452;
Best Local Similarity   89.2%;  Pred. No. 1.4e-128;
Matches  411;  Conservative  16;  Mismatches  23;  Indels  11;  Gaps  3;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
            ||||||:|||||||||||||: ::|||:||| |||||||:||||| ||:|
Db    1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYI--DPSNGET 58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTSYISHCRGG--GVCYGGYFEF 137
            :|||:||||||||||:|:|| ||:||:|::|:|||||||:  |  ||     ||  |
Db   59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC------ARGYRYNGDWFPDV 111

Qy  138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
            |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 171

Qy  198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
            |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db  172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 231

Qy  258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  232 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291

Qy  318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351

Qy  378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
            ||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||
Db  352 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411

Qy  438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
            |||||||||||||||||||||||||||||||||||||||||
Db  412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
```

RESULT 6
AAB30322
ID   AAB30322 standard; Protein; 452 AA.
XX
AC   AAB30322;
XX
DT   12-FEB-2001 (first entry)
XX
DE   Humanised anti-IL-8 antibody related protein SEQ ID NO: 71.
XX
KW   Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KW   adult respiratory distress syndrome; multiple organ failure;
KW   bacterial pneumonia; inflammatory bowel disease.
XX
OS   Unidentified.
XX
PN   US6113426-A.
XX
PD   17-OCT-2000.
XX
PF   20-FEB-1998;   98US-0026995.
XX
PR   21-FEB-1997;   97US-0038664.
PR   22-JAN-1998;   98US-0074330.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Presta LG, Leong SR, Gonzalez TN;
XX
DR   WPI; 2000-686027/67.
XX
PT   Humanized anti-interleukin 8 monoclonal antibody variant useful for
PT   treating inflammatory disorders, such as adult respiratory distress
PT   syndrome, hypovolemic shock and ulcerative colitis -
XX
PS   Disclosure; Column 199-202; 240pp; English.
XX
CC   The present invention provides a number of humanised monoclonal anti-IL-8
CC   antibodies which can be used in the diagnosis and treatment of
CC   inflammatory disorders, including adult respiratory distress syndrome,
CC   septic shock, multiple organ failure, bacterial pneumonia and
CC   inflammatory bowel disease. The present sequence comprises one of the
CC   antibodies of the invention.
XX
SQ   Sequence   452 AA;

Query Match   85.3%;   Score 2184.5;   DB 21;   Length 452;
Best Local Similarity 89.2%;   Pred. No. 1.4e-128;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
Db   1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYI--DPSNGET 58

Qy   80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
Db   59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC------ARGDYRYNGDWFFDV 111

Qy   138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
Db   112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 171

Qy   198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
Db   172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 231

Qy   258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
Db   232 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291

Qy   318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAPIEKTISKAGQPREP 377

Db   292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAPIEKTISKAGQPREP 351

Qy   378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
Db   352 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411

Qy   438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
Db   412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452

RESULT 7
AAY77766
ID   AAY77766 standard; Protein; 452 AA.
XX
AC   AAY77766;
XX
DT   06-JUN-2000 (first entry)
XX
DE   Humanised anti-IL-8 antibody related protein seq ID No:71.
XX
KW   Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4V1N35A;
KW   inflammatory disorder; adult respiratory distress syndrome;
KW   affinity purification.
XX
OS   Homo sapiens.
XX
PN   US6025158-A.
XX
PD   15-FEB-2000.
XX
PF   20-FEB-1998;   98US-0027449.
XX
PR   21-FEB-1997;   97US-0038664;
PR   22-JAN-1998;   98US-0074330.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Presta LG, Leong SR, Gonzalez TN;
XX
DR   WPI; 2000-181809/16.
XX
PT   New nucleic acid molecule encodes a polypeptide which is an
PT   anti-interleukin-8 monoclonal antibody or antibody fragment useful for
PT   the production of anti-interleukin-8 monoclonal antibodies or fragments
PT   -
XX
PS   Examples; Columns 199-202; 188pp; English.
XX
CC   The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
CC   (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs
CC   (complementarity determining regions) of the humanized anti-IL-8
CC   6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized
CC   anti-IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 MAbs and fragments
CC   can be used in diagnosis, for affinity purification of IL-8 from
CC   recombinant cell culture or natural sources and for the treatment of
CC   inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic
CC   acids encoding the anti-IL-8 MAb can be associated in a vector with
CC   another gene encoding another protein or protein fragment to produce a
CC   fusion protein which can make isolation and/or purification of the
CC   protein an easier process.
XX
SQ   Sequence   452 AA;

Query Match   85.3%;   Score 2184.5;   DB 21;   Length 452;
Best Local Similarity 89.2%;   Pred. No. 1.4e-128;
Matches 411; Conservative 16; Mismatches 23; Indels 11; Gaps 3;

Qy   20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGTT 79
Db   1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYI--DPSNGET 58

Qy   80 EYAASVKDRFTISRDDSKSIAVLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137

```
Db    59  TYNQKPFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC------ARGDYRYNGDWFFDV  111
               |||||   |||| :|||| :||||||||||||||             | | :|:|

Qy   138  WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  197
          ||||.||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   112  WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  171

Qy   198  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC  257
          |||||||||||||||||||||||||||||||||||||||||||||||| :||||||||||
Db   172  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC  231

Qy   258  PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN  317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   232  PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN  291

Qy   318  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   292  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  351

Qy   378  QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  437
          |||||||| ::||||||||||||||||||||||||||||||||||||||||||||||||
Db   352  QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL  411

Qy   438  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
          |||||||||||||||||||||||||||||||||||||||||
Db   412  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  452
```

RESULT 8
AAO14065
ID   AAO14065 standard; Protein; 474 AA.
XX
AC   AAO14065;
XX
DT   07-MAY-2002 (first entry)
XX
DE   Heavy chain protein of the monoclonal antibody from clone JA.
XX
KW   HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW   human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW   light chain; central nervous system; CNS; prophylactic therapy; clone JA.
XX
OS   Homo sapiens.
XX
PN   WO200188132-A2.
XX
PD   22-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US14468.
XX
PR   16-MAY-2000; 2000US-204518P.
XX
PA   (UXJE-) UNIV JEFFERSON THOMAS.
XX
PI   Hooper DC, Dietzschold B;
XX
DR   WPI; 2002-062381/08.
DR   N-PSDB; AAK98701.
XX
PT   Novel isolated human monoclonal rabies virus neutralising antibody
PT   useful for treating individual exposed to rabies virus and for
PT   preventing spread of rabies virus to central nervous system -
XX
PS   Claim 4; Page 23-24; 25pp; English.
XX
CC   This sequence represents the heavy chain protein of the monoclonal
CC   antibody from clone JA. The invention relates to an isolated human
CC   monoclonal rabies virus neutralising antibody (virucide) derived from
CC   cDNA clones encoding the antibody heavy and light chains expressed in
CC   heterologous expression systems and purified away from deleterious
CC   contaminants. The invention provides a fused gene encoding a chimeric
CC   immunoglobulin light chain and a fused gene encoding a chimeric
CC   immunoglobulin heavy chain. The antibody of the invention is useful for
CC   treating an individual exposed to a rabies virus by administering to the
CC   individual a therapeutically effective amount of the antibody, and
CC   preventing a spread of the rabies virus to the central nervous system
CC   (CNS). The antibody of the invention provides a safe and efficacious post
XX   -exposure prophylactic therapy for individuals exposed to a rabies virus.
SQ   Sequence 474 AA;

```
Query Match             85.2%;  Score 2183;  DB 23;  Length 474;
Best Local Similarity   86.7%;  Pred. No. 1.8e-128;
Matches  418;  Conservative   18;  Mismatches   34;  Indels   12;  Gaps   3;

Qy     1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
          | :||  |||| ||| | ||||||:|||||||||||||:|||:||||||:: || :|||||
Db     1  MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP  60

Qy    61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCT--  118
          ||| ||| :| ::  ::.|  ||||:|||||||||:||: |||:||| |||||||||     
Db    61  GKGLEWVSAI--SASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD  118

Qy   119  --TSYISHCRGGVCVGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL  176
            ::  |   ||  |    ||:|||||:|||||||||||||||||||||||||||||||||
Db   119  REVTMIVVLNGG------FDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL  172

Qy   177  VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK  236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173  VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK  232

Qy   237  PSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD  296
          |||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233  PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD  292

Qy   297  VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN  356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293  VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN  352

Qy   357  KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG  416
          |||||||||||||||||||||||||||||| ::|||||||||||||||||||||||||||
Db   353  KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG  412

Qy   417  QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413  QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  472

Qy   477  GK  478
          ||
Db   473  GK  474
```

RESULT 9
AAU14288
ID   AAU14288 standard; Protein; 477 AA.
XX
AC   AAU14288;
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human novel protein #159.
XX
KW   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.
XX
OS   Homo sapiens.
XX
PN   WO200155437-A2.
XX
PD   02-AUG-2001.
XX

PF
XX   25-JAN-2001; 2001WO-US02623.
PR
XX   25-JAN-2000; 2000US-0491404.
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-451939/48.
DR   N-PSDB; AAS22593.
XX
PT   Isolated polypeptides useful for treating anti-inflammatory diseases,
PT   nervous system disorders, and for regenerating bone and cartilage -
XX
PS   Example 4; Page 611-612; 894pp; English.
XX
CC   The invention relates to polynucleotides encoding novel human
CC   proteins or their active domains. The polypeptides, polynucleotides and
CC   antibodies raised against the polypeptides are used in a method of
CC   treatment of a mammal and prevention of disorders caused by the aberrant
CC   protein expression or activity. The polypeptides can be used as
CC   molecular weight markers, food supplements, and in antibody production.
CC   The polypeptides are used to identify compounds which bind to the
CC   polypeptides. Polynucleotides of the invention are used as probes and
CC   primers, for sequencing, for chromosome or gene mapping, in the
CC   production of recombinant proteins, and in generating anti-sense DNA or
CC   RNA and in gene therapy. Polypeptides of the invention can be used to
CC   target drugs to a tumour, in assays to determine biological activity, to
CC   raise antibodies/elicit an immune response, to determine quantitative
CC   protein levels, as tissue markers, and to isolate receptors or ligands.
CC   Polypeptides of the invention may also be useful in treating platelet
CC   disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC   ligament and/or nerve tissue, wound healing, treating burns, promoting
CC   the proliferation, differentiation and survival of stem cells, as a
CC   contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC   Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC   sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC   fungal infection or from autoimmunity, cancer, allergy, asthma,
CC   graft-versus-host disease, eczema, haemophilia, thrombosis,
CC   anti-inflammatory diseases, nervous system disorders, and infection.
CC   The present sequence represents a protein of the invention.
XX
SQ   Sequence   477 AA;

Query Match   85.0%; Score 2177.5; DB 22; Length 477;
Best Local Similarity   85.6%; Pred. No. 4e-128;
Matches 416; Conservative   20; Mismatches 33; Indels   17; Gaps 3;

```
Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                       ||| ||| |::|:| :|:||||||||||||||   ||||| ||:|: .:|:|:|
Db    1 MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
           ||| ||  || ||   .|| |||||||||||||||||: :||||| |:.|| ||||||||
Db   61 GKGLEWVAAIWY--DGSNKYYADSVKGRFTISRDNSKNTLYMQNSLRAEDTAVYYC--- 115

Qy  121 YISHCRGG------VCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAA 172
                       |::|  |:|:|:|||||||||||||||||||||||||||||||||
Db  116 ---AREGRWVRYTVTTIGYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA 171

Qy  173 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN 232
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  172 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN 231

Qy  233 VNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 292
         ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  232 VNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 291

Qy  293 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 352
         |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db  292 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 351

Qy  353 KVSNKALPAPIEKTISKAKGQPREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 412
         |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db  352 KVSNKALPAPIEKTISKAKGQPREPQVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW 411

Qy  413 ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 472
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  412 ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 471

Qy  473 SLSPGK 478
         ||||||
Db  472 SLSPGK 477
```

RESULT 10
AAW69316
ID   AAW69316 standard; protein; 452 AA.
XX
AC   AAW69316;
XX
DT   15-FEB-1999 (first entry)
XX
DE   Anti-IL-8 humanised antibody 6G4V11N35A.choSD.9.
XX
KW   Humanised antibody; chimeric antibody; monoclonal antibody; mouse;
KW   human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;
KW   inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW   ischaemic reperfusion; adult respiratory distress syndrome;
KW   dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
KW   rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
KW   leukocyte diapedesis; multiple organ injury syndrome; septicaemia;
KW   trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
KW   vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
KW   therapy; 6G4V11N35A.choSD.9.
XX
OS   Chimeric - Mus sp.
OS   Chimeric - Homo sapiens.
XX
PN   WO9837200-A2.
XX
PD   27-AUG-1998.
XX
PF   20-FEB-1998; 98WO-US03337.
XX
PR   22-JAN-1998; 98US-0012116.
PR   21-FEB-1997; 97US-0804444.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Hsei V, Koumenis I, Leong SR, Presta LR, Shahrokh Z;
PI   Zapata GA;
XX
DR   WPI; 1998-467563/40.
DR   N-PSDB; AAV44956.
XX
PT   New conjugates of antibody fragments - having covalently attached
PT   non-proteinaceous polymer molecules, particularly polyethylene
PT   glycol, for improving the residence time in the circulation.
XX
PS   Example P; Fig 48A-Z; 328pp; English.
XX
CC   This polypeptide is encoded by vector plasmid p6G4V11N35A.choSD.9
CC   (see AAV44956). It comprises a humanised 6G4V11N35A IgG containing
CC   complementarity determining regions of murine anti-interleukin-8
CC   (IL-8) monoclonal antibody (MAb) 6G5.2.5 (see AAW69309-10) in a human
CC   template. Humanised anti-IL-8 MAbs (see AAW69301-04) are described
CC   for use in diagnostic applications and in the treatment of
CC   inflammatory disorders. The invention provides conjugates of an
CC   antibody fragment and a polymer, such as PEG, that have improved
CC   half-life, mean residence time, and/or clearance rate. The
CC   conjugates can be used for immune therapy of e.g. psoriasis,
CC   responses associated with inflammatory bowel disease (such as
CC   Crohn's disease and ulcerative colitis), ischemic reperfusion,
CC   adult respiratory distress syndrome, dermatitis, meningitis,
CC   encephalitis, uveitis, autoimmune diseases such as rheumatoid

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CC    arthritis, Sjorgen's syndrome, vasculitis, diseases involving
CC    leukocyte diapedesis, central nervous system inflammatory disorder,
CC    multiple organ injury syndrome secondary to septicaemia or trauma,
CC    alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
CC    mediated diseases, inflammations of the lung, including pleurisy,
CC    alveolitis, vasculitis, pneumonia, chronic bronchitis,
CC    bronchiectasis, and cystic fibrosis.
XX
SQ    Sequence     452 AA;

Query Match        84.9%;   Score 2175.5;  DB 19;  Length 452;
Best Local Similarity  88.7%;  Pred. No. 5.1e-128;
Matches 409;  Conservative  17;  Mismatches  24;  Indels  11;  Gaps  3;

Qy    20  EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT  79
              ||||||||||||||||| :||| |:|: :|||||||||| : :||
Db     1  EVQLVQSGGGLVQPGGSLRLSCAASGYSFSHYMHWVRQAPGKGLEWVGYI--DPSNGET  58

Qy    80  EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
              ||||| | :|||:|| ::| : |:|            |  :|:
Db    59  TYNQKFKGRFTISRDNSKNTAYLQMNSLRAEDTAVYYC------ARGDYRYNGDWFFDV 111

Qy   138  WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
              ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   112  WGGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSA 171

Qy   198  VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257
              :|||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   172  LHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 231

Qy   258  PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   232  PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291

Qy   318  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   292  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351

Qy   378  QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
              |||||| :|:||||||||||||||||||||||||||||||||||||||||||||||||||
Db   352  QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411

Qy   438  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
              |||||||||||||||||||||||||||||||||||||||||
Db   412  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 11
AAR20057
ID    AAR20057  standard; Protein; 475 AA.
XX
AC    AAR20057;
XX
DT    25-MAR-1992  (first entry)
XX
DE    Heavy chain of 3D6 anti-HIV antibody.
XX
KW    Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;
KW    complementarity determining region.
XX
OS    Homo sapiens.
XX
FH    Key            Location/Qualifiers
FT    Peptide        1..19
FT                   /label= signal
FT    Region         20..49
FT                   /label= Framework_1
FT    Region         50..54
FT                   /label= CDR-1
FT    Region         55..68
FT                   /label= Framework_2
FT    Region         69..85
FT                   /label= CDR_2
```

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FT    Region         86..117
FT                   /label= Framework_3
FT    Region         118..134
FT                   /label= CDR_3
FT    Region         135..145
FT                   /label= Framework_4
FT    Region         146..475
FT                   /label= Constant_region
XX
PN    WO9118983-A.
XX
PD    12-DEC-1991.
XX
PF    28-MAY-1991;  91WO-1000067.
XX
PR    29-MAY-1990;  90AT-0001178.
XX
PA    (JUNG/) JUNGBAUER A.
XX
PI    Felgenhauer M,  Himmler G,  Kohl J,  Steindl F;
XX
DR    WPI; 1992-007468/01.
DR    N-PSDB; AAQ20066.
XX
PT    Recombinant protein which binds to complex viral antigen and
PT    HIV-1 - contains variable region of antibody derived from 3D6
PT    cell line, used for detecting HIV-1 antigen
XX
PS    Claim 2; Page 24; 52pp; German.
XX
CC    The variable region of the heavy chain is used in a recombinant
CC    protein with the variable region from the kappa light chain of 3D6,
CC    the two V regions being joined by a linker. The recombinant protein
CC    binds to HIV gp160.
CC    See also AAQ20067 and AAQ20068.
XX
SQ    Sequence     475 AA;

Query Match        84.8%;   Score 2172.5;  DB 13;  Length 475;
Best Local Similarity  86.2%;  Pred. No. 8.3e-128;
Matches 417;  Conservative  18;  Mismatches  34;  Indels  15;  Gaps  4;

Qy     1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
             :||:|::  :|:    :|||||:||||||||||||||||| ||||| |:||||||||
Db     1  MELGLSWIFLLAILKGVQCEVQLVSGGGLVQPGGSLRLSCAASGFTFNDYAMHVRQAP  60

Qy    61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
             |||| || : ::|  :| ||  ||||||||:|||||   ||||||| :|| ||:|||:
Db    61  GKGLEWVSGI--SWDSSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMALYYCV-- 116

Qy   121  YISHCRGGVCY----GGY-FEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALG 174
             ||: |:| |:      ||  : |||||| |||||||||||||||||||||||||||||||
Db   117  ----KGRDYYDSGGYFTVAPDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG 171

Qy   175  CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN 234
             ||||||||||||||||||||||| :|||||||||||||||||||||||||||||||||||
Db   172  CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN 231

Qy   235  HKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 294
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   232  HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV 291

Qy   295  VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 354
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   292  VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 351

Qy   355  SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 414
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   352  SNKALPAPIEKTISKAKGQPRRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 411

Qy   415  NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 474
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   412  NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 471
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          Matches  415;  Conservative  15;  Mismatches  31;  Indels  17;  Gaps  2;

Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
         | |||   :|||| ||:| ||||||||||||||||||||| :||||||||||| : |||:|
Db    1  MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP  60

Qy   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120
         |||:|||| ||| : :|| :||| | |||||||||||||:| |||||| |||||||||:|
Db   61  GKGLEVVAQINSV--GNSTYYPDTVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCASG  118

Qy  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180
                              :::|||||||||||||||||||||||||||||||||||||
Db  119  --------------DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  163

Qy  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  164  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  223

Qy  241  KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  300
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  224  KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  283

Qy  301  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  284  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  343

Qy  361  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  344  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  403

Qy  421  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  404  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  461
```

```
Qy   475  SPGK  478
          ||||
Db   472  SPGK  475

RESULT 12
AAU07745
ID   AAU07745 standard; Protein; 461 AA.
XX
AC   AAU07745;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Humanised monoclonal antibody Hu266, heavy chain.
XX
KW   Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
KW   Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KW   gene therapy.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Signal_peptide
FT   Protein         20..461
FT                   /label= Mature Hu266 heavy_chain
FT                   /note= "This sequence is specifically claimed in
FT                   claim 17"
XX
PN   WO20162801-A2.
XX
PD   30-AUG-2001.
XX
PF   26-FEB-2001; 2001WO-US06191.
XX
PR   24-FEB-2000; 2000US-0184601.
PR   08-DEC-2000; 2000US-0254465.
PR   08-DEC-2000; 2000US-0254498.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
PI   Vasquez M;
XX
DR   WPI; 2001-550087/61.
XX
PT   New humanised antibody for the treatment of Alzheimer's comprises the
PT   inhibition and reduction of the formation of amyloid plaques  -
XX
PS   Example 13; Fig 5; 63pp; English.
XX
CC   The invention relates a humanised antibody that specifically binds
CC   an epitope contained within positions 13-28 of amyloid beta peptide,
CC   Abeta. The antibody is useful to inhibit and reduce the formation of
CC   amyloid plaques or the effects of toxic soluble Abeta species in humans
CC   their fragments are used for the manufacture of a medicant. This includes
CC   the prolonged expression of recombinant sequences of them in human
CC   tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
CC   Down's syndrome or pre clinical cerebral amyloid angiopathy.
CC   Specifically, the antibody is used to sequester Abeta into plasma, brain
CC   or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
CC   peptide within the brain thereby improving cognition. The present
CC   sequence is the heavy chain of a humanised monoclonal antibody, Hu266,
CC   based on the mouse antibody 266.
XX
SQ   Sequence   461 AA;
```

```
RESULT 13
AAR22757
ID   AAR22757 standard; Protein; 470 AA.
XX
AC   AAR22757;
XX
DT   20-OCT-1992  (first entry)
XX
DE   Reshaped CAMPATH-1 antibody heavy chain.
XX
KW   Antigen; CDR; complementarity determining region; graft rejection;
KW   autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   Region          50..54
FT                   /note= "Complementarity determining region 1"
FT   Region          69..87
FT                   /note= "Complementarity determining region 2"
FT   Region          101..110
FT                   /note= "Complementarity determining region 3"
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Peptide         20..470
FT                   /note= "mature peptide"
XX
PN   WO9205274-A.
XX
PD   02-APR-1992.
XX
PF   16-SEP-1991; 91WO-GB01578.
XX
PR   17-SEP-1990; 90GB-0020282.
XX
PA   (GORM/) GORMAN S D.
XX
PI   Clark M R, Cobbold S P, Gorman S D, Waldmann H;
```

Query Match   84.7%; Score 2169.5; DB 22; Length 461;
Best Local Similarity   86.8%; Pred. No. 1.2e-127;

```
XX
DR   WPI; 1992-132139/16.
DR   N-PSDB; AAQ23570.
XX
PT   Humanisation of antibodies binding to human CD4 antigen - by
PT   mutation of framework-encoding regions of DNA encoding variable
PT   domain of rat or mouse antibody chain
XX
PS   Disclosure; Fig 5; 74pp; English.
XX
CC   The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.
CC   Reshaped CD4 antibody can be used to induce tolerance against an
CC   antigen. It can also be used to alleviate autoimmune diseases such
CC   as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC   to a graft, e.g. an organ graft or a bone marrow transplantation can
CC   also be useful to alleviate allergies. Tolerance to allergens could
CC   also be achieved. See also AAR22754-R22763.
XX
SQ   Sequence  470 AA;

Query Match        84.4%;  Score 2162;  DB 13;  Length 470;
Best Local Similarity  86.0%;  Pred. No. 3.7e-127;
Matches  411; Conservative  18; Mismatches  41; Indels  8; Gaps  2;

Qy     1 MGWSLILLFLVAVATRVQCEVOLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP  60
          |||||| |:|||:||  :|:||   :|| ||:|| :| : | :|||||||| :|||
Db     1 MGWSCIILFLVATATGVHSQVQLEESGPGLVRPSQTLSLTCTVSGFTFTDFYMNVRQPP  60

Qy    61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
          || ||| :| ||: ||||    ||| |||:| :|: |  ::  :|    |||||||:|
Db    61 GRGLEWIGFIRDKAKGYTTEYNPSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARE 120

Qy   121 YISHCRGGVCVGGYFEWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
              |  |  :||: ||| ||||||||||||||||||||||||||||||||
Db   121 --GHT-----AAPFDYWGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 172

Qy   181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 232

Qy   241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 292

Qy   301 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   293 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 352

Qy   361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   353 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 412

Qy   421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   413 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 14
AAY32263
ID   AAY32263 standard; Protein; 444 AA.
XX
AC   AAY32263;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Humanised anti-CD23 MAb C11 heavy chain.
XX
KW   CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
KW   monoclonal antibody; chimeric antibody; humanised antibody;
KW   complementarity determining region; CDR; autoimmune disease;
KW   inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW   Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW   urticaria; nephrotic syndrome; glomerulonephritis;
```

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KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW   Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis;
KW   graft-versus-host disease; COPD; bronchitis; diabetes;
KW   B-cell malignancy; therapy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /note= "framework region 1"
FT   Region          31..35
FT                   /note= "CDR 1"
FT   Region          36..49
FT                   /note= "framework region 2"
FT   Region          50..68
FT                   /note= "CDR 2"
FT   Region          69..100
FT                   /note= "framework region 3"
FT   Region          101..103
FT                   /note= "CDR 3"
FT   Region          104..111
FT                   /note= "framework region 4"
FT   Region          112..444
FT                   /note= "constant region"
XX
PN   WO958679-A1.
XX
PD   18-NOV-1999.
XX
PF   07-MAY-1999;  99WO-GB01434.
XX
PR   09-MAY-1998;  98GB-0009839.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Bonnefoy JMP,  Crowe SJ,  Ellis JH,  Rapson NT,  Shearin J;
XX
DR   WPI; 2000-053101/04.
DR   N-PSDB; AAZ34748.
XX
PT   Cell receptor specific antibodies useful for treating e.g. arthritis,
PT   diabetes, multiple sclerosis and psoriasis -
XX
PS   Claim 9; Fig 4; 81pp; English.
XX
CC   This amino acid sequence represents the heavy chain of humanised
CC   anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
CC   framework (HSIGKVII) and the heavy chain complementarity
CC   determining regions (see AAY32257-59) of murine antibody C11. The
CC   DNA was constructed by splice overlap PCR. The invention provides
CC   altered antibodies, such as chimeric or humanised antibodies, which
CC   comprise sufficient of the amino acid sequences of the C11 light
CC   and heavy chain complementarity determining regions to render them
CC   capable of binding to the CD23 type II molecule expressed on
CC   haematopoietic cells. The antibodies are used to block soluble
CC   CD23 formation in human therapy, for the treatment of arthritis,
CC   lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
CC   diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
CC   syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
CC   colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
CC   asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
CC   eczema, graft-versus-host disease, COPD, insulitis, bronchitis
CC   (particularly chronic bronchitis) or diabetes (particularly type 1
CC   diabetes), and B-cell malignancies (claimed). They are also useful
CC   for studying interactions between CD23 and various ligands and
CC   determining the binding agents.
XX
SQ   Sequence  444 AA;

Query Match        84.4%;  Score 2161.5;  DB 21;  Length 444;
Best Local Similarity  89.8%;  Pred. No. 3.7e-127;
Matches  412; Conservative  7; Mismatches  25; Indels  15; Gaps  1;
```

```
CC    region having an antibody variable light (VL) or heavy (VH) region,
CC    or a complementarity determining region (CDR) of VL or VH. MUC1-specific
CC    binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC    The binding of MUC1-specific binding member to MUC1 is detected by a
CC    detection method selected from enzyme-linked immunosorbent assay,
CC    magnetic resonance imaging, scintillation counting, and X-ray film.
CC    MUC1-specific binding member is useful for treating cancer, preferably
CC    adenocarcinoma, in an individual, where the cancer is present in tissue
CC    of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC    binding member is useful for diagnosing and imaging MUC1-expressing
CC    cancer cells and tissues, for purifying or isolating non-glycosylated,
CC    underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC    containing molecules, and for therapeutically or prophylactically
CC    treating cancer. The present sequence is human recombinant immunoglobulin
CC    (Ig) heavy chain region (variable VH and CH constant heavy chain).
XX
SQ    Sequence   451 AA;

Query Match             84.3%;  Score 2160;  DB 22;  Length 451;
Best Local Similarity   89.8%;  Pred. No. 4.7e-127;
Matches  412;  Conservative   12;  Mismatches   27;  Indels    8;  Gaps    3;

Qy     20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
           :|||||||||||||||||| ||||||  :  |  | |||||  |||||||||||||| ||
Db      1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSGYWMSWVRQAPGKGLEWVSGISG--SGGST 58

Qy     80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGGYFEFWG 139
           |||||||| |||||||||| ||||||||||||||| ||||||:|:||| :|| |:
Db     59 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA---KHTGGGV--WDPIDYWG 112

Qy    140 QGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199
           |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 172

Qy    200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP 259
           ||||||||||||||||||||||||||||||||||||||||||||||  |||:|||||||
Db    173 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 232

Qy    260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319
           ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CPAPELLAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 292

Qy    320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 352

Qy    380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 412

Qy    440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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Db    413 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

Search completed: March 29, 2003, 09:10:20
Job time : 51.1632 secs
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Qy     20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
           :|||||||||||||||||| ||||||  :  |  | |||||  ||||| | ||||| ||
Db      1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYWMSWVRQAPGKGLEWVAEIRLKSDNYAT 60

Qy     80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGGYFEFWG 139
           |||||| |||||||||||| ||||||:|:||| |||||||||:||||||||||| ||
Db     61 HYAESVKGKFTISRDDSKSRLYLQMNSLKTEDTAVYYCTD-----------FIDWG 105

Qy    140 QGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199
           |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    106 QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 165

Qy    200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP 259
           ||||||||||||||||||||||||||||||||||||||||||||||  |||:|||||||
Db    166 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 225

Qy    260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319
           ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 CPAPELLAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 285

Qy    320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 345

Qy    380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 405

Qy    440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
           |||||||||||||||||||||||||||||||||||||||
Db    406 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 444
```

```
RESULT 15
AAE12715
ID   AAE12715 standard; Protein; 451 AA.
XX
AC   AAE12715;
XX
DT   04-JAN-2002  (first entry)
XX
DE   Human recombinant immunoglobulin (Ig) heavy chain region.
XX
KW   Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
KW   heavy chain region; cancer; breast; ovary; lung; bladder;
KW   cytostatic; therapy; immunoglobulin; Ig.
XX
OS   Homo sapiens.
XX
PN   WO200175110-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10589.
XX
PR   30-MAR-2000; 2000US-0538911.
XX
PA   (DYAX-) DYAX CORP.
XX
PI   Hoogenboom HRJM,  Henderikx MPG;
XX
DR   WPI; 2001-626437/72.
DR   N-PSDB; AAD20745.
XX
PT   Novel isolated tumour-associated antigen mucin-1-specific binding member
PT   for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT   its portion for binding to an epitope of the protein core of mucin-1 -
XX
PS   Claim 12; Page 106-108; 126pp; English.
XX
CC   The invention relates to an isolated tumour-associated antigen mucin-1
CC   (MUC-1)-specific binding member comprising an antigen binding domain
```

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                 GenCore version 5.1.4 p5_4578
        Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          March 29, 2003, 09:06:23 ; Search time 43.353 Seconds
                                           (without alignments)
                                           2271.829 Million cell updates/sec

Title:           US-09-758-173-8
Perfect score:   2561
Sequence:        1 MGWSLILLFLVAVATRVQCE........MHEALHNHYTQKSLSLSPGK 478

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:      671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_21:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                10: sp_plant:*
                11: sp_rodent:*
                12: sp_virus:*
                13: sp_vertebrate:*
                14: sp_unclassified:*
                15: sp_rvirus:*
                16: sp_bacteriap:*
                17: sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2178.5	85.1	471	4	Q8TC77	Q8tc77 homo sapien
2	1838	71.8	473	4	Q8TC63	Q8tc63 homo sapien
3	1632.5	63.7	469	11	Q8R3V9	Q8r3v9 mus musculu
4	1495.5	58.4	473	11	Q9D8L4	Q9d8l4 mus musculu
5	1480.5	57.8	473	11	Q91Z05	Q91z05 mus musculu
6	1480	57.8	468	11	Q99L31	Q99l31 mus musculu
7	1472.5	57.5	473	11	Q99L25	Q99l25 mus musculu
8	1469.5	57.4	437	11	Q9R1A4	Q9r1a4 mus musculu
9	1458.5	57.0	463	11	Q99LC4	Q99lc4 mus musculu
10	1415	55.3	474	11	Q8R3H6	Q8r3h6 mus musculu
11	1268	49.5	701	4	Q96PQ8	Q96pq8 homo sapien
12	1262.5	49.3	337	6	Q95M34	Q95m34 equus cabal
13	879.5	34.3	597	4	Q96BB9	Q96bb9 homo sapien
14	845	33.0	613	4	Q8WUK1	Q8wuk1 homo sapien
15	805	31.4	494	4	Q96K68	Q96k68 homo sapien
16	792	30.9	484	11	Q8VEA0	Q8vea0 mus musculu
17	789.5	30.8	614	4	Q96GA6	Q96ga6 homo sapien
18	789	30.8	278	11	Q921K1	Q921k1 mus musculu
19	786.5	30.7	487	11	Q99KA4	Q99ka4 mus musculu
20	769.5	30.0	479	11	Q91WP5	Q91wp5 mus musculu
21	760	29.7	486	11	Q91Z07	Q91z07 mus musculu
22	731	28.5	613	11	Q8VCX7	Q8vcx7 mus musculu
23	727.5	28.4	480	11	Q91XE1	Q91xe1 mus musculu
24	719	28.1	500	4	Q9BRV0	Q9brv0 homo sapien
25	716.5	28.0	597	4	Q9BU10	Q9bu10 homo sapien
26	714.5	27.9	597	4	Q9BQB8	Q9bqb8 homo sapien
27	712	27.8	496	4	Q96DK0	Q96dk0 homo sapien
28	710.5	27.7	481	11	Q91WT1	Q91wt1 mus musculu
29	710.5	27.7	497	4	Q8WY24	Q8wy24 homo sapien
30	708	27.6	613	4	Q96EY0	Q96ey0 homo sapien
31	706.5	27.6	588	4	Q8WUX4	Q8wux4 homo sapien
32	706.5	27.6	618	4	Q96AA6	Q96aa6 homo sapien
33	687	26.8	488	11	Q91WR1	Q91wr1 mus musculu
34	671.5	26.2	481	11	Q8VCV5	Q8vcv5 mus musculu
35	670.5	26.2	489	11	Q8VCX4	Q8vcx4 mus musculu
36	669	26.1	484	11	Q99LA6	Q99la6 mus musculu
37	666.5	26.0	481	11	Q91WT3	Q91wt3 mus musculu
38	650.5	25.4	482	11	Q91X92	Q91x92 mus musculu
39	645	25.2	573	4	Q8WU38	Q8wu38 homo sapien
40	641	25.0	496	4	Q96KX8	Q96kx8 homo sapien
41	625	24.4	479	11	Q99M22	Q99m22 mus musculu
42	600.5	23.4	416	4	Q9NPP6	Q9npp6 homo sapien
43	516	20.1	426	11	Q9DCD9	Q9dcd9 mus musculu
44	481.5	18.8	147	4	Q9Y509	Q9y509 homo sapien
45	469.5	18.3	384	4	Q9UP60	Q9up60 homo sapien

ALIGNMENTS

```
RESULT 1
Q8TC77
ID   Q8TC77           PRELIMINARY;        PRT;     471 AA.
AC   Q8TC77;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.8 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024289; AAH24289.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 471 AA;  51791 MW;  38BF7F4CF588660E CRC64;

Query Match             85.1%;  Score 2178.5;  DB 4;  Length 471;
Best Local Similarity   87.2%;  Pred. No. 7.1e-181;
Matches  416;  Conservative  15;  Mismatches  27;  Indels  19;  Gaps  3;

Qy      8 LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWV 67
          :|||::||||||||||||||||||| :|||||||||: :||:|||: :|:|:|||||||||
Db      8 VFLVAILEGVQCEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWV 67

Qy     68 GFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCT------TSY 121
          ||:|| :: .|::|.||||:||:||.::.::|.|||.|||.|.|||||||      |||
Db     68 SSMSS--SSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSY 125

Qy    122 ISHCRGGVCYGGYPEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 181
          |||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    126 ----------WYFDLWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 174

Qy    182 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 241
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  175 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 234
        ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Qy  242 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 301
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  235 VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 294

Qy  302 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 361
        ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db  295 PEVKFNWYVVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 354

Qy  362 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 421
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  355 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 414

Qy  422 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  415 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
```

RESULT 2
Q8TC63
```
ID   Q8TC63       PRELIMINARY;     PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 473 AA;  51986 MW;  E29920B09BA369F5 CRC64;
```

```
Query Match             71.8%;
Best Local Similarity   75.5%;     Pred. No. 2.9e-151;   DB 4;   Length 473;
Matches  357;  Conservative  33;  Mismatches  67;  Indels  16;  Gaps  4;
```

```
Qy    8 LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSG--FTFSDHYMYWFRQAPGKGPE 65
        ||:|| || :: : : :|| :|| || :|:|: || ||   ||
Db   15 LLLVAAPRWVLSRLQIQESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQPPGKGLE 74

Qy   66 WVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHC 125
        | | | |   : : :|| :|:: :::   :: ||:  |:|:
Db   75 WIGTIN---FSGNMYSPSLRSRVTMSADMSENSFYLKLDSVTAADTAVYYCAAGHL--- 128

Qy  126 RGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 185
                  :|: :|||| |:|| :|||||||||||| ::|||||:|||||||||||||||
Db  129 -----VMGFGAHWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV 183

Qy  186 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK 245
        |||||||||||||||||||||||||||||||||||||||||:||:|||:|||||||||||
Db  184 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKR 243

Qy  246 AEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 305
        :  |    : ||| |||||:||||||||||||||||||||||||||||||||:|||||:
Db  244 VESK---YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ 300

Qy  306 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 365
        |||||||||||||||||||||:||||||||||||||||||||||||||||||| |:|:|:
Db  301 FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK 360

Qy  366 TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 425
        |||||||||||||||||||: ::::||||||||||||||||||||||||||||||||||
Db  361 TISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 420

Qy  426 PPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
```

```
Db  421 PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 473
```

RESULT 3
Q8R3V9
```
ID   Q8R3V9       PRELIMINARY;     PRT;   469 AA.
AC   Q8R3V9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024405; AAH24405.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 469 AA;  51976 MW;  534793F155D05457 CRC64;
```

```
Query Match             63.7%;
Best Local Similarity   63.0%;     Pred. No. 2.1e-133;   DB 11;   Length 469;
Matches  303;  Conservative  69;  Mismatches  90;  Indels  19;  Gaps  7;
```

```
Qy    1 MGWSLILFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
         | :   ::|| :|  ||||:||||||||||||||||:|:|||:|||||:|:||::||||
Db    5 LNW----IFIVTLLNGIQCEVNLVESGGGLVQPGGSLRLSCAASGFTFTDYYMSWVRQPP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
        |||  || ||||||||||||||||||| ||||| ||| ||||||||: :||:| ||| ||  ||
Db   61 GKALEWLGFIRNKANGYTTEYAASVKGRFTISRDNSQSILYLQMNALRAEDSATYYCARD 120

Qy  121 YISHCRGGVCYGG-YFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 179
           :    : ::  |:: ||||| |||||| : : :|: ||| :|: :||||||||||
Db  121 R----RSSYYYSGTSFAYWGQGTLVTVSAAKTPPSVVPLAPGSAAQTNSMVTLGCLVKG 176

Qy  180 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN 239
        ||||||||:|||| |:||||||||||||  ||:|||:||||||: | || |||| ||:
Db  177 YFPEPVTVTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTWPSQTVTCNVAHPASS 235

Qy  240 TKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 297
        ||||||  : :|  ||:|      | |::  ||||:|||||||:| : | ||:|||||||
Db  236 TKVDKKIVPRDCG----CKPCICTVPEV--SSVFIFPPKPKDVLTITLTPKVTCVVVDI 288

Qy  298 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 357
        |::|||| |:|::|:||||:|:|||||||:|||:| ||:| :|:|||||||||:|:| :
Db  289 SKDDPEVQFSWFVDDVEVHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSA 348

Qy  358 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 417
        | ||||||||||:||:|: ||||| ||| :: ::| |||||:::  |||:| ||| |||
Db  349 AFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMTDFFPEDITVEWQWNGQ 408

Qy  418 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 477
        | :|||:| |::|:||| |:||||:|:||:| | ||| ||::||:|||| |::|||| ||
Db  409 PAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 468

Qy  478 K 478
        |
Db  469 K 469
```

RESULT 4
Q9D8L4
```
ID   Q9D8L4       PRELIMINARY;     PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810060009Rik protein.
```

```
GN   IGH-1 OR 1810060O09RIK.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez J., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

Query Match             58.4%;  Score 1495.5;  DB 11;  Length 473;
Best Local Similarity   57.4%;  Pred. No. 1.7e-121;
Matches  278;  Conservative   79;  Mismatches 110;  Indels  17;  Gaps 5;

Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP   60
         |  |::||||::|:| :|:|||||||||||||||::||||||| |:|:||||::: :: :
Db    1  MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRP   60

Qy   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120
         | | ||:|:|  ||:|: | |::::: :|::||: ||:|:|:|:|:|::| |:|:|:||
Db   61  GQGLEWIGKI--GPSGSGTYYNEKFKGKATLTADKSSSTAYMQLSSLITSEDSAVYFC--  115

Qy  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180
            ::  || ||  :: :|||||:|||:|:  | |||:||||  |: |||::||||||:|
Db  116  ---ARSGYDY-DWFAYWGQGTLVTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGY   170

Qy  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
         |||||| :|||| |:||||||||:||:||||:|||:|||:|:: :||||:||||:| |:|
Db  171  FPEPVTLTWNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASST  229

Qy  241  KVDKKAEPK------SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  294
         |||||:||:      ||    || |||| ||||||||::|||| ||:|||| :|:|||||
Db  230  KVDKKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVV  289

Qy  295  VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  354
         ||||::|| |:::|:|:||||||::|: :||:|||| ||||:: :: |||::||| ||||
Db  290  VDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKV  349
```

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Qy  355  SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES  414
         .||.||:|||||||| :| |  |||||||||:: |||:: |||||: ||:|::|||:|:|
Db  350  NNRALPSPIEKTISKPRGPVRAPQVYVLPPAAEMTKKEFSLTCMITGFLPAEIAVDWTS   409

Qy  415  NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL  474
         ||: |:||| |::|||||||:|:|||| |:||:|: |:|::|||:||.||||:|:|:||:
Db  410  NGRTEQNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTKTISR   469

Qy  475  SPGK  478
         | ||
Db  470  SLGK  473
```

```
RESULT 5
Q91Z05
ID   Q91Z05       PRELIMINARY;      PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.9 kDa protein.
GN   AU044919.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE  473 AA;  51946 MW;  CF625F008932AF12 CRC64;

Query Match             57.8%;  Score 1480.5;  DB 11;  Length 473;
Best Local Similarity   59.2%;  Pred. No. 3.5e-120;
Matches  286;  Conservative   69;  Mismatches 105;  Indels  23;  Gaps 6;

Qy    5  LILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGP   64
         | | |||.|   |||||||||||||||:||| :|  ||| .|||||||:| :::|:||.|:
Db    5  LNLVFLVLILKGVQCEVQLVESGGGLVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGL   64

Qy   65  EWVGFIRNKPNGGTTE--YAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYI  122
         |||. |    ||.:|  |||.:|. |||||||:.|:.. |:| ||: |||| |||:.
Db   65  EWVAYI----NSGSTTIYYADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARE--  118

Qy  123  SHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  182
               ::       | :.:|||||:||||   | |||:||||  |  .|||:||||||:|||
Db  119  ------LWLRRIDYWGQGTTITVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFP  171

Qy  183  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  242
         | ||| :|||| |:|||||||:||:||||::||:|||||::  :||| |||:| | ::.:
Db  172  ESVTVTWNSGSLSSGVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTV  230

Qy  243  DKKAEPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV  295
         |||.||    || ||:||      |||| |:||||||:|||: ||:|||| :|:|||||
Db  231  DKKLEPSGPISTINPCPPCKECHCCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVV  290

Qy  296  DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS  355
         |||::||.|:::|:|:||||||::|: :||:|||| :||||: :: |||::|||.||||.
Db  291  DVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVN  350

Qy  356  NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN  415
         || ||:|||:||||.:| |  |||| ||||:: | :  |||||: ||:|. |::|||:|N
Db  351  NKDLPSPIERTISKIKGLVRAPQVYILPPAAQLSRKDVSLTCLVVGFNPGDISVEWTSN   410

Qy  416  GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS  475
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Db  411  GHTEENYKDTAPVLDSDGSYPIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRS  470
          |||| ||||   |||||||| |:|||  ||  ||  |:  | ::|| |||: |:|| :||
Qy  476  PGK  478
          |||
Db  471  PGK  473
```

RESULT 6
Q99L31
```
ID   Q99L31         PRELIMINARY;      PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
```

```
Query Match             57.8%;  Score 1480; DB 11; Length 468;
Best Local Similarity   58.3%;  Pred. No. 3.8e-120;
Matches  280;  Conservative  69;  Mismatches 117;  Indels  14;  Gaps  5;
```

```
Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP   60
          ||||||| ||  | :||||:||||||||||| :||||||||| |||||||||||||||||
Db    1  MKCSWVIPFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRP   60

Qy   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS   120
          |||||||||||||||||:  : || |||||||| ||| ||:: ::: |::|||||||:
Db   61  EQGLEWIGYI--YPRDGSTKYNEKFGKATLTADKSSNTAYLQLSSLTSEDTAIYYCARN   118

Qy  121  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY  180
          ||:      |||:||:|||||||||||||||||||||||||| :: ||:|||||| |
Db  119  LL------YGGYDYWGQGTTITVSSAKTAPSVYPLAPVCGDTTGSSVTLGCLVKGY     170

Qy  181  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT  240
          |||||||||||| |||||||||||||:|||:|||||||||||:| |||:||||:|| ||
Db  171  FPEPVLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASST   229

Qy  241  KVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS  298
          ||||| | |  || ||| |   |||  |||||||:|||| || :||| ||||||||||||
Db  230  KVDKKIEPRG-PTIKPCPPCKPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVS   288

Qy  299  HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA  358
          ||||:||:||:|||:|||| || |||||||| |||:||: |||| |||||||:||||||:
Db  289  EDDPDVQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKA   348

Qy  359  LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP  418
          ||||||:||||  |  ||:||| | ||  |||| ||: || |||||||| ||:|  |
Db  349  LPAPIERTISKPKGSVRAPQVVLPPEEEMTKKQVTLTCMVTDFMPEDIYEWTN        408

Qy  419  ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPGKA  478
          | ||| |||||||||| |:||||  |||  | ||  | :|:||| |||: |:||| |||
Db  409  GHTEENYKDTAPVLDSDGSYPIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRS  470
```

```
Db  409  ELNYKNTEPVLDSDGSFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK  468
          | ||| ||||||||||| |:||||  |||  | ||  | :|:||| |||: |:|| ||
```

RESULT 7
Q99L25
```
ID   Q99L25         PRELIMINARY;      PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
```

```
Query Match             57.5%;  Score 1472.5; DB 11; Length 473;
Best Local Similarity   57.6%;  Pred. No. 1.7e-119;
Matches  279;  Conservative  74;  Mismatches 114;  Indels  17;  Gaps  6;
```

```
Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP   60
          ||||||| ||  | :|||| :|| :::  :|| |||| |:||| |||||||| |||||||
Db    1  MEWSWVFLFFLSVTTGVHSQVQLQQSGASVKISCKVSGYTFDHTIHWVKQRP          60

Qy   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSKSIAYLQMSSLKIEDTAVYYCTTS  120
          :| |||||| |     ||||:|  |  ||| |||||| ||::::: :||: :|| |:
Db   61  EQGLEWIGYI--YPRDGSTKYNEKFGKATLTADKSSSTAYMQLNSLTSEDSAVCFCS--   116

Qy  121  YISHCRGGVCYGG----YFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL  176
           ||:  |||  |||     |:||||||||||||| |:|||| || |||  |:|||||:|
Db  117  ---RGGSIYYGVGLYYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCL   171

Qy  177  VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK  236
          |||||||||:||||||| |:||||||||||| ||| |||||||:|||  | | | ||| |
Db  172  VKGYFPEPVLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHP  230

Qy  237  PSNTKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  294
          ||:|||||| | |  || ||| |   |||  |||||||:|||| ||:|||| || ||||
Db  231  ASSTKVDKKIEPRG-PTIKPCPPCKPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVV  289

Qy  295  VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  354
          ||||:|||:|| ||:|||:|||| || |||||||| |||:||:|||| |||||||:|||
Db  290  VDVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKV  349

Qy  355  SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES  414
          :|||||||||:||||  |  ||:||| | ||  |||| ||: || |||||||| ||:|  |
Db  350  NNKALPAPIERTISKPKGSVRAPQVVLPPEEEMTKKQVTLTCMVTDFMPEDIYEWTN     409

Qy  415  NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL  474
          || :   |||||||||||||| |:|||  |||  | || | :|:||| ||||  | |
Db  410  NGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR  469

Qy  475  SPGK  478
          ||||
Db  470  TPGK  473
```

RESULT 8
Q9R1A4
ID   Q9R1A4   PRELIMINARY;   PRT;   437 AA.
AC   Q9R1A4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update).
GN   IGH-4.
DE   Gamma1 heavy chain of Mab7 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFv).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152372; AAD40243.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER   1   1
FT   NON_TER   437   437
SQ   SEQUENCE   437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match   57.4%; Score 1469.5; DB 11; Length 437;
Best Local Similarity   59.8%; Pred. No. 2.8e-119;
Matches 275; Conservative 68; Mismatches 92; Indels 25; Gaps 6;

Qy   21 VQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTTE 80
          |||||||||||||||||||||:|||||:||||||||||||||||||||||:|||||||
Db   1 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVA--SFSSSGIIY 57

Qy   81 YAASVKDRFTISRDDSKSIAVLQMSLKIEDTAVYYCTTSYISHCRGGVCYGGYFEFWGQ 140
          | |||||| ||| :|:|:| |||||||:|||||| | : ||
Db   58 YTDSVKGRFTIYKDKDRNILSLQMSSLRSEDTAMYYCAR---------GDYSAYWGP 105

Qy   141 GALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 200
          | |||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db   106 GTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHT 165

Qy   201 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP- 259
          |||||||||||||:|||||||||||||:||||||||||:| :||: |||||||
Db   166 FPAVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPC 220

Qy   260 -CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYYDGVEVHNA 318
           || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 ICTVPEV--SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTA 277

Qy   319 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQREPQ 378
          :|||:||||||||||:|||||||||||||||||||||:|||||||||||||:|||
Db   278 QTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQ 337

Qy   379 VVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 438
          :||:|| |:|||||||||||||||||||||||||||||||||||||||||||||||||
Db   338 VVTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVY 397

Qy   439 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
          ||| |||||||||||||||||||||||||||||:|||||
Db   398 SKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK 437

RESULT 9
Q99LC4
ID   Q99LC4   PRELIMINARY;   PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match   57.0%; Score 1458.5; DB 11; Length 463;
Best Local Similarity   56.5%; Pred. No. 2.8e-118;
Matches 272; Conservative 80; Mismatches 108; Indels 21; Gaps 7;

Qy   1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                :|:|:|:|::||||||||||||||||||:||||||||||:||||||||||||
Db   1 MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRT 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCT-T 119
          |:|||||| ||||| |: : ||||||||||||:||:||:| :::|||:|||||
Db   61 GQGLEWVGEI--YPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARS 118

Qy   120 SYISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 179
          | : :|| |: |:||||:|:|| |||||||||||||||||||||||
Db   119 SYYSY-------DLFAYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKG 170

Qy   180 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN 239
          |||||||||:|||||||||||||||||||||||||:||||||||||||:||||||||
Db   171 YFPEPVTVTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASS 229

Qy   240 TKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 297
          ||||||| ||||||| || || |||||||||||||||||||||||||||||
Db   230 TKVDKKIVPRDCG-----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDI 282

Qy   298 SHEDPEVKFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 357
          |:|||||:|||:||||||||:|||:||||||||||:||||||||||||||||||:||||
Db   283 SKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSA 342

Qy   358 ALPAPIEKTISKAKGQREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 417
          |:||||||||||:||| |:||||:| |:|||||||||||||||||||||||||||
Db   343 AFPAPIEKTISKTKGRPKAPQVVTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQ 402

Qy   418 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 477
          | :||||:|||||||||:|||||| ||||||||||||||||||||||||||:||||
Db   403 PAENYKNTQPIMDTDGSYFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPG 462

Qy   478 K 478
          |
Db   463 K 463

RESULT 10
Q8R3H6
```
ID   Q8R3H6      PRELIMINARY;      PRT;   474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.7 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA;  51748 MW;  8608B57C6CD2874A CRC64;

Query Match             55.3%;  Score 1415;  DB 11;  Length 474;
Best Local Similarity   55.9%;  Pred. No. 1.7e-114;
Matches  271;  Conservative  73;  Mismatches 123;  Indels  18;  Gaps  5;

Qy     1 MGWSLILLFLAVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
           ||| ||:|| ||||:  |||||||||  | ::  :||  ||  ||  : | :
Db     1 MEWPCILLFLLSVTEGVHSQVOLLQSGPELVKPGASVKISCRASGYAFSKSWMNWVKRRP 60

Qy    61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
           ||:|| :  |::  :|: ::|   :||| | ::::| |:||:||||:|||:|:: |||
Db    61 GKGLEWIG--RIFPGDGDTHYSGKFQGKAKLTADKSSVTAFLQLTSLTSEDSAVYFCARD 118

Qy   121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
           || ::  :  |||:||||||||| | :|||  | :::|:::: ||
Db   119 --------SDYGDYFDDWGQGATVTVSSAKTPPSVYPLAPGCGDTTGSSVTLGCLVKGY 170

Qy   181 FEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 240
           ||| |:||||||||||||| |||:|||||||||||||| :|| |||| :|||||| ::
Db   171 FPSVTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASST 229

Qy   241 KVDKKAEPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 293
           |||| :|  |   |  |:|||::||| |:|||||||||::|||: ||:|||| |||||
Db   230 TVDKKLEPSGP1STINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCV 289

Qy   294 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 353
           |||||: || || :| |:::|||:||: :|:||||| |||| | |  :||||:||||||
Db   290 VVDVSEDDPDVQISWFVNNVEVHTAQTQTHRDYNSTIRVVSALPIQHQDWMSGKEFKCK 349

Qy   354 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 413
           |:||:||:|||:||||  | |||||:: ||| ::|:::||||||||| ||:| ||:||
Db   350 VNNKDLPSPIERTISKIKGLVRAPQVVILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWT 409

Qy   414 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 473
           |||: ||||| | ||||||||:|:||||  | |:||:  .|||.|  ||:||:| | || 
Db   410 SNGHTEENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTIS 469

Qy   474 LSPGK 478
         ||:||
Db   470 RSPGK 474
```

RESULT 11
Q96PQ8
```
ID   Q96PQ8      PRELIMINARY;      PRT;   701 AA.
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21477448; PubMed=11593034;
RA   Hu Z.; Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR   EMBL; AF272274; AAK58686.1; -.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   SMART; SM00181; EGF; 2.
DR   PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW   Hydrolase; Serine protease.
SQ   SEQUENCE   701 AA;  77826 MW;  94AC6CEB42CC992F CRC64;

Query Match             49.5%;  Score 1268;  DB 4;  Length 701;
Best Local Similarity   82.7%;  Pred. No. 1.8e-101;
Matches  244;  Conservative   4;  Mismatches 29;  Indels  18;  Gaps  3;

Qy   187 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS--NTKVD 243
           |||  | .. |        ||:          || :|  | : :
Db   422 VSWGQGCATVG--------HFGVY------TRVSQYIEWLQKLMRSEPRPGVLLRAPFP 466

Qy   244 KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 303
           |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   467 GSAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 526

Qy   304 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   527 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 586

Qy   364 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 423
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   587 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 646

Qy   424 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   647 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 701
```

RESULT 12
Q95M34
```
ID   Q95M34      PRELIMINARY;      PRT;   337 AA.
AC   Q95M34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Immunoglobulin gamma 1 heavy chain constant region
DE   (Fragment).
GN   IGHC1.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
```

```
Matches 208;   Conservative 82;   Mismatches 179;   Indels 119;   Gaps 18;

Qy    1  MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMWFRQAP  60
         :|: ||| ||||: | |||||||| ||||||||||||||:||| ||| |:  :  :||||
Db    1  MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAP  60

Qy   61  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS  120
         |||.||| :||.  :||:|  ||:||.|||||||:|:  : |||:||: |:||||||||
Db   61  GKGLEWVSAISG--SGGSTYYADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCA--  116

Qy  121  YISHCRGGVCYGGYF-EFWGQGALVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLV  177
          :. : |.      :  :|||||:|||||. :.|| : |||:|::.  .| ||::|.||
Db  117  --KDPRGYSASGNYTREDYWGQGTLVTVSSGGSASAPTLFPLVSCENSPDTSSVAVGCLA  174

Qy  178  KDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICN  232
          | : |. || |  |.  :.   |.||:||: .|| ::.   :.||. .:  |||:| : |
Db  175  QDFLPDSITFSWKYKNNSDISSTRGFPSVLR-GGKYAATSQVLLPSKDVMQGTDEHVCCK  233

Qy  233  VNHKPSN----------------TKVDKKAEPKS---------CDKTHTCP--------  258
         |:| .:                 ||:||                                
Db  234  VQHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWL  293

Qy  259  --------------PCPAPELLGGPS----------------  270
                       ||:|    .|||                   
Db  294  REGKQVGSGVTTDQVQABAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQN  353

Qy  271  ------VFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH  316
              |: |.  :|:  :|  :.   | ||:.  : |::                 
Db  354  ASSMCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAV  411

Qy  317  NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-R  375
          . |::  .. :.  :. |..:     |.: | .  . :  .   | :.     ..: :
Db  412  KTHTNISESHPNATFSAVGEASICEDDWNSGERFTCVTHTDLPSPLUKQTISRPKGVALH  471

Qy  376  EPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--  430
         .|.||:||| .:.   :.: :.|| | |||| |: ||  .||||  | .| .:.. :.   
Db  472  RPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMEPQ  531

Qy  431  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         ..|.:| : .:|| |. |: |: |:|.|.|||| |.||| : . : ||
Db  532  APGRYFAHSIILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK  579
```

RESULT 14
Q8WUK1
```
ID   Q8WUK1           PRELIMINARY;       PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 67.3 kDa protein.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020240; AAH20240.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;   67296 MW;   60C7F595067IE315 CRC64;
```

```
RP   SEQUENCE FROM N.A.
RA   Wagner B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RX   MEDLINE=98383416; PubMed=9717671;
RA   Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA   Leibold W., Radbruch A.;
RT   "Organization of the equine immunoglobulin heavy chain constant region
RT   genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL   Immunobiology 199:105-119(1998).
DR   EMBL; AJ300675; CAC44624.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT   NON_TER   1   1
SQ   SEQUENCE   337 AA;   37438 MW;   A60BF2B01DEFD1F6 CRC64;
```

```
Query Match   49.3%;   Score 1262.5;   DB 6;   Length 337;
Best Local Similarity   69.2%;   Pred. No. 1.9e-101;
Matches  234;   Conservative  42;   Mismatches  53;   Indels  9;   Gaps  3;
```

```
Qy  149  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  208
         |||. |.||.||| . :||||:|||||||.:.||||||.||||||:|||||||||.||||
Db    1  ASTTAPKVFALAPGCGTTSDSTVALGCLVSGYFPEPVKVSWNSGSLTSGVHTFPSVLQSS  60

Qy  209  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP------KSCDKTHTCPPCPA  262
         |.||||| ||||.: .|:.||||||.|.|.|.|||| ||||      | |    || ||
Db   61  GFYSLSSMVTVPASTWTSETYICNVVHAASNFKVDKRIEPIPDNHQKVCDMS-KCPKCPA  119

Qy  263  PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP  322
         |||||||||| |||:||||||| |||||||||||||| ::|:||||||:|||||..|.:|
Db  120  PELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTRP  179

Qy  323  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL  382
         :|||:||||||||||..:||||| |||:|||| |:||| |||:||.|.||: .|||||.|
Db  180  KEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTKGRSQEPQVYVL  239

Qy  383  PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK  440
         .|::||| |.||.|||||||||| :| .|| |||||  |.:| :|...::|||| ||||||
Db  240  APHDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK  299

Qy  441  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  478
         |:||:.|||||. |:| |||||||||||||:..: ||
Db  300  LSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSKNPGK  337
```

RESULT 13
Q96BB9
```
ID   Q96BB9           PRELIMINARY;       PRT;   597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 65.0 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-CELL;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;   65039 MW;   4FCA3AD8ECE263D9 CRC64;
```

```
Query Match   34.3%;   Score 879.5;   DB 4;   Length 597;
Best Local Similarity   35.4%;   Pred. No. 8.7e-68;
```

```
Query Match          33.0%; Score 845; DB 4; Length 613;
Best Local Similarity 34.5%; Pred. No. 9e-65;
Matches 201; Conservative 84; Mismatches 178; Indels 120; Gaps 18;

Qy    1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
          |: :|||:| |||: ::|||||||||||||| |||||| ||||: |:|:||||||||
Db    1 MEFGLSWVFLVALLRGVQCQVQLVESGGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAP 60

Qy   61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
          |||:|||: |   :|:| :||| ||| ||||||||:|:| ||||:||| ||||||||| |
Db   61 GKGLEWVAVI---SYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD 118

Qy  121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKD 179
          ::| |  |||  :   :||||| |||||||:| |||||:|:|| | : ||:|| |  |:|
Db  119 WSE----GV---ETFDIWGQGTMVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQD 171

Qy  180 YFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVN 234
          :||: : ||  ||  :  |: ||:|| ||| :|| | ::| |   :   |: ::  |  |
Db  172 FLPDSIIFSWKYKNNSDISSTRGFPSVLR-GGKYAATSQVLLPSKDVMQGTDEHVCVKVQ 230

Qy  235 HKPSN----------------TKVDKAEPKS---------------CDKTHTCP------ 258
          | ||                 |||| |  |                 || ||||
Db  231 HPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLRE 290

Qy  259 --------------PCPAPELLGGPS---------------------------------- 270
                        ||||||||||||
Db  291 GKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNAS 350

Qy  271 --------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 318
                  |||||||:: :||: ::|  :  :     |    ||  :  :  :  ::
Db  351 SMCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLITYD-SVTISWTRQNGEAVKT 408

Qy  319 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REP 377
          ||||| | || |||:  ::|:  |    :     | : :| |:   |:|: ||:|  ::|
Db  409 HTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRP 468

Qy  378 QVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SD 432
          :||:|||:|::| :|:||:||| ||||| | : :: |   ||  | ::|||| |   ::
Db  469 DVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKVVTSAPMPEPQAP 528

Qy  433 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 475
          | :| :| ||:| |:|  | ||||| |||:|:| ||:|:|  |
Db  529 GRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS 571
```

RESULT 15

Q96K68

```
ID   Q96K68      PRELIMINARY;    PRT;    494 AA.
AC   Q96K68;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo
DE   sapiens SNC73 protein (SNC73) mRNA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida K., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK027379; BAB55072.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   494 AA;  53088 MW;  9AID7AEB5AEE4C0E CRC64;
```

```
Query Match          31.4%;  Score 805;  DB 4;  Length 494;
Best Local Similarity 40.3%;  Pred. No. 2e-61;
Matches 199; Conservative 68; Mismatches 179; Indels 48; Gaps 19;

Qy    8 LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWV 67
          :||||   |||||||||||||||| ||||||:|||| |: :|: |::|:||||||| |||
Db    8 VFLVAFLEGVQCEVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWV 67

Qy   68 GFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRG 127
            :  :  : :|  :|||||:|||||||:|: |:|:||:|||:|||||||||    ::| |
Db   68 SSISSRSD--YIYYRDSVKGRFTISRDNAKNSLYILQMNSLRVDDTAVYYCAR---DSCNG 122

Qy  128 GVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP-EPVT 186
          | ||   | ||||| ||||||||  | ||||:| :   : |:  : :|||   || ||::
Db  123 AICYG--FSPWGQGTLVTVSSASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEPLS 179

Qy  187 VSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSS-LGTQTYICNVNH--KPSNTKV 242
          |:| |:| :   :||| | |:|| ||: |||:| |:|: |:|:  |  |      |::
Db  180 VTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQ--- 236

Qy  243 DKKAEPKSCDKTHTC----PPCPAPELLGGPS--------VFLFPPKPKDTLMISRTPEV 290
           :    |:| : :|     ||||  | : | |        |:| |    |:| ||::|:
Db  237 -------DVTVPCPVPSTPPTPSPTSPSCCHPRLSLHRPALED-LLLGSEANL 286

Qy  291 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEY 350
          || :  :  :   :::  | :|    : : |||: |   :  |:  | | ||  : |::
Db  287 TCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSSVLPGCAEPWNHGKTF 343

Qy  351 KCCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIA 409
          || ::   :|  |:  |:| |      ||| : || |::| |:  ::||||| |||| |:
Db  344 TCTAAVPESKTPLTATLSKS-GNTRPEVHLLPPSEELALNELVTLTCLARGFSPKDVL 402

Qy  410 VEWESNGQ-PENNYKTTPPVLD-SDG-SFFLYSKLTVDKSRWQQGNVFSCSVMHEALH 464
          | |   |: | :::  |  :|   :  :||| | :|:::::   |   :||:| ||||
Db  403 VRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALP 462

Qy  465 NHYTQKSLSLSPGK 478
            :||:| :  |:|
Db  463 LAFTQKTIDRLAGK 476
```

Search completed: March 29, 2003, 09:14:40
Job time : 45.353 secs

```
         GenCore version 5.1.3
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      April  5, 2003, 19:13:54 ; Search time 2735.1 Seconds
                                         (without alignments)
                                         8508.978 Million cell updates/sec

Title:          US-09-758-173-7
Perfect score:  1437
Sequence:       1 ATGGGTTGGAGCCTCATCTT.........CCCTGTCTCCGGTAAATGA 1437

Scoring table:  IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched:       16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:   32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
          1:  em_estba:*
          2:  em_esthum:*
          3:  em_estin:*
          4:  em_estmu:*
          5:  em_estov:*
          6:  em_estpl:*
          7:  em_estro:*
          8:  em_htc:*
          9:  gb_est1:*
         10:  gb_est2:*
         11:  gb_htc:*
         12:  gb_est3:*
         13:  gb_est4:*
         14:  gb_est5:*
         15:  em_estfun:*
         16:  em_estom:*
         17:  gb_gss:*
         18:  em_gss_hum:*
         19:  em_gss_inv:*
         20:  em_gss_pln:*
         21:  em_gss_vrt:*
         22:  em_gss_fun:*
         23:  em_gss_mam:*
         24:  em_gss_mus:*
         25:  em_gss_other:*
         26:  em_gss_pro:*
         27:  em_gss_rod:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	902	62.8	1020	14	BQ062878	BQ062878	AGENCOURT
2	864	60.1	947	14	BQ709771	BQ709771	AGENCOURT
3	850.4	59.2	958	14	BQ706140	BQ706140	AGENCOURT
4	842.4	58.6	926	12	BG755166	BG755166	602711488
5	837.4	58.3	988	14	BQ708857	BQ708857	AGENCOURT
6	830.8	57.8	901	13	BM007892	BM007892	603617577
7	824.4	57.4	1029	14	BQ063185	BQ063185	AGENCOURT
8	823.8	57.3	918	14	BQ708022	BQ708022	AGENCOURT
9	822.8	57.3	887	14	BQ711255	BQ711255	AGENCOURT
10	819	57.0	995	14	BM914540	BM914540	AGENCOURT
11	808.8	56.3	881	14	BQ711291	BQ711291	AGENCOURT
12	800.2	55.7	1031	14	BQ064886	BQ064886	AGENCOURT
13	797.4	55.5	936	14	BQ711727	BQ711727	AGENCOURT
14	796	55.4	940	14	BQ705928	BQ705928	AGENCOURT
15	787.4	54.8	977	14	BQ710532	BQ710532	AGENCOURT
16	786.4	54.7	980	14	BM914504	BM914504	AGENCOURT
17	785.2	54.6	843	13	BM007897	BM007897	603617582
18	779.6	54.3	930	13	BM007597	BM007597	603616995
19	778.8	54.2	991	14	BQ708936	BQ708936	AGENCOURT
20	777.2	54.1	973	14	BQ706204	BQ706204	AGENCOURT
21	770.6	53.6	981	14	BM914528	BM914528	AGENCOURT
22	764.6	53.2	926	14	BQ710304	BQ710304	AGENCOURT
23	764.2	53.2	917	14	BQ708169	BQ708169	AGENCOURT
24	759.4	52.8	961	14	BQ710233	BQ710233	AGENCOURT
25	756.8	52.7	945	14	BQ712403	BQ712403	AGENCOURT
26	752.4	52.4	1012	14	BM914556	BM914556	AGENCOURT
27	752.2	52.3	895	14	BQ708303	BQ708303	AGENCOURT
28	750.4	52.2	783	13	BM007838	BM007838	603617519
29	749.4	52.2	1026	14	BM914288	BM914288	AGENCOURT
30	741.4	51.6	914	14	BQ712363	BQ712363	AGENCOURT
31	740.2	51.5	913	14	BQ707472	BQ707472	AGENCOURT
32	739.6	51.5	906	14	BQ711709	BQ711709	AGENCOURT
33	733.8	51.1	855	13	BM007689	BM007689	603617119
34	733.2	51.1	944	14	BQ712397	BQ712397	AGENCOURT
35	733.6	51.1	919	14	BQ709339	BQ709339	AGENCOURT
36	733.6	51.1	924	14	BQ710668	BQ710668	AGENCOURT
37	732.8	51.0	936	14	BQ707530	BQ707530	AGENCOURT
38	731.8	50.9	1014	14	BM914505	BM914505	AGENCOURT
39	731	50.9	933	14	BQ710248	BQ710248	AGENCOURT
40	730.4	50.8	973	14	BQ708902	BQ708902	AGENCOURT
41	729.6	50.8	888	12	BG757604	BG757604	602714780
42	729	50.7	936	14	BQ707915	BQ707915	AGENCOURT
43	728.8	50.7	941	14	BQ712021	BQ712021	AGENCOURT
44	728.6	50.7	925	14	BQ709853	BQ709853	AGENCOURT
45	728.4	50.7	991	14	BQ707621	BQ707621	AGENCOURT

ALIGNMENTS

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RESULT 1
BQ062878

LOCUS       BQ062878     1020 bp    mRNA      linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6825949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
            5', mRNA sequence.
ACCESSION   BQ062878
VERSION     BQ062878.1  GI:19890085
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1020)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094 row: h  column: 21
            High quality sequence start: 21
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FEATURES             Location/Qualifiers
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source          1..1020
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:592420"
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                /tissue_type="lymphoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Size-selected >500bp for average insert size
                1.8kb. Library constructed by Ling Hong in the laboratory
                of Gerald M. Rubin (University of California, Berkeley)
                using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                II RT (Life Technologies). Note: this is a NIH_MGC
                Library."
BASE COUNT      239 a          344 c          269 g          166 t          2 others
ORIGIN

Query Match             62.8%;   Score 902;   DB 14;   Length 1020;
Best Local Similarity   98.0%;   Pred. No. 7.8e-211;
Matches 923;   Conservative    0;   Mismatches   17;   Indels    2;   Gaps    1;

Qy   495  CACCCTCGGGGCAACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGT  554
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Db    36  CACCCTCGGGGCAACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGT  95

Qy   555  GACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT  614
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Db    96  GACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT  155

Qy   615  ACAGTCCTCAGGACTTCTACTCCCTCAGACAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  674
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Db   156  ACAGTCCTCAAGACTTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  215

Qy   675  CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGACACAGAA  734
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Db   216  CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACACAGAA  275

Qy   735  AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT  794
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Db   276  AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT  335

Qy   795  CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC  854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   336  CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC  395

Qy   855  CCGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA  914
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Db   396  CCGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA  455

Qy   915  GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA  974
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Db   456  GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA  515

Qy   975  GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT  1034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   516  GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT  575

Qy  1035  GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAA  1094
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Db   576  GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAA  635

Qy  1095  AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC  1154
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Db   636  AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC  695

Qy  1155  CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC  1214
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Db   696  CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC  755

Qy  1215  CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA-GAACAACTACAAGACC  1272
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Db    69  GACTCTTACTCCTCAGCAGCGTGGCGTGACCGTGGACGTGACCGTGGCACCCAGACCT  128
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Db   756  CAGCGGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAAACTACTACTAGACC  815
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Qy  1273  ACGCCTCCCGTGCTGACTCCGACCGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC  1332
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Db   816  ACGCCTCNCGTGCTGACTCCGACCGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGGA  875

Qy  1333  AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGAGTCATGAGGCTCTGCAC  1392
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Db   876  CAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCGTGATGATGCATGAAGCTCTGCAC  935

Qy  1393  AACCACTACACGCAGAGAGAGCCTCCCCGTGTCTCCGGGTAAA  1434
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Db   936  AACCACTACACGCAGAGAGCCTCCCCCGTGTCTTCGGGGTAA  977
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RESULT 2
BQ709771
LOCUS       BQ709771                  947 bp    mRNA        linear    EST 16-JUL-2002
DEFINITION  AGENCOURT 8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
            5', mRNA sequence.
ACCESSION   BQ709771
VERSION     BQ709771.1  GI:21848670
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 947)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466 row: m column: 16
            High quality sequence start: 3
            High quality sequence stop: 675.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278583"
                     /clone_lib="NIH MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      225 a          320 c          252 g          150 t
ORIGIN

Query Match             60.1%;   Score 864;   DB 14;   Length 947;
Best Local Similarity   99.4%;   Pred. No. 1.6e-201;
Matches 867;   Conservative    0;   Mismatches    5;   Indels    0;   Gaps    0;

Qy   566  GGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG  625
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Db     9  GGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG  68

Qy   626  GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCT  685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    69  GACTCTACTCCTCAGCAGCGTGGCGTGACCGTGGACGTGACCGTGGCACCCAGACCT  128
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464   row: a   column: 01
High quality sequence stop: 705.
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                /clone_lib="NIH_MGC_113"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT    229 a    319 c    256 g    150 t    4 others
ORIGIN
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Query Match        59.2%;   Score 850.4;   DB 14;   Length 958;
Best Local Similarity  99.2%;   Pred. No. 3.6e-198;
Matches  865;   Conservative  0;   Mismatches  6;   Indels  1;   Gaps  1;
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Qy   564  GTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCGGCTGTCCTACAGTCCTC   623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    11  GTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCGGCTGTCCTACAGTCCTC    70

Qy   624  AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCCAGCAGCTTGGGCACCCAGAC   683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71  AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCCAGCAGCTTGGGCACCCAGAC   130

Qy   684  CTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGCAGAGCC   743
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Db   131  CTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGTTGAGCC   190

Qy   744  CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGG   803
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191  CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGG   250

Qy   804  ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCTCATGATCTCCGGACCCC   863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   251  ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCTCATGATCTCCGGACCCC   310

Qy   864  TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG   923
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Db   311  TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG   370

Qy   924  GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACACCGCGGGAGGAGCAGTACAA   983
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Db   371  GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACACCGCGGGAGGAGCAGTACAA   430

Qy   984  CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA   1043
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Db   431  CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA   490

Qy  1044  GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC   1103
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Db   491  GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC   550

Qy  1104  CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA   1163
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Db   551  CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA   610

Qy  1164  GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTATCCCAGCGACAT   1223
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   611  GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT   670
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Qy   686  ACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGCAGAGCCCA   745
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Db   129  ACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGTTGAGCCCA   188

Qy   746  AATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC   805
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Db   189  AATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC   248

Qy   806  CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCGGACCCCTG   865
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Db   249  CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCGGACCCCTG   308

Qy   866  AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT   925
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Db   309  AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT   368

Qy   926  ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA   985
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Db   369  ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA   428

Qy   986  GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG   1045
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Db   429  GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG   488

Qy  1046  AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA   1105
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Db   489  AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA   548

Qy  1106  AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC   1165
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Db   549  AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC   608

Qy  1166  TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG   1225
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Db   609  TGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG   668

Qy  1226  CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC   1285
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Db   669  CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC   728

Qy  1286  TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC   1345
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Db   729  TGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGC   788

Qy  1346  AGCAGGGGAACGTCTTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAACTACACGC   1405
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Db   789  AGCAGGGGAACGTCTTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAACTACACGC   848

Qy  1406  AGAAGAGCCTCTCCGTGTCCCCGGGTAAATGA   1437
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Db   849  AGAAGAGCCTCTCCGTGTCCCCGGGTAAATGA   880
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RESULT 3
BQ706140
LOCUS       BQ706140               958 bp    mRNA    linear    EST 16-JUL-2002
DEFINITION  AGENCOURT_8352177 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277512
            5', mRNA sequence.
ACCESSION   BQ706140
VERSION     BQ706140.1   GI:21845039
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 958)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
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Qy      1224 CGCCGTGGAGTGGGAGGCAGCAATGGGCAGCGGAGACAACTACAAGACCACGGCCTCCCGT 1283
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Db       671 CGCCGTGGAGTGGGAGGCAGCAATGGGCAGCGGAGACAACTACAAGACCACGGCCTCCCGT 730

Qy      1284 GCTGGACTCCGACGGCTCCTTCTTCCTCTCACAGCAAGCTCACCGTGGACAAGAGCAGGTG 1343
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Db       731 GCTGGACTCCGACGGCTCCTTCTTCCTCTCACAGCAAGCTCACCGTGGACAAGAGCAGGTG 790

Qy      1344 GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 1403
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Db       791 GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 850

Qy      1404 GCAG-AAGAGCCTCTCCCTGTCTCCGGGTAAA 1434
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Db       851 ACAGAAAGAGCCTCTCCCTGTCTCCGGGTAA 882

RESULT 4
BG755166
LOCUS       BG755166                 926 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602711488F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',
            mRNA sequence.
ACCESSION   BG755166
VERSION     BG755166.1  GI:14065819
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 926)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1695 row: o column: 21
            High quality sequence stop: 888.
FEATURES             Location/Qualifiers
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                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      225 a    309 c    244 g    148 t
ORIGIN

Query Match        58.6%;  Score 842.4;  DB 12;  Length 926;
Best Local Similarity  98.2%;  Pred. No. 3.3e-196;
Matches  852;  Conservative  0;  Mismatches 16;  Indels  0;  Gaps  0;

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            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        2 CTCAGGCGCCCTGACCAGCGGCGTGCACACTTCCCGCGTCTTCCCGCGTCCTACAGTCCTCCAGGACT 61

Qy      630 .CTACTCCCTCCAGCAGCGTGGTGACCCGTGGCCCTCCAGCAGCGTTGGGCACCCAGGACTACAT 689
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Db        62 CTACTCCCTCCAGCAGCGTGGTGACCGTGGCCCTCCAGCAGCTTGGCACCCAGGACCTACAT 121

Qy       690 CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAAGAGAGCCCAAATC 749
             |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db       122 CTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTGAGCCCAAATC 181

Qy       750 TTGTGACAAAACTCACACATGCCACGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC 809
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       182 TTGTGACAAAACTCACACATGCCACGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC 241

Qy       810 AGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCAGACCCCTGAGGT 869
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       242 AGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCAGACCCCTGAGGT 301

Qy       870 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       302 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT 361

Qy       930 GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC 989
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       362 GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC 421

Qy       990 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 1049
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       422 GTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA 481

Qy      1050 CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCCGAGAAACCATCTCCAAAGC 1109
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       482 CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCCGAGAAACCATCTCCAAAGC 541

Qy      1110 CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC 1169
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       542 CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC 601

Qy      1170 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT 1229
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       602 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT 661

Qy      1230 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 1289
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       662 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA 721

Qy      1290 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 1349
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       722 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 781

Qy      1350 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACGCGAGAA 1409
             ||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||
Db       782 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACACTTACACGCAGAA 841

Qy      1410 GAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
             ||||||||||||||||||||||||||||
Db       842 AAAGCCTCTCCGTGTCTCCGGGTAAATGA 869

RESULT 5
BQ708857
LOCUS       BQ708857                 988 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8352194 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277561
            5', mRNA sequence.
ACCESSION   BQ708857
VERSION     BQ708857.1  GI:21847756
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 988)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Dr. Mark Watson
               cDNA Library Preparation: Dr. Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM2464 row: c  column: 02
               High quality sequence stop: 716.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6277561"
                     /clone_lib="NIH_MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT     230 a    338 c    258 g    162 t
ORIGIN

Query Match      58.3%;  Score 837.4; DB 14; Length 988;
Best Local Similarity  95.1%;  Pred. No. 5.7e-195;
Matches 908;  Conservative 0; Mismatches 41; Indels 6; Gaps 4;

Qy    400 TACTTCGAATTCTGGGGCCAGGGCGCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGC 459
          |||| |||||  ||||||||||||| |||||||||||||||||| ||||| ||||||||
Db      6 TACTTGACTACTGGGGCCAGGGCAACCGTCGGTCACCGTCTCCTCGGCCTCCACCAAGGGC 65

Qy    460 CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG 125

Qy    520 GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC 579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC 185

Qy    580 CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC 245

Qy    640 AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG 305

Qy    700 AATCACAAGCCCAGCAACACCAAGGTGGACAGAAAGCAGCCCAAATCTTGTGACAAA 759
          ||||||||||||||||||||||||||||||| ||||   ||||||||||||||||||
Db    306 AATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA 365

Qy    760 ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTC 819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTC 425

Qy    820 TTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG 879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 TTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG 485

Qy    880 GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG 939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG 545

Qy    940 GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG 999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG 605

Qy   1000 GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG 665

Qy   1060 GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG 1119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG 725

Qy   1120 CCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAG 1179
          |||||||||  ||||||||||||||||||||||||||||||||||||||||||||| |||
Db    726 CCCCGAGAAACACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAA-CAG 784

Qy   1180 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG 844

Qy   1240 AGCAATGGGCAG-CCGGAGAACAACTACAAGACCACGCCTCCCGTG---CTGGACTCCGA 1295
          ||| ||||||||  |||||||||||||||| | |||||  |||||||    |||| |||||
Db    845 AGCCATGGGCAGCCGGAGAACAACTACAACTACCAGCCACCACGCCTCCCGTGGAACTCCGA 904

Qy   1296 CGGG-TCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 1349
          ||| |||||||||||||||||| |||||| || ||||| |||||||| |||||||
Db    905 CGGCTCCTTCTTCCTCTACAGAAAAGCTCCCGGGGAACAAAGCAGGGGTGGCA 959


RESULT 6
BM007892

LOCUS       BM007892              901 bp   mRNA   linear   EST 30-OCT-2001
DEFINITION  603617577F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450611 5',
            mRNA sequence.
ACCESSION   BM007892
VERSION     BM007892.1  GI:16522233
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 901)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1939 row: j  column: 20
            High quality sequence stop: 834.
FEATURES             Location/Qualifiers
     source          1..901
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5450611"
                     /clone_lib="NIH_MGC 113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT     209 a    315 c    234 g    143 t
ORIGIN

Query Match      57.8%;  Score 830.8; DB 13; Length 901;
Best Local Similarity  97.3%;  Pred. No. 2.3e-193;
Matches 866;  Conservative 0; Mismatches 22; Indels 2; Gaps 2;
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REFERENCE   1 (bases 1 to 1029)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2095 row: g column: 10
             High quality sequence stop: 723.

FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_99"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."

BASE COUNT   237 a   350 c   276 g   165 t   1 others
ORIGIN

Query Match   57.4%; Score 824.4; DB 14; Length 1029;
Best Local Similarity 99.0%; Pred. No. 9.1e-192;
Matches 861; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

Qy   408 ATTCTGGGGCCAGGGCGGCCCTGGTCACCGTGTCCTCAGCTAGCACCAAGGGCCCATCGGT 467
          ||||| || || ||||| |||||||||||||||||||| ||||||||||||||||||||
Db   13 ATTACTGGGGCCAGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT 72

Qy   468 CTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCGCCCTGGGCTGCCT 527
          |||||||||| ||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   73 CTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCGCCCTGGGCTGCCT 132

Qy   528 GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAG 587
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   133 GGTCAAGGACTACTTCCCCGACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAG 192

Qy   588 CGGCGTGCACACCTTCCCGGCTGTCCTACAGCTCCTCAGGACTCTACTCCCTCAGCAGCGT 647
          |||| ||||||||||||||||||||| |||||||| |||||||||||||||||||||||||
Db   193 CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTTCAGGACTCTACTCCCTCAGCAGCGT 252

Qy   648 GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA 707
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   253 GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA 312

Qy   708 GCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACAC 767
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 GCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACAC 372

Qy   768 ATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCTTCCCCCC 827
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373 ATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCTTCCCCCC 432

Qy   828 AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGA 887
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   433 AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGA 492

Qy   888 CGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA 947
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493 CGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA 552

Qy   948 TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGT 1007
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Db   553 TAATGCCAAGACACAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGT 612

Qy   1008 CCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA 1067
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Db   613 CCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA 672

Qy   1068 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA 1127
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Db   673 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC-AAGGGCAGCCCCGAGA 731

Qy   1128 ACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT 1187
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   732 ACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT 791

Qy   1188 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG-CCGTGGAGTGGGAGAGCAATG 1246
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Db   792 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCCGTGGAGTGGGAGAGCAATCC 851

Qy   1247 GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC 1296
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   852 GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC 901

RESULT 7
BQ063185
LOCUS   BQ063185   1029 bp   mRNA   linear   EST 02-APR-2002
DEFINITION AGENCOURT_6876667 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924769
            5', mRNA sequence.
ACCESSION   BQ063185
VERSION   BQ063185.1 GI:19890681
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Best Local Similarity 95.5%;   Pred. No. 1.2e-191;
Matches   868; Conservative   0; Mismatches   39;   Indels   2;   Gaps   2;

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Qy   404 TGAATTCTGGGGCCAGGCGCCCTGTCACCGTCTTCCTCAGCTAGCACCAAGGCCCAT 463
         |||   |||||||||||    || |||||||||||||||||||||   ||||||||||||
Db     1 TTGACCGCTGGGGCCAGGGAACGCTGGTCACCGTCTTCCTCAGCCTCCCACCAAGGCCCAT 60

Qy   464 CGGTCTTCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGGGCGCCCTGGGCT 523
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CGGTCTTCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGGGCGCCCTGGGCT 120

Qy   524 GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGA 583
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGA 180

Qy   584 CCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA 643
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Db   181 CCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA 240

Qy   644 GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC 703
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC 300

Qy   704 ACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATTGTGACAAAACTC 763
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Db   301 ACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTC 360

Qy   764 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 823
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC 420

Qy   824 CCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 883
         ||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   421 CCCCAAAACCCAAGGACACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG 480

Qy   884 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 943
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 540

Qy   944 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA 1003
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA 600

Qy  1004 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 1063
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT 660

Qy  1064 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1123
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Db   661 CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 720

Qy  1124 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 1183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCA 780

Qy  1184 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT-GGAGTGGGAGAGC 1242
         |||||  ||||||||||||||||||||||||||||||||| ||| | |||||||||||||
Db   781 GCCTGGACCTGGTCAAAGGCTTCTATCCCAGCGACATCNCCGNGGAGTGGGAGAGC 840

Qy  1243 AATGGGCAG-CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC 1301
         |||||||| |||||||||||||||||||||||||||||||| |||||||||||||||
Db   841 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGGGCTGGGACTCCCGACGG 900

Qy  1302 CTTCTTCCT 1310
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Db   901 GTCCTTTCT 909
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RESULT 9
BQ711255
LOCUS   BQ711255   887 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
            5', mRNA sequence.

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Db   484 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCCACCGTCCTGCACCAGGA 543
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Qy  1029 CTCGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1088
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   544 CTCGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 603

Qy  1089 CGAGAAAACCATCTCCAAAGCCAGCAGCAGGAGAACCACAGGTGTACACCCTGCC 1148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   604 CGAGAAAACCATCTCCAAAGCCAGCAGCAGGAGAACCACAGGTGTACACCCTGCC 663

Qy  1149 CCCATCCCGGGATGAGCTGACCTGCCTGGTCAAGGCAGCAATGGGCAGCGCCTGA 1208
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664 CCCATCCCGGGATGAGCTGACCTGCCTGGTCAAGGCAGCAATGGGCAGCGCCTGA 723

Qy  1209 CTATCCCAGCGACACGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAA 1268
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   724 CTATCCCAGCGACACGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAA 783

Qy  1269 GACCACGCCT-CCCGTGCTGGACTCCGACGGCTCCTTCCTCTCCTTCTCCTTCTCTACAGGCAAGCTCACC 1326
         | ||||||||  |||||||||||||||||                    |||||||| |||||||||||
Db   784 GAACACGCCTCCCCGTGCTGGACTCCGACTCCTTCCTCTCCTTCTCCTTCTCTACAGGCAAGCTCACC 843

Qy  1327 GTGGACAAGAGCA-GGTGGCAGCAGGGGAA 1355
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Db   844 GTGGACCAGGAGGGGTTGGCAGCAGGGGGA 873
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RESULT 8
BQ708022
LOCUS   BQ708022   918 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8353641 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279643
            5', mRNA sequence.
ACCESSION   BQ708022
VERSION   BQ708022.1 GI:21846921
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 918)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469 row: i column: 20
            High quality sequence stop: 667.
FEATURES   Location/Qualifiers
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                    /db_xref="taxon:9606"
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                    /clone_lib="NIH_MGC_113"
                    /lab_host="DH10B (phage-resistant)"
                    /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCCACGAG(G). Library constructed by Ling Hong in the
                    laboratory of Gerald M. Rubin (University of California,
                    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                    Superscript II RT (Life Technologies). Note: this is a
                    NIH_MGC library."
BASE COUNT   208 a   316 c   245 g   147 t   2 others
ORIGIN

Query Match   57.3%; Score 823.8; DB 14; Length 918;

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Db    421  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  480

Qy   1027  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCAAGTCTTCCAACAAAGCCCTCCAGCCCCC 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCAAGTCTTCCAACAAAGCCCTCCAGCCCC  540

Qy   1087  ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGTGTACACCCTG  1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGTGTACACCCTG  600

Qy   1147  CCCCCATCCCGGATGAGTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1206
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CCCCCATCCCGGGATGAGTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC  660

Qy   1207  TTCTATCCCAGCGACATCCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TTCTATCCCAGCGACATCCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC  720

Qy   1267  AAGA-CCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC 1325
           |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  NAGACCCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAC  780

Qy   1326  CGT-GGACAAGAGCAGGTGGCAGC-AGGGGAACGTTCTTCATGCTCCGTGATGCATGAG 1383
           ||| ||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    781  CGTGGGACAAAAGCAAGTGGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAA  840

Qy   1384  GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGTGTCCGGG 1430
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Db    841  GCTCTGCACAACCACTACACGCCGAGAAGAGCTTCCCCGGTCCGG  887
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RESULT 10
BM914540
LOCUS   BM914540   995 bp   mRNA   linear   EST 12-MAR-2002
            AGENCOURT_6615506 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480223
DEFINITION 5', mRNA sequence.
ACCESSION   BM914540
VERSION   BM914540.1 GI:19364919
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 995)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2002 row: l column: 16
            High quality sequence stop: 718.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5480223"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a

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ACCESSION   BQ711255
VERSION     BQ711255.1  GI:21850154
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 887)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474 row: m  column: 20
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT    218 a    295 c    230 g    143 t     1 others
ORIGIN
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Query Match   57.3%; Score 822.8; DB 14; Length 887;
Best Local Similarity 97.6%; Pred. No. 2.1e-191;
Matches 866; Conservative   0; Mismatches 18; Indels 3; Gaps 3;

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Qy    547  GAACCGGTGCACGGTGCGTGGAACTCAGGCGCCCTGACCAGCGGCGCCGTGCACACCTTCCCG 606
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Db      1  GAACCGGTGCACGGTGCGTGGAACTCAGGCGCCCTGACCAGCGGCGCCGTGCACACCTTCCCG  60

Qy    607  GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 120

Qy    667  AGCTTGGGCACCCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AGCTTGGGCACCCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 180

Qy    727  GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 786
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 240

Qy    787  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTC 846
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Db    241  CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAACCCAAGGACACCCTC 300

Qy    847  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 360

Qy    907  GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 420

Qy    967  CGGGAGGAGCAGTACAACAGCACGTACCGTGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1026
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ACCESSION      BQ711291
VERSION        BQ711291.1  GI:21850190
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 881)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Dr. Mark Watson
               cDNA Library Preparation: Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM2468  row: c  column: 01
               High quality sequence stop: 721.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G).Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT        220 a     285 c     237 g     139 t
ORIGIN
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Query Match           56.3%;  Score 808.8;  DB 14;  Length 881;
Best Local Similarity 99.8%;  Pred. No. 5.8e-188;
Matches  810;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

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Db      1 GTCCTCAGGACTTCTACTTCCCTCAGCAGCGTGTGTGACCGTGCCCTCCAGCAGCTTGGGCAC 60

Qy    678 CCAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACACCAAGGTGCAACAAGAAAGC 737
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Db     61 CCAGACCTACATCTGCAACGTGAATCACAGCCCAGCAACACACCAAGGTGCAACAAGAAAGT 120

Qy    738 AGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAGTGCCCAGCACCTGAACTCCT 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 180

Qy    798 GGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 240

Qy    858 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 917
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Db    241 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 300

Qy    918 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 977
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Db    301 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 360

Qy    978 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAGGACTGGCTGAA 1037
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BASE COUNT        241 a     330 c     259 g     165 t
ORIGIN

Query Match           57.0%;  Score 819;  DB 14;  Length 995;
Best Local Similarity 96.4%;  Pred. No. 1.9e-190;
Matches  859;  Conservative  0;  Mismatches  30;  Indels  2;  Gaps  2;

Qy    400 TACTTCGAATTCTGGGGCCAGGCGCCCTGGTCACCGTCCTCCAGCTAGCACCAAGGGC 459
          ||||||     ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 TACTTTGACGATTGGGGCCAGGGAAGCCTGGTCACCGTCCTCCAGCCTCCACCAAGGGC 66

Qy    460 CCATCGGCTTCCCCTGGCACCCTCCTCCAAGAGCACTTCTGGGGGCACAGCGGCCCTG 519
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Db     67 CCATCGGCTTCCCCTGGCACCCTCCTCCAAGAGCACTTCTGGGGGCACAGCGGCCCTG 126

Qy    520 GGCTGCCTGGTCAAGGACTACTTCCCCGACAACCGGTGCACGGTGTCGTGGAACTCAGGCGC 579
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Db    127 GGCTGCCTGGTCAAGGACTACTTCCCCGACAACCGGTGCACGGTGTCGTGGAACTCAGGCGC 186

Qy    580 CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC 246

Qy    640 AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG 699
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Db    247 AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG 306

Qy    700 AATCACAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAA 759
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Db    307 AATCACAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA 366

Qy    760 ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTC 819
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Db    367 ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTC 426

Qy    820 TTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG 879
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Db    427 TTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG 486

Qy    880 GTGGTGGACGTGAGCCACGAGGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG 939
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Db    487 GTGGTGGACGTGAGCCACGAGGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG 546

Qy    940 GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG 999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG 606

Qy   1000 GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG 1059
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Db    607 GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG 666

Qy   1060 GTCTCCAACAAAGCCCTCCCAGCCCCCATCTCGAGAAAAACCATCTCCAAAGCCAAAGGGCAG 1119
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Db    667 GTCTCCAACAAAGCCCTCCCAGCCCCCATCTCGAGAAAAACCATCTCCAAAGCCAAAGGGCAG 726

Qy   1120 CCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAG 1179
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Db    727 CCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAG 786

Qy   1180 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG-A 1238
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Db    787 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCATCCCAGCGACTTCCCCGTGGGAGTGGGAA 846

Qy   1239 GAGCAATGGCAGCCGAGAACAACTACAAGA-CCACGCCTCCCGTGCTGG 1288
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Db    847 AAGCAATGGGAAGCCGGAAAAAAAAACTACAAGACCCCCGCCTCCCGTGCTTG 897
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RESULT 11
BQ711291    BQ711291
LOCUS       AGENCOURT_8347186 NIH_MGC_113  881 bp  mRNA  linear  EST 16-JUL-2002
DEFINITION  AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096
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Db    421  TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC   480

Qy   1098  CATCTCCAAAGCCAAGGGCCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG  1157
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Db    481  CATCTCCAAAGCCAAGGGCCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG   540

Qy   1158  GGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG  1217
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Db    541  GGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG   600

Qy   1218  CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC  1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC   660

Qy   1278  TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG  1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG   720

Qy   1338  CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA  1397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA   780

Qy   1398  CTACACGCAGAAGAGCCTCTCCCTGTCTCCGG  1429
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Db    781  CTACACGCAGAAGAGCCTCTCCCTGTCTCCGG   812
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RESULT 12
BQ064886
LOCUS   BQ064886   1031 bp   mRNA   linear   EST 02-APR-2002
DEFINITION AGENCOURT_6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343
            5', mRNA sequence.
ACCESSION   BQ064886
VERSION   BQ064886.1 GI:19893932
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1031)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2107 row: e column: 24
            High quality sequence stop: 573.
FEATURES   Location/Qualifiers
     source   1..1031
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_99"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."

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BASE COUNT      248 a    349 c    271 g    162 t     1 others
ORIGIN

Query Match             55.7%;   Score 800.2;  DB 14;   Length 1031;
Best Local Similarity   94.4%;   Pred. No. 8.1e-186;
Matches   840;   Conservative   0;  Mismatches  49;   Indels   1;   Gaps   1;
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Qy    497  CCCTGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGGACTACTTCCCGAACCGGTGA  556
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Db     11  CCCTGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGGACTACTTCCCGAACCGGTGA   70

Qy    557  CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC  616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71  CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC  130

Qy    617  AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA  676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131  AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA  190

Qy    677  CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAG  736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191  CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAG  250

Qy    737  CAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC  796
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Db    251  TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC  310

Qy    797  TGGGGGGACCGTCAGTCTTCCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC  856
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311  TGGGGGGACCGTCAGTCTTCCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC  370

Qy    857  GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGGACCCTGAGGTCAAGT  916
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Db    371  GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAGGACCCTGAGGTCAAGT  430

Qy    917  TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC  976
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431  TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC  490

Qy    977  AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA  1036
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491  AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA  550

Qy   1037  ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA  1096
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Db    551  ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA  610

Qy   1097  CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC  1156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611  CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC  670

Qy   1157  GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA  1216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671  GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA  730

Qy   1217  GCGACATCGCCGT-GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG  1275
           ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    731  GCGACATCGCCCNTGGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGAACCCG  790

Qy   1276  CCTCCCGTGCTGGACTTCGACGGCTCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG  1335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791  CCTCCCGTGCTGAACTCGACGGCTCTCCTTCTTCCTCTACACGCAAAGCTCACCGGGGGACA  850

Qy   1336  AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC  1385
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Db    851  AAAGCAGGGGGGCAACCGGGGGGCAACCGGGGGAGAACGTCTTTCTCAAATGCTCCGTGATGC  900
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RESULT 13
BQ711727
BQ711727
LOCUS   BQ711727   AGENCOURT_8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
                936 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
            5', mRNA sequence.

ACCESSION   BQ711727
VERSION   BQ711727.1 GI:21850626
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 936)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2518 row: k column: 18
            High quality sequence stop: 547.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301961"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   231 a   306 c   245 g   152 t   2 others
ORIGIN

Query Match   55.5%; Score 797.4; DB 14; Length 936;
Best Local Similarity   98.3%; Pred. No. 3.8e-185;
Matches   826; Conservative   0; Mismatches   12; Indels   2; Gaps   2;

Qy   599 CCTTCCCGGCTGTCCTACAGTCCTCCAGGACTTCTACTCCCTCCAGCAGCGGTGGTGACCGTGC 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10 CCTTCCCGGCTGTCCTACAGTCCTCCAGGACTTCTACTCCCTCCAGCAGCGGTGGTGACCGTGC 69

Qy   659 CCTTCCAGCAGCTTGGGCACCCAGCCAGACCTACATCGCAACGTGAATCACAAGCCCAGCAACA 718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   70 CCTCCAGCAGCTTGGGCACCCAGCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACA 129

Qy   719 CCAAGGTGACAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT 778
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Db   130 CCAAGGTGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT 189

Qy   779 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 838
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 249

Qy   839 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACG 898
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Db   250 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACG 309

Qy   899 AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 958
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Db   310 AAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 369

Qy   959 CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC 1018
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC 429

Qy   1019 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC 1078

Db   430 TGCACCAGGACTGGCTGAATGGCAAGGATACAAGGTGCAAGGTCTTCCAACAAAGCCCTCC 489
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1079 CAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT 1138
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Db   490 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT 549

Qy   1139 ACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGG 1198
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   550 ACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGG 609

Qy   1199 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGGAGA 1258
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   610 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGGAGA 669

Qy   1259 ACAACTACAAGACCA-CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 1317
          |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   670 ACAACTACNAGACACCGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 729

Qy   1318 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG 1377
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Db   730 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGGGATG 789

Qy   1378 CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   790 CATGAGGGTCTGGAC-ACCACTAACCCGAGAAGAGCCTCTTCCTCCTGTCTCCGGGAAATGA 848

RESULT 14
BQ705928
LOCUS   BQ705928   AGENCOURT_7976186 NIH_MGC_113   940 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION AGENCOURT_7976186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214795
            5', mRNA sequence.
ACCESSION   BQ705928
VERSION   BQ705928.1 GI:21844827
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 940)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2382 row: k column: 20
            High quality sequence stop: 619.
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT   235 a   318 c   240 g   147 t
ORIGIN

Query Match   55.4%;   Score 796;   DB 14;   Length 940;
Best Local Similarity 99.3%;   Pred. No. 8.4e-185;
Matches 810; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Db      1 CAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCAGCAGCTTGGCACCCAGA 60

Qy    683 CCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGACAAGAAAGCAGAGC 742
              ||||||||||||||||||||||||||||||||||||||||||| ||||
Db     61 CCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAGAAAGTTGAGC 120

Qy    743 CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGG 802
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCAACTCCTGGGG 180

Qy    803 GACCGTCAGTCTTCCTCTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GACCGTCAGTCTTCCTCTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC 240

Qy    863 CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT 922
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Db    241 CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT 300

Qy    923 GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACACAAAGCCGGGAGGAGCAGTACA 982
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Db    301 GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACACAAAGCCGGGAGGAGCAGTACA 360

Qy    983 ACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCA 1042
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Qy   1043 AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCT 1102
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Db    421 AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCT 480

Qy   1103 CCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATG 1162
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Db    481 CCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATG 540

Qy   1163 AGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACA 1222
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Qy   1223 TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG 1282
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Db    601 TCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG 660

Qy   1283 TGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGT 1342
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Db    661 TGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGT 720

Qy   1343 GGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA 1402
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Qy   1403 CGC-AGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
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RESULT 15
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LOCUS   BQ710532   AGENCOURT_8352211 NIH_MGC_113   977 bp   mRNA   linear   EST 16-JUL-2002
DEFINITION   5', mRNA sequence.   AGENCOURT_8352211 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277538
ACCESSION   BQ710532
VERSION   BQ710532.1   GI:21849431
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

FEATURES   Location/Qualifiers
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                     /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT   227 a   331 c   264 g   154 t   1 others
ORIGIN

Query Match   54.8%;   Score 787.4;   DB 14;   Length 977;
Best Local Similarity 92.5%;   Pred. No. 1.1e-182;
Matches 886; Conservative   0; Mismatches 57; Indels 15; Gaps   5;

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Qy    481 CCCTCCTCCAGAGCACCTCTTGGGGGCACAGCGGCCCCTGGCCTGCCTGTCAAGGACTAC 540
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Db     11 CCCTGCTCCAGAGCACCTCCGGAGCACAGCACCTGGGCTGCCTGTCAAGGACTAC 70

Qy    541 TTCCCGGAACCGTGACGGTCGTGGAACTCAGGCGGCCCTGACCAGCCGGTGCACACC 600
              |||||||||||||||||||||||| |||| |||||||||||| ||||||||||||||
Db     71 TTCCCGGAACCGTGACGGTCGTGGTGAACTCAGGCGTCGCCCTGACCAGCCGCGTCACACC 130

Qy    601 TTCCCGGCTGTCCTACAGTCCTCACTCCTCCTCAGCAGGACTGCCC 660
              ||||||||||||||||||||| |||||||||| ||||||| |||||
Db    131 TTCCCGGCTGTCCTACAGTCCTCACTCCTCCTCAGCAGCGTGACCGTGACCGTGACCGTGCCC 190

Qy    661 TCCAGCAGCTTGGCACCCAGCACCCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 720
              |||||||||||| |||| |||||||||||| ||||||  ||||||||||||||||||||
Db    191 TCCAGCAGCTTCGGCACCCAGCGACCTACACCTGCAACGTGATCAAGCCCAGCAACACC 250

Qy    721 AAGGTGGACAAGAAACAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 780
              |||||||||||||| ||||||||||   | ||| |||
Db    251 AAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGA-----GTGCCACCGTGTC 301

Qy    781 ACCCTCATGATCTCCCGGGACCCCTGAGGTCGTGGTGGTGGTGGACCTGAGCCACGAA 840
              |||| ||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    302 CCAGCACC---ACCTGCGGACCAGGGACCAGTGAGGTCGTGGTGGTGGACCTGAGCCACGAA 358

Qy    841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGACGTGAGGTGCATATAGCCAAGACA 900
              ||||| ||||||||||||| |||||||||||   || ||| |||||| ||||||||||||
Db    359 ACCCTCATGATCTCCCGGGCCCCTGAGGTCACGTGCAGTCGCGTGCATATAGCCAAGACA 418

Qy    901 GACCCTGAGGTCAAGTTCAACTGGTACGTGACGTGGACGGCGTGGAGGTGCATATAGCCAAGACA 960
              |||||| |||||||||||||||| |||||| |||||| |||||| |||||||||||||||
Db    419 GACCCCGAGGTCCAGTTCAACTGGTACGTGACGTGGACGGCGTGGAGGTGCATATAGCCAAGACA 478

Qy    961 AAGCCGCGGAGGAGCAGTACAACAGCACGTACCCGTCTCCTCACCGTCCTG 1020
              |||||| ||||||||||||||| |||||| |||||| |||| |||||||||
Db    479 AAGCCACCGGAGGAGGAGCAGTTCAACAGCACGTTCCGTGTGTGGTCAGCAGCTCCTCACCGTCGTG 538
```

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Qy  1021  CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAACAAAGCCCTCCCA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   539  CACCAGGACTGGCTGAACGGCAAGGAGTACAAGTCCAAGGTCTCCAACAAAGGCCTCCCA  598

Qy  1081  GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599  GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTAC  658

Qy  1141  ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   659  ACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC  718

Qy  1201  AAAGGCTTCTATCCCAGCGACATC-GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA 1259
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   719  AAAGGCTTCTACCCCAGCGACATCTCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA  778

Qy  1260  CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAA 1319
          ||||||  |||||||||||||||||  |||||||||||||||||||||||||||||||
Db   779  CAACTANCAGACCACACCTCCCATGCTGGACTCCGACGGCTCTTTCTTCCTCTACAGC-A  837

Qy  1320  GCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCATGCTCCGTGATGCA 1379
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   838  GCTCACCGTGGACAAGAGCAAGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA  897

Qy  1380  TGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
          ||||||||| ||||||||||||||||||      ||||||||||||||||||||||||
Db   898  TGAGGCTCTGGCCCCACCCCTACACACA-AAGAGCCTCTCCCTGTCTCCGGGTAAATGA  954
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Search completed: April 6, 2003, 06:20:36
Job time : 2744.1 secs

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                 GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April  5, 2003, 18:12:24 ; Search time 394.366 Seconds
                                       (without alignments)
                                       8205.894 Million cell updates/sec

Title:          US-09-758-173-7
Perfect score:  1437
Sequence:       1 ATGGGTTGGAGCCTCATCTT.........CCCTGTCTCCGGGTAAATGA 1437

Scoring table:  IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2185239 seqs, 1125599159 residues

Total number of hits satisfying chosen parameters:    4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_101002:*
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     24:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1437	100.0	1437	AAV35487	Macaque primatized
2	1437	100.0	1437	AAS17245	DNA sequence of a
3	1435.4	99.9	1437	AAT13847	Primatised anti-hu
4	1219	84.8	7521	AAF30315	Bicistronic chimer
5	1216	84.6	1616	AAS62785	cDNA sequence #572
6	1199.2	83.5	1386	AAQ49834	Anti-HIV-1 recombi
7	1186	82.5	1798	AAC98220	Human colon cancer
8	1185	82.5	1430	AAK98701	cDNA of the heavy
9	1184	82.4	1644	AAS22593	Human cDNA encodin
10	1183	82.3	1549	13 AAQ20066	Encodes heavy chai
11	1182.2	82.3	19035	19 AAV61794	Traget plasmid Man
12	1171.4	81.5	1427	19 AAV41431	Plasmid Hu19CHcpcd
13	1171.4	81.5	1427	19 AAV41429	Plasmid Hu19DHcpcd
14	1169.8	81.4	1427	19 AAV41432	Plasmid Hu19BHcpcd
15	1169.4	81.4	1442	22 AAC84208	Plasmid Glambda-1B
16	1166.2	81.2	6281	22 AAC84206	Plasmid Glambda-1A
17	1165.4	81.1	1615	24 ABK34973	Human cDNA encodin
18	1163	80.9	1617	24 AAS62784	cDNA sequence #571
19	1158.4	80.6	6284	19 AAV41427	Plasmid Hu19AHcpcd
20	1155.8	80.4	1576	14 AAQ49944	Human anti-HBs hea
21	1155.4	80.4	1641	15 AAQ54655	chiT84.12 H3 heavy
22	1153.4	80.3	2974	22 AAH98397	Synthetic EST-deri
23	1147.2	79.8	1335	21 AA234748	Humanised anti-CD2
24	1142.8	79.5	1598	24 ABK34965	Human cDNA encodin
25	1142.8	79.5	1634	24 AAS62516	cDNA sequence #303
26	1141.4	79.4	1356	22 AAD20745	Human recombinant
27	1139.4	79.3	1412	13 AAQ25692	Sequence of the ch
28	1138.6	79.2	1347	21 AAZ60599	cDNA encoding a ra
29	1138.6	79.2	1590	24 ABK34976	Human cDNA encodin
30	1138.6	79.2	1640	24 ABK35183	Human cDNA encodin
31	1133.4	78.9	1599	24 ABK64550	Human benign prost
32	1133.4	78.9	1599	24 ABL62673	Colon adenocarcino
33	1133.4	78.9	1599	24 ABL65479	Lung cancer relate
34	1133.4	78.9	1599	24 ABL66294	Lung cancer relate
35	1131.8	78.8	1617	14 AAQ35099	Antibody D heavy c
c 36	1130.2	78.6	1449	20 AAX06951	Monoclonal antibod
c 37	1130.2	78.6	1449	20 AAX06952	Monoclonal antibod
38	1129.2	78.6	9182	24 ABK10574	Baculovirus expres
39	1127.8	78.5	1467	13 AAQ23570	Reshaped CAMPATH-1
c 40	1127.6	78.5	9182	24 ABL55051	Plasmid pTRABac/9F
41	1127	78.4	1428	22 AAH74680	Nucleotide sequenc
42	1125.8	78.3	9201	15 AAQ65629	Vector contg. TCAE
43	1125.8	78.3	19001	19 AAV61793	Traget plasmid Mol
44	1122.6	78.1	1413	21 AAA63531	DNA encoding a dim
c 45	1121	78.0	2912	22 AAS22718	Human cDNA encodin

ALIGNMENTS

```
RESULT 1
AAV35487
ID   AAV35487 standard; DNA; 1437 BP.
XX
AC   AAV35487;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Macaque primatized 7B6 heavy chain DNA.
XX
KW   Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
KW   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW   T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW   immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
KW   T cell proliferation; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1437
FT                   /*tag= a
FT                   /product= 7B6 heavy chain
XX
PN   WO9819706-A1.
XX
PD   14-MAY-1998.
XX
PF   29-OCT-1997;  97WO-US19906.
XX
PR   08-NOV-1996;  96US-0746361.
XX
PA   (IDEC-) IDEC PHARM CORP.
```

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XX
PI   Anderson DR, Brams P, Hanna N;
XX
DR   WPI; 1998-286601/25.
DR   P-PSDB; AAW63763.
XX
PT   New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT   inhibiting binding to CD28 - useful as specific immunosuppressants
PT   for treating diseases that involve interactions between T and B
PT   cells, e.g. graft rejection or tumours
XX
PS   Example 7; Fig 4b; 87pp; English.
XX
CC   This sequence encodes a primatized form of the antibody 7B6 heavy chain
CC   from macaque. This sequence is used in a method which studies new
CC   monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to
CC   B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC   Mab's are specific immunosuppressants for treatment of diseases involving
CC   T cell/B cell interactions, particularly autoimmune disease, specifically
CC   idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC   I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC   inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC   host diseases, B cell lymphoma, infections (including by human immune
CC   deficiency virus) or inflammatory disease and tumours. Optionally the
CC   MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can
CC   also be used as imaging agents and as vaccines or immunogens to develop
CC   anti-idiotype reagents. MAb's are optionally combined with other proteins
CC   or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC   induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC   production of interleukin-2 (IL-2), T cell proliferation and
CC   antigen-specific immunoglobulin G (IgG) responses.
XX
SQ   Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;

Query Match       100.0%;  Score 1437;  DB 19;  Length 1437;
Best Local Similarity  100.0%;  Pred. No. 1.3e-277;
Matches 1437;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 ATGGGTGGAGCTCATCTTGCTCTTCCTTGTCGCTGTTGTACGCGTGTCCAGTGTGAG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGGTGGAGCTCATCTTGCTCTTCCTTGTCGCTGTTGTACGCGTGTCCAGTGTGAG 60

Qy   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120

Qy  121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180

Qy  181 GGGAAGGGGCCGAATGGGTAGGTTCATTAGAAACAAACGAACGGTGGGACAACAGAA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GGGAAGGGGCCGAATGGGTAGGTTCATTAGAAACAAACGAACGGTGGGACAACAGAA 240

Qy  241 TACGCCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCAAAAGCATCGCC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TACGCCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCAAAAGCATCGCC 300

Qy  301 TATCTGCAAATGAGCAGCCTGAAAATGCGAGGACACGCCGTCTTATTACTGTACATCC 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TATCTGCAAATGAGCAGCCTGAAAATGCGAGGACACGCCGTCTTATTACTGTACATCC 360

Qy  361 TACATTTCACATTGTCGGGGTGGTCTGCTATGGAGGTTACTTCGAATTCTGGGGCCAG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 TACATTTCACATTGTCGGGGTGGTCTGCTATGGAGGTTACTTCGAATTCTGGGGCCAG 420

Qy  421 GGCGCCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GGCGCCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCA 480

Qy  481 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 540

Qy  541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 600

Qy  601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 660
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Db  601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 660

Qy  661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 720

Qy  721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 780

Qy  781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCCCCCCAAAACCCAAGGAC 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCCCCCCAAAACCCAAGGAC 840

Qy  841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 900

Qy  901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 960
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Db  901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 960

Qy  961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 1020

Qy 1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1080

Qy 1081 GCCCCCATCGAGAAAACCATCTCAAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 GCCCCCATCGAGAAAACCATCTCAAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1140

Qy 1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200

Qy 1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260

Qy 1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320

Qy 1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380

Qy 1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGGGTAAATGA 1437
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGGGTAAATGA 1437


RESULT 2
AAS17245
ID   AAS17245 standard; DNA; 1437 BP.
XX
AC   AAS17245;
XX
DT   12-MAR-2002  (first entry)
XX
DE   DNA sequence of a primatised form of the heavy chain of 7B6 antibody.
XX
KW   Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
```

KW   neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
KW   B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;
KW   tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
KW   graft-vs-host disease; immunosuppression; organ rejection;
KW   interleukin-2; IL-2; mutant; ds.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Macaca sp.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1437
FT   /*tag= a
FT   /product= "Heavy chain of 7B6 antibody"
XX
PN   WO200189567-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16364.
XX
PR   22-MAY-2000; 2000US-0576424.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Hanna N, Brams P;
XX
DR   WPI; 2002-089895/12.
DR   P-PSDB; AAU11644.
XX
PT   Use of monoclonal antibody which specifically binds to B7.1 antigen
PT   CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT   treating cancer, graft-vs-host disease and autoimmune disease such as
PT   allergy -
XX
PS   Example 8; Fig 4b; 89pp; English.
XX
CC   The present invention relates to a new use of a monoclonal antibody
CC   which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC   (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC   useful for treating diseases such as B cell cancer, lymphoma, a
CC   cancer where B cells promote the growth and/or metastasis of tumours,
CC   B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC   idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC   type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC   anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC   or graft-vs-host disease. The antibody is useful for immunosuppression
CC   in a human or animal and for treating or preventing resistance to or
CC   rejection of transplanted organ or tissue for treating proliferative
CC   and hyperproliferative diseases, for treating reversible obstructive
CC   airways disease, intestinal inflammations and allergies e.g. Crohn's
CC   disease and ulcerative colitis, food-related allergies e.g. migraine,
CC   rhinitis and eczema, and other types of allergies. The present nucleic
CC   acid sequence encodes the heavy chain of 7B6, a primatised antibody
CC   used in the invention to induce apoptosis.
XX
SQ   Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;

Query Match   100.0%; Score 1437; DB 24; Length 1437;
Best Local Similarity 100.0%; Pred. No. 1.3e-277;
Matches 1437; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGGCGTGTCCAGTGTGAG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGGCGTGTCCAGTGTGAG   60

Qy   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGAGTCTCC   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGAGTCTCC   120

Qy   121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA   180

Qy   181 GGGAAGGGGCCGGAATGGGTAGGTTCATTAGAAACAAACCGAACGGTGGACAACAGAA   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGAAGGGGCCGGAATGGGTAGGTTCATTAGAAACAAACCGAACGGTGGACAACAGAA   240

Qy   241 TACGGCCGCTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TACGGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC   300

Qy   301 TATCTGCAAATGAGCAGCCGAAAATGAGGACACGGCCGTCTATTACTGTACTACATCC   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TATCTGCAAATGAGCAGCCTGAAAATGAGGACACGGCCGTCTATTACTGTACTACATCC   360

Qy   361 TACATTTCACATTGTCGGGGTGGTGTCGTCTATGGAGGTTACTTGCAATTCTGGGGCCAG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TACATTTCACATTGTCGGGGTGGTGTCGTCTATGGAGGTTACTTGCAATTCTGGGGCCAG   420

Qy   421 GGCGCCCTGGTCACGGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GGCGCCCTGGTCACGGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA   480

Qy   481 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC   540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC   540

Qy   541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC   600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC   600

Qy   601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC   660

Qy   661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC   720

Qy   721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC   780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC   780

Qy   781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC   840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC   840

Qy   841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA   900

Qy   901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA   960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA   960

Qy   961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG   1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG   1020

Qy   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA   1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA   1080

Qy   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC   1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC   1140

Qy   1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC   1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC   1200

Qy   1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC   1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC   1260

Qy   1 ATGGGTTGGAGCTGCATCATCTTCTTGTCTCCGTGTTGCTACGCGTGTCCAGTGTGAG   60
Db   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC   120
Qy   61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC   120
Db   121 TGTGCAGTCTCTGGATTCACCTTCAGTGACGCCACTACATGTATTGGTTCCGCCAGGCTCCA   180
Qy   121 TGTGCAGTCTCTGGATTCACCTTCAGTGACGCCACTACATGTATTGGTTCCGCCAGGCTCCA   180
Db   181 GGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACGAACGGTGGACAACAGAA   240
Qy   181 GGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACGAACGGTGGACAACAGAA   240
Db   241 TACGCGCGTCTGTGAAAGACAGATTCACCATTCCAGAGATGATTCAAAAGCATCGCC   300
Qy   241 TACGCGCGTCTGTGAAAGACAGATTCACCATTCCAGAGATGATTCAAAAGCATCGCC   300
Db   301 TATCTGCAAATGAGCAGCCTGAAAATGCAGGACACGGCCGTCTATTACTGTACTACATCC   360
Qy   301 TATCTGCAAATGAGCAGCCTGAAAATGCAGGACACGGCCGTCTATTACTGTACTACATCC   360
Db   361 TACATTTCACATTGTCGGGGTGGTCTGCTATGGAGGTTACTTCGAATTCTGGGGCCAG   420
Qy   361 TACATTTCACATTGTCGGGGTGGTCTGCTATGGAGGTTACTTCGAATTCTGGGGCCAG   420
Db   421 GGGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA   480
Qy   421 GGCGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA   480
Db   481 CCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTGCAAGGACTAC   540
Qy   481 CCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTGCAAGGACTAC   540
Db   541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC   600
Qy   541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC   600
Db   601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC   660
Qy   601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC   660
Db   661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC   720
Qy   661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC   720
Db   721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC   780
Qy   721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC   780
Db   781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC   840
Qy   781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC   840
Db   841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA   900
Qy   841 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA   900
Db   901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA   960
Qy   901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA   960
Db   961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG   1020
Qy   961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCGTCCTG   1020
Db   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA   1080
Qy   1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA   1080
Db   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC   1140
Qy   1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC   1140

Qy   1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG   1320
Db   1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG   1320
Qy   1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT   1380
Db   1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT   1380
Qy   1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1437
Db   1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1437

RESULT 3
AAT13847
ID   AAT13847 standard; DNA; 1437 BP.
XX
AC   AAT13847;
XX
DT   25-MAY-1997 (first entry)
XX
DE   Primatised anti-human B7.1 antigen antibody 7B6 heavy chain DNA.
XX
KW   Monoclonal antibody; cynomolgus monkey; macaque; 7B6;
KW   primatised antibody; B7 antigen; CD28; immunosuppressive;
KW   autoimmune disease; idiopathic thrombocytopaenia purpura;
KW   systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW   type 1 diabetes mellitus; graft versus host disease;
KW   hetero-hybridoma; transfectoma; ss.
XX
OS   Chimeric Macaca cynomolgus;
OS   Chimeric Homo sapiens.
XX
PN   WO9640878-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996; 96WO-US10053.
XX
PR   07-JUN-1995; 95US-0487550.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
DR   WPI; 1997-108638/10.
DR   P-PSDB; AAW01820.
XX
PT   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT   useful for treating autoimmune disease or graft-versus-host disease
XX
PS   Claim 8; Fig 9B; 81pp; English.
XX
CC   2 DNA sequences (AAT62511 and AAT13847) respectively code for
CC   primatised forms (AAW01819 and AAW01820) of the light and heavy chains
CC   of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC   7B6. Cloned 7B6 light and heavy variable genes are inserted into
CC   an expression vector (pref. NEOSPLA) which contains human light and
CC   heavy chain constant region genes to allow prodn. of primatised
CC   antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
CC   antibodies have also been produced (see also AAW01817-18 and AAW01821-
CC   22). The primatised antibodies inhibit the B7:CD28 pathway, making
CC   them useful immunosuppressants for the treatment of autoimmune
CC   disorders and graft-versus-host disease.
XX
SQ   Sequence 1437 BP; 329 A; 452 C; 387 G; 269 T; 0 other;

Query Match   99.9%; Score 1435.4; DB 18; Length 1437;
Best Local Similarity   99.9%; Pred. No. 2.6e-277;
Matches 1436; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

Qy   1 ATGGGTTGGAGCTGCATCATCTTCTTGTCTCCGTGTTGCTACGCGTGTCCAGTGTGAG   60
Db   1 ATGGGTTGGAGCTGCATCATCTTCTTGTCTCCGTGTTGCTACGCGTGTCCAGTGTGAG   60

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Qy  1141 ACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 ACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200

Qy  1201 AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260

Qy  1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320

Qy  1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380

Qy  1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGTGTCCGGGTAAATGA 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGTGTCCGGGTAAATGA 1437
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RESULT 4

AAF30315

ID   AAF30315 standard; cDNA; 7521 BP.
XX
AC   AAF30315;
XX
DT   14-MAY-2001 (first entry)
XX
DE   Bicistronic chimeric idiotype plasmid VR1623.
XX
KW   Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KW   immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1623;
KW   antibody; idiotype; vector; ss.
XX
OS   Chimeric - Cytomegalovirus.
OS   Chimeric - Mus musculus.
OS   Chimeric - Bos taurus.
XX
PN   WO200109303-A2.
XX
PD   08-FEB-2001.
XX
PF   31-JUL-2000; 2000WO-US20679.
XX
PR   30-JUL-1999; 99US-0146170.
XX
PA   (VICA-) VICAL INC.
XX
PI   Hermanson GG;
XX
DR   WPI; 2001-123319/13.
XX
PT   Immunogenic compositions comprising Flt-3 ligand encoding
PT   polynucleotide and one or more antigen, or cytokine encoding
PT   polynucleotides, useful for suppressing tumour growth and for treating
PT   autoimmune diseases (e.g. rheumatoid arthritis) -
XX
PS   Example 1; Page 92-97; 149pp; English.
XX
CC   The present sequence is that of bicistronic chimeric idiotype
CC   plasmid VR1623, which includes the cytomegalovirus immediate-early
CC   promoter, enhancer and 5' untranslated sequences, driving the
CC   expression of mouse chimeric immunoglobulin light and heavy chain
CC   coding sequences. The transcriptional terminator region includes
CC   polyA and termination signals from the bovine growth hormone gene.
CC   The plasmid expresses a functional chimeric idiotype immunoglobulin
CC   that stimulates a partially protective B and T cell response to
CC   38C13 tumour. Co-administration of VR1623 with plasmid VR6200 (see
CC   AAF30313) encoding a secreted form (see AAB20187) of mouse Fms-like
CC   tyrosine kinase (Flt-3 ligand), demonstrated the ability of the
CC   present invention to enhance protection from tumour challenge in a
CC   mouse B-cell lymphoma model. Thus, the invention is directed to
CC   enhancing the immune response of a vertebrate to an antigen or a
CC   cytokine by administering in vivo a Flt-3 ligand-encoding
CC   polynucleotide such as VR6200, and 1 or more antigen- or
CC   cytokine-encoding polynucleotides.
XX
SQ   Sequence 7521 BP; 1879 A; 1988 C; 1858 G; 1796 T; 0 other;

Query Match   84.8%;   Score 1219; DB 22;   Length 7521;
Best Local Similarity 91.3%;   Pred. No. 4.6e-234;
Matches 1307; Conservative   0; Mismatches 115; Indels   9; Gaps   1;

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Qy    7 TGGAGCCTCATCTTGCTCCTCCTTGTCGTGTGCTGTGCTACGGCCGTGTGCAGTGTGAGGTGCAA 66
         ||||||||||||| ||||||||| ||||  ||  |||||| ||||||||||||||||||||||||
Db 2739 TTGTGCTGAACTGGATTTTCCTTGTAACACTTTAAATGTATCCAGTGTGAGGTGAAG 2798

Qy   67 CTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCCTGTGCA 126
         |||||||||||| |||||| ||||||||||||  ||||||||||||||||||||||||
Db 2799 CTGGTGGAGTCTGAGGGAGGCTTGGTACAGCCTCGGGGGTCTTCTCTGAGTCTCTGTGCA 2858

Qy  127 GTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCAGGGAAG 186
         ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db 2859 GCTTCTGGATTCACCTTCACTGATTACTACATGAGCTGGGTCCGCCAGCCTCCAGGGAAG 2918

Qy  187 GGGCCGGAATGGGTAGGTTTCATTAGAAACAAACCGAACGGTGGGACAACAGAATACGCC 246
         ||||||  |||||||||||  || ||||| | || ||||||||||||  ||   |||||
Db 2919 GCACTTGAGTGGTTGGCTTTGATTAGATTAGAAACAAAGCTAATGGTTACACAACAGAGTACAGT 2978

Qy  247 GCGCTCGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCCTATCTG 306
         |||||||||| ||||||||||||||| |||| |||||||  |||||||||||||||||||
Db 2979 GCATCTGTGAAGGGTCGGTTCACCATCTCCAGAGATAATTCCAAAAGCATCCTCTATCTT 3038

Qy  307 CAAATGAGCAGCCTGAAAATCGAGGACACGGCCGTCTATTACTGTGTACTACATCCTACATT 366
         ||||||||||| | |||||||||||||||||||| ||   | |  |||||| |
Db 3039 CAAATGAATCGCCTGAGAGCTGAGGACACAGTGCCACTTATTATTACTGTGCAAGAGATCCCAAT 3098

Qy  367 TCACATTGTCGGGGTGGTGCTGTCTATGGAGGTTACTTGGAATTCTGGGGCCAGGGCGCC 426
         |  |   | |  |||  |||     ||| ||||   || |||||||||||||||||||||
Db 3099 TACTA--------CGATGGTAGCTACGAAGGGTACTTTGACTACTGGGGCCAAGGTACC 3149

Qy  427 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 486
         ||||||||||||| ||||||||| ||||||||||||  |||||||||||||||||||||
Db 3150 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCACCCTCC 3209

Qy  487 TCCAAGAGCACCTCTGGGGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3210 TCCAAGAGCACCTCTGGGGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 3269

Qy  547 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3270 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 3329

Qy  607 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3330 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 3389

Qy  667 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 726
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3390 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 3449

Qy  727 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3450 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 3509

Qy  787 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 846
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3510 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 3569

Qy  847 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 906
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3570 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 3629

Qy  907 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 966
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CC   The present invention relates to the isolation of novel cDNA sequences
CC   which encode human secreted proteins. The cDNA sequences have been
CC   derived from a variety of human tissues. The invention also provides
CC   a method for producing proteins from these polynucleotide sequences.
CC   The proteins are useful for identifying compounds that modulate their
CC   activity and production, and the cell is also useful for identifying
CC   compounds that modulate expression of the polynucleotide sequences
CC   encoding the secreted proteins. The sequences of the invention are
CC   useful for treating diseases such as hyperproliferative disorders
CC   (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC   immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC   sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC   disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
CC   The polynucleotide sequences of the invention are also useful in gene
CC   therapy. AAS62214-AAS62838 represent the cDNA sequences of the
CC   invention that encode for novel human secreted proteins.
XX
SQ   Sequence 1616 BP; 369 A; 503 C; 441 G; 298 T; 5 other;
```

Query Match   84.6%; Score 1216; DB 24;   Length 1616;
Best Local Similarity   91.0%; Pred. No.1.6e-233;
Matches 1307; Conservative 0; Mismatches 118; Indels 12; Gaps 1;

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Qy      1 ATGGGTTGGAGCCTCATCTTGCTTCCTTCCTTGTCCGTGTCCAGTGTGAG 60
          ||||||||||||||||||||||||||||   |||||||||||||||||||
Db     66 ATGGAGTTTGGGCTTAGCTCGGTTTTCCTTGTTGTCTATTTTAAAAGGTGTCAATGTGAG 125

Qy     61 GTGCAACTGGTGGAGTCTCGGGGAGGCTTGGTCCAGCCTGCGGGTCCCTCTGAGAGTCTCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 GTGCAGCTGGTGGAGTCTCGGGGAGGCCTGATCACAACCAGCGGGTCCCTCCTGAGACTCTCC 185

Qy    121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGGCCAGGCTCCA 180
          |||||||||||||||||||||||||  ||  |||| | ||||||||||||||||||||||
Db    186 TGCAGAGGTTCTGGATTCCCGTTTGGATTATGTGTGAGCTGGGTCCGCCCAGGCTCCA 245

Qy    181 GGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAACAAACCGAACGGTGGACAACAGAA 240
          |||||||||||||||||||||||||||||||||||||||   ||||||||||||  |||
Db    246 GGGAAGGGGCTGGAGTTGGGTAGGGTAGGGTCAATGAGAACCGAGGCTTATGGTGGGACAAGAAAT 305

Qy    241 TACGCCGGCTGTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC 300
          ||||||||||||||| ||| |||||||||||||||||||||||| ||||||||||||||
Db    306 TACGCCCGGCTGTCTGTGACGGGCAGATTCACCATCTCAAGAGACGATGATTCCAAAGCCATCGCC 365

Qy    301 TATCTGCAAATGAGCAGCCTGAAAATGGACAGCAGCGGGCGCGTCTATTACTGTACACATCC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 TATCTGCAGATGAGCAGCCTGAAAACCGAGGACACACAGGCCTTTATCACTGTAGTA---- 420

Qy    361 TACATTTCACATTGTCGGGTGGTCTCGTCTATGGAGGTTACTTCGAATTCTGGGGCCAG 420
          ||||| ||| |||||||||||  |||||||  ||||||  ||||||||||||||||||
Db    421 ------AACATTACTATGATGATACTGGTTATCACGAATACTTCCAACACTGGGGCGAG 473

Qy    421 GGGCGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474 GGCACCCTGGTCATCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 533

Qy    481 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTGAAGGACTAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTGAAGGACTAC 593

Qy    541 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGCGGCCCTGACCAGCGGCGTGCACACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGCGGCCCTGACCAGCGGCGTGCACACC 653

Qy    601 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTCGTGACCGTGCCC 660
          ||||||||||||||||||||||||||||||||| || ||||||||||||||||||||||
Db    654 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 713

Qy    661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    714 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 773

Qy    721 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 780
          |||||||  ||||||||||||||||||| ||  |||||||||||||||||||||||||||
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Db   3630 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 3689
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    967 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1026
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   3690 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 3749
Qy   1027 GACTGGCTGAATGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3750 GACTGGCTGAATGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 3809
Qy   1087 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3810 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 3869
Qy   1147 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3870 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 3929
Qy   1207 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3930 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 3989
Qy   1267 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3990 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 4049
Qy   1327 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4050 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 4109
Qy   1387 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
          |||||||||||||||||||||||||||||||||||||||||||| ||
Db   4110 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGATCCTGA 4160
```

```
RESULT 5
AAS62785
ID   AAS62785 standard; cDNA; 1616 BP.
XX
AC   AAS62785;
XX
DT   14-FEB-2002  (first entry)
XX
DE   cDNA sequence #572 encoding novel human secreted protein.
XX
KW   Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW   immune deficiency disorder; blood disorder; inflammatory disorder;
KW   infectious disorder; gene therapy; antimicrobial; hepatotropic;
KW   immunosuppressive; antirheumatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200177291-A2.
XX
PD   18-OCT-2001.
XX
PF   29-MAR-2001; 2001WO-US10485.
XX
PR   06-APR-2000; 2000US-195604P.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI   Gulukota K, Graham JR;
XX
DR   WPI; 2002-010900/01.
XX
PT   New polynucleotides encoding secreted proteins useful for treating e.g.
PT   asthma, HIV and Crohn's disease -
XX
PS   Claim 1; Page 363-364; 391pp; English.
XX
```

```
Db   774 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 833

Qy   781 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   834 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 893

Qy   841 ACCCTCATGATCTCCCGGACCCCTGAGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   894 ACCCTCATGATCTCCCGGACCCCTGAGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 953

Qy   901 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   954 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 1013

Qy   961 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTG 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1014 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTG 1073

Qy  1021 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1074 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1133

Qy  1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1134 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1193

Qy  1141 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1194 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC 1253

Qy  1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1254 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1313

Qy  1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320
             ||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  1314 AACTACAAGACCACNCGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAG 1373

Qy  1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
             |||||||||||||||||||||||||| ||||||||| ||||||||||||||||
Db  1374 CTCNCCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1433

Qy  1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
             ||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db  1434 GAGGCTNTGTTCAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAATGA 1490
```

RESULT 6
AAQ49934
ID   AAQ49934 standard; cDNA; 1386 BP.
XX
AC   AAQ49834;
XX
DT   27-APR-1994 (first entry)
XX
DE   Anti-HIV-1 recombinant antibody 447-52D heavy chain coding sequence.
XX
KW   Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW   HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW   acquired immune deficiency syndrome; chimeric antibody;
KW   surface glycoprotein gp120; V3 loop; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1386
FT   /*tag= a
FT   /note= "encodes recombinantly modified 447-52D
FT   heavy chain"
XX
PN   WO9319785-A.
XX
PD   14-OCT-1993.

```
Query Match             83.5%;  Score 1199.2;  DB 14;  Length 1386;
Best Local Similarity   92.1%;  Pred. No. 3.5e-230;
Matches 1277;  Conservative   0;  Mismatches 103;  Indels   6;  Gaps   1;

Qy    58 GAGGTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGTCCCTGAGAGTC 117
            | ||||||||||||||||||||||| ||||||||||| ||||||||| |||||||||
Db     1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTCAGACTC 60

Qy   118 TCCTGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCT 177
            | |||||| |||||||  ||||| |||||| || || ||||| |||| ||||||||||
Db    61 ACCTGTGTAGCCTCTGGTTTCACGTTCAGTGATGTGTCGGCTGAACTGGAGTCCGCCAGGCT 120

Qy   178 CCAGGGAAGGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACGAACGATGTGGGACAACA 237
            ||||||||||||||| | ||||||||| |||||||| ||||| ||||||||||||||||
Db   121 CCAGGGAAGGGGCTGGAGTGGGTTGGCCGTATTAAAAGCAAAGCAGAACTGATGTGGGACAACA 180

Qy   238 GAATACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATC 297
            ||||| || || ||||  ||||||||| |||||||||||||||||| ||||||||| ||
Db   181 GACTACGCTGCATCCGTGAAAGGCAGATTCACCATCTCCAGAGACAATGACTCAAAAAACACG 240

Qy   298 GCCTATCTGCAAATGAGCAGCCTGAAAATCGAAGACACGGCCGTCTATTACTGTACTACA 357
            ||||| ||||||| ||||||| |||||| |||||||| ||||| ||||| ||||| ||||
Db   241 CTATATCTGCAAATGAATAGCCTGAAAACAGAGGACACAGCCGTGTTTATTCTGCACCACA 300

Qy   358 TCCTACATTCACATTGTCGGGG------TGTGTCTGCTATGGAGGTTACTTCGAATTC 411
            | |||| || |||  ||||||       |||| || ||||| |||||| |||||||||
Db   301 GATGGTTTTTATTATGATTCGGGAGAGTCCCAGGACTACTACTACTACATCGACGTT 360

Qy   412 TGGGGCCAGGGGCGCCCTGGTCACCGTCTCCTCAGTGAGCACCAAGGGCCCATCGGTCTTC 471
            ||||| ||||||| ||||||||||| |||| |||| |||||||||| ||||||||||||||
Db   361 TGGGGCAAGGGACCACGGGTCACCGTCTCAGTGAGCCTCCAGCCCAGGGCCCATCGGTCTTC 420

Qy   472 CCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC 531
            |||||||| |||||||||||||||| ||||||||||||||||| ||||||||||||||||
Db   421 CCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC 480

Qy   532 AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGC 591
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGC 540
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KW   immunomodulatory; muscular; gynaecological; gastrointestinal;
KW   nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW   neural disorder; immune system disorder; muscular disorder;
KW   reproductive disorder; gastrointestinal disorder; renal disorder;
KW   infectious disease; cardiovascular disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055351-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05883.
XX
PR   12-MAR-1999;    99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587534/55.
DR   P-PSDB; AAB53463.
XX
PT   Colon cancer associated gene sequences, referred to as colon cancer
PT   antigens, useful for the treatment, prevention, and diagnosis of colon
PT   disorders such as colon cancer -
XX
PS   Claim 1; Page 652; 2104pp; English.
XX
CC   AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC   called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC   human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC   neuroprotective, immunomodulatory, gynaecological, gastrointestinal
CC   vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC   can be used in gene therapy. The colon cancer antigen polynucleotides,
CC   proteins and antibodies to the proteins are useful for the prevention,
CC   treatment and diagnosis of colon disorders, such as colon cancer. The
CC   polynucleotides may be used in diagnostics and research, such as for
CC   chromosome identification, and as hybridisation probes. The proteins
CC   may also be used to prevent diseases such as neural disorders, immune
CC   system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, wounds, renal disorders, infectious
CC   diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC   AAB54007 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 1798 BP; 477 A; 529 C; 458 G; 311 T; 23 other;
```

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Query Match             82.5%;  Score 1186;  DB 21;  Length 1798;
Best Local Similarity   90.2%;  Pred. No. 1.5e-227;
Matches 1296;  Conservative   9;  Mismatches 115;  Indels  17;  Gaps  3;

Qy      1 ATGGGTTGGAGCCTCATCTTGCTCTTCCTGTTGCTTCGCTGTTGCTACGCGTGTCCAGTGTGAG 60
          ||||||||||||||||||||  ||||||||||||||| |||||||||||||||||||||||||
Db    148 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGAGGTGTCCAGTGTCAG 207

Qy     61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGAGGTCCCTGAGACTCTCC 267

Qy    121 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180
          ||||||| :|||||||| |||||||||||||| |||| ||| |||||||||||||||||
Db    268 TGTGCAGCSTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCA 327

Qy    181 GGGAAGGGGCCGGAATGGGTAGTTCATTAGAGAAACAAACCGAACGGTGGGACAACAGAA 240
          |||||||| ||:||| |||| |||:   |: ::|||
Db    328 GGCAAGGGGCTGAGTGGGTGGCAGTTATATSRTA-----TGATGGAAGTAATAAATAC 381

Qy    241 TACGGCGCCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC 300
          |||| | ||||| |||||||||| |||||||||||||||| ||||| |||||||||| |||
Db    382 TATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTG 441

Qy    301 TATCTGCAAATGAGCAGCCTGAAAATCGAGGACACGGCCGTCTATTACTGTACTACATCC 360
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Qy    592 GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTG 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTG 600

Qy    652 ACCGTGCCTCCAGCAGCTTGGCACCACCCAGACCTACATCTGCAACGTGAATACAAAGCCC 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACCGTGCCTCCAGCAGCTTGGCACCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC 660

Qy    712 AGCAACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGC 771
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    661 AGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGC 720

Qy    772 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAA 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTCTTCCTCTTCCCCCCAAAA 780

Qy    832 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATCGTGTGGTGGACGTG 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG 840

Qy    892 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    841 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT 900

Qy    952 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTC 960

Qy   1012 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1020

Qy   1072 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1080

Qy   1132 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1140

Qy   1192 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1200

Qy   1252 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1260

Qy   1312 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1320

Qy   1372 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1380

Qy   1432 AAATGA 1437
          ||||||
Db   1381 AAATGA 1386
```

```
RESULT 7
AAC98220
ID   AAC98220 standard; cDNA; 1798 BP.
XX
AC   AAC98220;
XX
DT   09-MAR-2001   (first entry)
XX
DE   Human colon cancer antigen nucleotide sequence SEQ ID NO:230.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   identification; cytostatic; cardioactive; neuroprotective; vulnerary;
```

```
Db  293 DVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVN 352
            |||||:|:  :::|:|  :|||    |||  |||:|:||||||||||||||:|||||
Qy  354 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 413
            ||:|||||||||||||||:|||: |||  |  ::: ||||||||||||||||||||
Db  353 NKDLPAPIERTISKIKGIVRAPQVVILSPPPEQLSRKDVSLTCLAVGFSPEDISVEWTSN 412

Qy  414 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
            |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db  413 GHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNVYLKKTISRS 472

Qy  474 PGK 476
            |||
Db  473 PGK 475
```

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
F;133-202/Domain: immunoglobulin homology <IMM>

```
Query Match             48.9%;  Score 1259;  DB 2;  Length 328;
Best Local Similarity   69.3%;  Pred. No. 2.2e-67;
Matches  230;  Conservative  43;  Mismatches  53;  Indels  6;  Gaps  2;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
            |: || |||  || ::  || |  | ||||||||:||||||:|||:|||||:|||
Db    1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVLQPS 60

Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
            ||||||||  | || || | |||||||| |  ||| |  :| || ||||| |||
Db   61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy  267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
            |||| ||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db  117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176

Qy  327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
            |||||||| :|||||||||||:|||||||||||||||||||||||||||||||||||||
Db  177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236

Qy  387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
            | |||||| |:|| : |:| ||||||||:   ||||||||||||||||||||||||
Db  237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296

Qy  445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            || ||| || ||||||||||||||:|||:|||
Db  297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
```

RESULT 15
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.

submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

```
Query Match             48.7%;  Score 1256;  DB 4;  Length 255;
Best Local Similarity   97.1%;  Pred. No. 2.5e-67;
Matches  232;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy  238 TKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 297
            |||||||||||||||||||||||||||||||:|||||||||||||||||||
Db   17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76

Qy  298 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 357
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136

Qy  358 PAPIEKTISKAKGQPREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  137 PAPIEKTISKAKGQPREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

Qy  418 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  197 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255
```

Search completed: March 29, 2003, 09:16:17
Job time : 23.3633 secs

R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from n
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglo
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A;Reference number: A26233; MUID:82173203; PMID:6801173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Yamamoto, C.; Yamamoto, K.; Irimura, T.; Takahash
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:9216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F;1-19/Domain: immunoglobulin homology <IM1>
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   52.0%;   Score 1341;   DB 1;   Length 474;
Best Local Similarity   53.4%;   Pred. No. 4.9e-72;
Matches   258; Conservative   71; Mismatches 138; Indels 16; Gaps   4;

```
Qy    1 MKHLWFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
          |: :|| | |:  || |:|||:|| | |:| :: |||||||:||: ::| ::|
Db    1 MEWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKMSCKASGYTFI-YVMHWVKQK 59

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
         ||:||||||:| |: : :|:|: |:|:|||| ||:|| |:| :|:|||||||||||
Db   60 PGQGLEWIGYINPNKDGTKFNEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARDY 119

Qy  121 RPDCTTICYGGWDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
         | || |: ||||:||||||||||||||||||||| ||||||||||||
Db  120 DYD------WPAYWGQGTLVTVSAAKTPPSVVPLAPGCGDTTGSSVTSGCLVKGYFP 171

Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
         | ||||||||||||||||||||||||||:|||||||||||:|| |||||:|||||||
Db  172 ESVTVTWNSGSLSSSVHTLSQALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTV 231

Qy  241 DKKAEPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 293
         |||  | |: |  : |||      |||| | |||||| |||:|||| ||| | ||||||
Db  232 DKKLEPSGPISTINPCPPCKECHKCCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVV 291

Qy  294 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 353
         ||| ||| | ::: |:|:|||| || ||| |||||:|||| | | |||| |||| :||||
Db  292 DVSEDDPDVQISWFVNNVEVHTAQTQHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVN 351

Qy  354 NKALPAPIEKTISKAKGQPREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 413
         || |  |||:|||| | :: :|||| ||::| |||| |||||:| | ||  ||| :|
Db  352 NKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVTCLLVVGFNPGDISVEWTSN 411

Qy  414 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALNHYTQKSLSLS 473
          : |||| |:|||||||||:|:||:| |  : : | |: || || |  |||  ||| |
Db  412 GHTENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRS 471

Qy  474 PGK 476
         |||
Db  472 PGK 474
```

RESULT 13
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed ag
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>

Query Match   51.6%;   Score 1329.5;   DB 2;   Length 475;
Best Local Similarity   53.4%;   Pred. No. 2.3e-71;
Matches 258;   Conservative   79;   Mismatches 131;   Indels 15;   Gaps   7;

```
Qy    1 MKHLWFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
         |:: :|| | |: |: |:|||:|| | |:| :| : ||| :::|: ::| ::|
Db    1 MEWIWIFLFILSGTAGVQSQVQLQQSGAELARPGASVKLSCKASGYTLTSYGI-SWVKQR 59

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
         | :|||||| || |: : |:|: | |:|||| ||:: || | :|:|||||| ||  ||
Db   60 TQQGLEWIGEIYPGSGNSYFNEKFKFGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCA-GP 118

Qy  121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
         |  || | ||| :||||||||| ||:||||||||| ||||||||||||
Db  119 R-QVGLLPFG----YWGQGTLVTASAAKTPPSVVPLAPGCGDTTGSSVTLGCLVKGYFP 173

Qy  181 EPVTVSWNSGALTSGVHTFPAVLQSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
         | ||||||||| |||||||||||| ||||:|||||||||:|| |||||:|||||||
Db  174 ESVTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTV 232

Qy  241 DKKAEPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 293
         |||  |  : |  : |||      |||| | |||||| |||:|||| ||| | ||||||
Db  233 DKKLEPSGPTSTINPCPPCKECHKCCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVV 292

Qy  294 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 353
Db  294 ...
```

```
Db  356  RTISKPKGGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN 415
Qy  423  TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||||||||||||| |:| |||:| :||:|||||||||||||: |||:| ||||
Db  416  TEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 469
```

RESULT 10
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr...
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again...
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

Query Match   53.4%;   Score 1376.5;   DB 2;   Length 444;
Best Local Similarity   55.6%;   Pred. No. 3.6e-74;
Matches 260;   Conservative 73;   Mismatches 100;   Indels 35;   Gaps 9;

```
Qy  20  QVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEWIGHI------YG 73
            |::|| ||:| | |:|:|||   :| |||:|| ||
Db   1  EVQXVETGGGLVRPGNSLKLSCLTSGFTFSN-YRMHWLRQPPGKRLEWIAVITVKSDNYG 59

Qy  74  NGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGQPRPDCTTICYGGWV 133
            |:|| || |:|:|| ||| :|   :| |||:||||||||||| || |  |:  || ||
Db  60  ----AKYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCRTP--------WV 104

Qy  134  ---DVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 190
           |||:| |||||||||||||||:| :|:| ||||||||||||||||
Db  105  YAMDCWGQGTSVIVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSG 164

Qy  191  ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCD 250
           :|||||||||||| :|| :||||||| ||||||||||||||||| :| || |||  | |
Db  165  SLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG 223

Qy  251  KTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 308
           |  |||   |||| |||||||| |||||| ||:|||||||||||||||||||||:|||
Db  224  ----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFV 276

Qy  309  DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 368
           |||:||  || |:|||:|||| |||||||||||||||||||||:|   |||||||||:|
Db  277  DDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKT 336

Qy  369  KGQPREEQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 428
           ||| ||:|||||| |:| :|| |:|||||||||||||:  |||||||||||:|| |||
Db  337  KGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMD 396

Qy  429  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           :|||:|||||| ||:||| |||||||||||||||||||| |:|| :||
Db  397  TDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHTEKSLSHSPGK 444
```

RESULT 11
S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi...
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: S40295

A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid <MAT>
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match   53.2%;   Score 1370;   DB 2;   Length 446;
Best Local Similarity   57.0%;   Pred. No. 8.8e-74;
Matches 261;   Conservative 66;   Mismatches 117;   Indels 14;   Gaps 5;

```
Qy  20  QVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEWIGHIYGNGATTN 79
            |::|| ||:|| | |:|:|||   :| |||:|| |::|||
Db   1  QIQLQQSGPELVRPGASVKISCKASGYTFDYYI-HWVKQRPGEGLEWIGWIYPGSGNTK 59

Qy  80  YNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGQPRPDCTTICYGGWVDVWGPG 139
           |||  ||||| |:||:  |:| :||:||||||||||||| | |::      |   |
Db  60  YNEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGK------FAMDYWGQG 110

Qy  140  DLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 199
           |:|||||:|||| :||  ||| :| |||||||||||:||||||||| |||||:||||||
Db  111  TSVTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTF 170

Qy  200  PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP-- 257
           |||| || :|||||| |||  : |:|||||:|||:||::||||  | :|   | ||
Db  171  PAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCK 228

Qy  258  CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317
           |||  |||||||| |||||||:|| || |||:|||||||| || ||:||  | |||||
Db  229  CPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQ 288

Qy  318  TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 377
           | |:|||:||||  |||||||||||||||||||||:|   ||||||||||  |||||:|
Db  289  TQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQV 348

Qy  378  YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 437
           |||| |:| :|| |:|||||||||||||  |||||||||||:|| |||||:|||:|||
Db  349  YVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS 408

Qy  438  KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
           ||||:|| : |||||||||||| :|||||||||||||
Db  409  KLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 446
```

RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific mo...
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

```
Best Local Similarity   61.6%;    Pred. No.  6.6e-83;
Matches   294;  Conservative   61;  Mismatches  112;  Indels  10;  Gaps  6;

Qy    4 LWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPGR 63
Db    2 LWTLLFVLSAPRGVLSQVRLQESGPSLATLLQTLSVTCTISGFSLNNYGV-DWVRQAPGK 60

Qy   64 GLEWIGHIYGNG--ATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPR 121
Db   61 ALEWLG--GSGYDEDIDYNPVLKSRLSITKDTSKSQVSLTLSVTTEDTAVYYCARVDY 117

Qy  122 PDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 181
Db  118 DSSHAFAYASY-DFWGPGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPE 176

Qy  182 PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD 241
Db  177 PVTVTWNSGALTSGVHTFPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVD 236

Qy  242 KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 301
Db  237 KRVEPGCPDPCKHC-RCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPE 295

Qy  302 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 361
Db  296 VQFSWFVDNVEVRTARTKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPI 355

Qy  362 EKTISKAKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENN 419
Db  356 VRTISRTKGQAREPQVVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDK 415

Qy  420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db  416 YGTTTSQLDADGSYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK 472
```

RESULT 8
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

```
Query Match           57.7%;    Score 1487;  DB 2;  Length 374;
Best Local Similarity  62.3%;    Pred. No.  8.9e-81;
Matches   297;  Conservative   24;  Mismatches  38;  Indels 118;  Gaps  7;

Qy    8 LLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSIS-----GYYWTWIRQTP 61
Db    8 LLLLTIPSWVLSQTLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVG-----WIRQPP 62

Qy   62 GRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPR 121
Db   63 GQALEWLALIFWDD-DKRYSPSLRTRLTITKDTSKNQVLTMNVDPADTATYYCGVSVE 121
```

```
Qy  122 PDCTTICYG-GW-VDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
Db  122 G------YGGGYRFHSWGQGTLVTVSS-------- 142

Qy  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
Db  143 -------------------- 142

Qy  240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHED 299
Db  143 -----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHED 197

Qy  300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
Db  198 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 257

Qy  360 PIEKTISKAKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
Db  258 PIEKTISKAKGQPREPQVVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 317

Qy  420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db  318 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374
```

RESULT 9
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

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Query Match           54.7%;    Score 1408.5;  DB 2;  Length 469;
Best Local Similarity  56.3%;    Pred. No.  5e-76;
Matches   267;  Conservative   70;  Mismatches 126;  Indels  11;  Gaps  5;

Qy    5 WFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPGRG 64
Db    5 WIFLFLLSGTAGVHCCQIQLQQSGPELVKPGASVKISCKASGYTFDYYI-NWVKQKPGQG 63

Qy   65 LEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGRPDC 124
Db   64 LKWIGWIYPASGNTKYNENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVFCARAMGATA 123

Qy  125 TTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 184
Db  124 TLL------DYWGQGTTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVT 177

Qy  185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA 244
Db  178 LTWNSGSLSSGVHTFPAVLQSD-LVTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKI 236

Qy  245 EPKSCDKTHTCPP--CPAPELLGGPSVFIFPPKDTLMISRTPEVTCVVVDVSHEDPEV 302
Db  237 EPRG-PTIKPCPPCPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDV 295

Qy  303 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 362
Db  296 QISWFVNNVEVHTAQFQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIE 355

Qy  363 KTISKAKGQPREPQVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 422
```

A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
C;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   61.6%;   Score 1586.5;   DB 1;   Length 327;
Best Local Similarity   90.6%;   Pred. No. 1e-86;
Matches 299;   Conservative 12;   Mismatches 16;   Indels 3;   Gaps 1;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
           ||||||||||| ||| | | ||||||||||||||||||||||||||||||||||||||
Db   1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS   60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
           ||||||||||||||| | |||||||||||||||||| ||: | | |||:
Db   61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK--YGPPCFSCPAPEFLGG   117

Qy   267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
           ||||||||||||||||||||||||||||| |||:|||||||||||||||||||:|
Db   118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy   327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
           ||||||||||||||||||||||||||| | | | |:||||||||||||||||||||:
Db   178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy   387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
           :| ||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy   447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ::|||||||||||||||||||||||| ||
Db   298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327

RESULT 6
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Accession: S22080
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   59.6%;   Score 1537;   DB 2;   Length 470;
Best Local Similarity   62.6%;   Pred. No. 1.3e-83;
Matches 299;   Conservative 60;   Mismatches 109;   Indels 10;   Gaps 7;

Qy   1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT   60
           | |:|:||||| |||| | | : : |:: |::|: :||||||:|| || | ||||
Db   1 MNPLWTLLFVLSAPIGVLSQVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYAL-TWVRQA   59

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
           ||| ||||| | | ||:|||| ||| ||||| : ::: | :: : :| |: |||| |
Db   60 PGKALEWVGGI-TSGGTTYYNPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARST 118

Qy   121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
           | : : || |: ||| ||:: :|:::   : | :: : : ||: |: ||: |
Db   119 YGE---VGDGAIADAWGQGLLVTVSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSVMP 175

Qy   181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
           |||||||||||||||||||||||||||||||||||||| |: || |||| |::|||
Db   176 EPVTVTWNSGALKSGVHTFPAVLQSSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTKV 234

Qy   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
           ||:| | | ||| | | :|||| ||:| |:| |:||:| || ||||| |:||
Db   235 DKAVDP-TC-KPSPCDCCPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVVDVGHDDP 292

Qy   301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
           |||:||| |||||| | ||||||| |||||||||||| |: |||||| | | |: |
Db   293 EVKFSWFVDDVEVNTATTKPREEQFNSTYRVVSALRIQHQDWTGGKEFPKCKVHNEGLPAP 352

Qy   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--EN 418
           | |||||||||||||| :: | : | | | | |:| |||||||||||||||||| :
Db   353 IVRTISRTGPAREPQVVVLAPPQEELSKSTVSLTCMVTSFYPDIAVEWQRNGQPESED 412

Qy   419 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           ||||||||||||||||||||||||||| | :||||||||||||||||||||||| ||
Db   413 KYGTTPPQLDADSSYFLYSKLRVDRNSWQEGDYTCVVMHEALHNHYTQKSTSKSAGK 470

RESULT 7
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

Query Match   59.2%;   Score 1525;   DB 2;   Length 472;

```
Query Match       63.0%;  Score 1624.5;  DB 2;  Length 377;
Best Local Similarity   81.7%;  Pred. No. 6.8e-89;
Matches 308;  Conservative  10;  Mismatches  12;  Indels  47;  Gaps  1;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
             ||||||||||||:|:||:||:||||||||||||||||||||||||||||||||||||||
Db     1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA------------------ 244
             ||||||||||||||||||||||||||||||||||:||:
Db    61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE-----------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 120

Qy   245 --------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 279
Db   121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTHTCPRCPEPKSC 180

Qy   280 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 339
             ||||||||||||||||:||||||:||||||:|||||||||||||||::||::||:||||
Db   181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy   340 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399
             |||||||||||||||||||||||||||:||||||||||||||||:||:|||||||||||
Db   241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREMTKNQVSLTCLVK 300

Qy   400 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 459
             ||||||||||||||||||||:|||||||||||||||:||||||||||:||||||||||
Db   301 GFYPSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360

Qy   460 ALHNHYTQKSLSLSPGK 476
             ||||:|||||||||||
Db   361 ALHNRFTQKSLSLSPGK 377


RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV', 60-85,132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
```

```
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation, Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:6906124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapi
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l8i
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted


Query Match       62.1%;  Score 1600;  DB 1;  Length 326;
Best Local Similarity   90.9%;  Pred. No. 1.6e-87;
Matches 300;  Conservative  12;  Mismatches  14;  Indels  4;  Gaps  2;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  60

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
             ||||||||||||:|||||||||||||||||||||||         ::
Db    61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy   267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
             ||||||||||||||||||||||||||||||||||:|||||||||||||||||:||||:
Db   117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFN 176

Qy   327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
             ||:|||||||||||||||||||||||||||||||||||||||:|||||||||||||:||
Db   177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy   387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
             :||||||||||||||||||||||||||||||||||:|||||||||||||||:|||||||
Db   237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy   447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
             ||||||||||||||||||||||||||||||
Db   297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
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igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',99-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match     68.4%;  Score 1763;  DB 1;  Length 330;
Best Local Similarity  99.7%;  Pred. No. 3.9e-97;
Matches  329;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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Db    1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy  267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy  327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy  387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy  447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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Db  301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match     63.1%;  Score 1626.5;  DB 2;  Length 377;
Best Local Similarity  81.7%;  Pred. No. 5.2e-89;
Matches  308;  Conservative  10;  Mismatches  12;  Indels  47;  Gaps  1;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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Db    1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA----------------------- 244
            ||||||||||||||||||||||||||||||||||||||
Db   61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy  245 -----------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 279
                                   ||:||||||||||||||||||||||||||||
Db  121 DTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy  280 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 339
            ||||||||||||||||||||:||||||||||||||||||||||||||||:||||||||||
Db  181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy  340 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399
            ||||||||||||||||||||||||||:::||||||||||||||||:|:||||||||||
Db  241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREEMTKNQVSLTCLVK 300

Qy  400 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 459
            ||||||||||||:||||||||:||||:|||||||||||||||||||||||||:||||||||
Db  301 GFYPSDIAVEWESSGQPENNYNTTPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE 360

Qy  460 ALHNHYTQKSLSLSPGK 476
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Db  361 ALHNRFTQKSLSLSPGK 377


RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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                    GenCore version 5.1.4_p5_4578
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:       March 29, 2003, 09:06:24 ; Search time 21.3633 Seconds
                                          (without alignments)
                                          2141.995 Million cell updates/sec

Title:        US-09-758-173-4
Perfect score: 2577
Sequence:     1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:     283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_73:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	% Match	DB	Length	ID	Description
1	1763	68.4		1	330	GHHU	Ig gamma-1 chain C
2	1626.5	63.1		2	377	A23511	Ig gamma-3 chain C
3	1624.5	63.0		2	377	A60764	Ig gamma-3 chain C
4	1600	62.1		1	326	G2HU	Ig gamma-2 chain C
5	1586.5	61.6		1	327	G4HU	Ig gamma-4 chain C
6	1537	59.6		4	470	S22080	Ig heavy chain pre
7	1525	59.2		2	472	S31459	Ig gamma-1 chain -
8	1487	57.7		2	374	S69339	Ig heavy chain V r
9	1408.5	54.7		4	469	S37483	Ig gamma-2a chain
10	1376.5	53.4		4	444	PC4436	monoclonal antibod
11	1370	53.2		2	446	S40295	Ig gamma-2a chain
12	1341	52.0		1	474	G2MS11	Ig gamma-2b chain
13	1329.5	51.6		2	475	S01321	Ig gamma-2b chain
14	1259	48.9		2	328	I47159	Ig gamma-2a chain
15	1256	48.7		4	255	S31866	Ig gamma-1 chain C
16	1253	48.6		2	328	I47160	Ig gamma-2b chain
17	1250	48.5		4	234	PT0207	Ig gamma chain C r
18	1227	47.6		2	328	I47158	Ig gamma-1 chain C
19	1226.5	47.6		1	323	GHRB	Ig gamma 1 chain C
20	1223	47.5		2	328	I47161	Ig gamma 3 chain C
21	1212.5	47.1		2	329	G2GP	Ig gamma-2 chain C
22	1157.5	44.9		2	308	C30554	Ig heavy chain C r
23	1152	44.7		4	289	G3HUWI	Ig gamma-3 heavy c
24	1148	44.5		2	326	PS0017	Ig gamma-1 chain C
25	1142.5	44.3		3	333	PS0018	Ig gamma-2b chain
26	1138	44.2		1	324	G1MS	Ig gamma-1 chain C
27	1137	44.1		2	329	G3MSC	Ig gamma-3 chain C
28	1133	44.0		1	393	G1MSM	Ig gamma-1 chain C
29	1126	43.7		1	398	G3MSM	Ig gamma-3 chain C
30	1122	43.5		1	330	G2MSA	Ig gamma-2a chain
31	1119.5	43.4		1	335	G2MSAB	Ig gamma-2a chain
32	1117	43.3		1	399	G2MSAM	Ig gamma-2a chain
33	1114.5	43.2		2	329	S00847	Ig gamma-2c chain
34	1108	43.0		2	327	PS0019	Ig gamma-2a chain C
35	1088.5	42.2		1	327	S06611	Ig gamma-2 chain C
36	1080	41.9		1	405	G2MSBM	Ig gamma-2b chain
37	1062	41.2		2	277	I47162	Ig gamma 4 chain C
38	908	35.2		2	548	S38864	Ig epsilon chain C
39	903	35.0		2	220	A49444	Ig gamma-1 heavy c
40	794.5	30.8		2	549	S04845	Ig heavy chain pre
41	771	29.9		2	592	S25705	Ig mu chain - shee
42	727.5	28.2		2	572	B46529	Ig Y heavy chain (
43	719	27.9		2	627	S14683	Ig mu chain precur
44	713.5	27.7		2	249	S69340	Ig heavy chain VHI
45	709.5	27.5		2	241	S69131	Ig heavy chain (DO

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                              ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36661; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, ;
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a g
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96; 'R', 98-135 <CUN>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R;Ponsting1, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
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Qy    494  CTGGGGCACAGCCGCCCTGGGCTGCCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGG  553
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Db    491  CTGGGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGG    550

Qy    554  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT  613
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Db    551  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT  610

Qy    614  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  673
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  670

Qy    674  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGTGGACAAGAAAGCAG   733
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Db    671  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  730

Qy    734  AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG  793
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731  AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG  790

Qy    794  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA  853
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Db    791  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA  850

Qy    854  CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  913
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Db    851  CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  910

Qy    914  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  973
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Db    911  ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  970

Qy    974  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1033
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAGTGGCTGAATG  1030

Qy   1034  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1093
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1090

Qy   1094  TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1153
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Db   1091  TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG  1150

Qy   1154  ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1213
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Qy   1214  ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC  1273
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Qy   1274  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1333
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Db   1271  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1330

Qy   1334  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331  GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1390

Qy   1394  ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
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Search completed: April 6, 2003, 06:25:14
Job time : 69.1566 secs

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   ADDRESSEE: Burns, Doane, Swecker & Mathis
   STREET: P.O. Box 1404
   CITY: Alexandria
   STATE: Virginia
   COUNTRY: United States
   ZIP: 22313-1404
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/335,697B
   FILING DATE:
   CLASSIFICATION:
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: 08/770,057
   FILING DATE:
ATTORNEY/AGENT INFORMATION:
   NAME: Teskin, Robin L.
   REGISTRATION NUMBER: 35,030
   REFERENCE/DOCKET NUMBER: 012712-150
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (703) 836-6620
      TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 1428 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
   MOLECULE TYPE: DNA (genomic)
   FEATURE:
      NAME/KEY: CDS
      LOCATION: 1..1428
US-09-335-697B-17

Query Match        78.5%;   Score 1123.6;  DB 4;   Length 1428;
Best Local Similarity 88.5%;   Pred. No. 2.8e-265;
Matches 1255;  Conservative 0;  Mismatches 154;  Indels 9;  Gaps 3;

Qy    17 TCTTCCTCCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGTGAAGCTGCAGCAGT   76
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Qy    77 GGGGCGAAGGACTTCTGGAGCCTTCGAGCCTTCGGAGACCCTGTCCCGCACCTGCGTTGTCTCTGGTG  136
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Db    77 CTGGTCCTGGTGGTGGTGAAACCCAGACCCTCAGCCTGACCTGCACCGTCTCTGGGT  136

Qy   137 GCTC---CATCAGCGGTTACTACTACTGGAGCTGGATCCGCCAGCCCCAGGAGGGGAC  193
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Qy   194 TGGAGTGGATTGGCCATATTTATGGTAATGGTGAGAGTGACGAAGTC---CTTCAGTCCTTCTCTGA  253
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Db   197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAAGTC---CTTCAGTCCTTCTCTGA  253

Qy   254 AGAGTGGAGTCACCATTCAAAAGACACGTCCAAGAACACAGTTCTTCTCGAACTTGAATT  313
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Qy   374 CAACCATTGTTATGGCGGCTGGGTCGATGTCTGGGGCCCCGGAGACGTCGGTCACCGTCT  433
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Db   371 TCAATGCTTATTACCTATACTGGATTATTGGGGGCAGGAGAACCCTGGTCACCGTCT  430

Qy   434 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCT  493
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Qy   614 CCTCAGGACTCTACTCCCTCAGCAGCCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  673
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Db   611 CCTCAGGACTCTACTCCCTCAGCAGCCGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  670

Qy   674 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  733
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Db   671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG  730

Qy   734 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG  793
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Qy   794 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA  853
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   791 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGA  850

Qy   854 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  913
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Db   851 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA  910

Qy   914 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  973
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Db   911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  970

Qy   974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1033
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Db   971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1030

Qy  1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA 1093
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Qy  1094 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1153
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Db  1091 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1150

Qy  1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1213
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Qy  1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
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Qy  1334 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393
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RESULT 15
US-09-335-697B-17
; Sequence 17, Application US/09335697B
; Patent No. 6413771
GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaima Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/335,697B
    FILING DATE: 06-Jul-2000
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/770,057
    FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
    NAME: Teskin, Robin L.
    REGISTRATION NUMBER: 35,030
    REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (703) 836-6620
    TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1428 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    FEATURE:
        NAME/KEY: CDS
        LOCATION: 1..1428
    SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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US-09-335-697B-17

Query Match   78.5%;   Score 1123.6; DB 4;   Length 1428;
Best Local Similarity   88.5%;   Pred. No. 2.8e-265;
Matches 1255; Conservative   0; Mismatches 154; Indels   9; Gaps   3;

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Qy     17 TCTTCCTCCCCTGGTGGCAGCTCCCAGATGGTCCTGTCCAGGTGAAGCTGCAGCAGT      76
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Db     17 TCTTGCTCTCCCTTGTCGCCGTGTGCTACGGCGTGTCCTGTCCAGGTGCAGTTGCAGGAGT      76

Qy     77 GGGGCGAAGGACTTCTGGAGACCCTCGGAGACACCCTCGTCCCGCACCTGACCTCGTCTGTG     136
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Db     77 CTGGTCCTGTGGCGTGGTGGAAACCCACAGAGACCCTCAGGCTGGACTGACCTGCTCTGGGT     136

Qy    137 GCTC---CATCAGCGGTACTACTACTGGACCTGGATCCGCCAGACCCCAGGGAGGGGAC     193
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Db    137 TCTCACTCAGCAACCCTAGAATGGGTGTGACCTGGATCCAGCCCCGCCCCGGGAAGGCCC     196

Qy    194 TGGAGTGGATTGGCCATATTATGGTAATGGTGACCACCAACTACATCCCTCCCTCA     253
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Db    197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGACGAAGAGTC---CTTCAGTCCTTCTCTGA     253

Qy    254 AGAGTCGAGTCACCATTTCAAAAGACACGTCAAGAACCAGTTCTTCCTGACTTGAATT     313
          |||||||| ||| ||||||||||||||| |||  |||||||||||||||||||||||
Db    254 AGAGCAGACTCACCACTCTCCAGGACACCTCCAAGAGCCAGGTGGTCCTAAGCTTGACCA     313

Qy    314 CTGTGACCGACGCGGACACGGCCGTCTATTACTGTGGAGAGGCCCTCGCCCGATTGCA     373
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Qy    374 CAACCATTGTTATGGCGGCTGGGTCGATGTCTGGGGCCCCGGGAGACCTGGTCACCGTCT     433
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Db    371 TCAATGCTTATTACCTATACTGGATTATTGGGGGCAGGAGGAACCCTGGTCACCGTCT     430

Qy    434 CCTCAGCTAGCACCAAGGGCCCATCGGTTCCCCCTGGCACCCTCCTCCAAGAGCACCT     493
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Db    431 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT     490

Qy    494 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG     553
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Db    491 CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG     550

Qy    554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT     613
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT     610
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Db    731 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG     790

Qy    794 GGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGA     853
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Db    791 GGGGACCGTCAGTCTTCTCCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGA     850

Qy    854 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA     913
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    851 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA     910

Qy    914 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT     973
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT     970

Qy    974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG    1033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG    1030

Qy   1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA    1093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA    1090

Qy   1094 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG    1153
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Qy   1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG    1213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG    1210

Qy   1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC    1273
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Db   1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC    1270

Qy   1274 CCGTGTGGACTCCAGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA    1333
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Db   1271 CCGTGTGGACTCCAGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA    1330

Qy   1334 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT    1393
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Db   1331 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT    1390

Qy   1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA    1431
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Db   1391 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA    1428
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RESULT 14
US-09-335-697B-17
; Sequence 17, Application US/09335697B
; Patent No. 6200804
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   CHAMAT, Soulaina Salim
;   PAN, Li-Zhen
;   WALSH, Edward E.
;   HEARD, Cheryl Janne
;   NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

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;    APPLICATION NUMBER:  US 08/488,376
;    FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-150
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO: 17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1428 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1428
;
US-08-770-057-17

Query Match       78.5%;    Score 1123.6;  DB 2;   Length 1428;
Best Local Similarity 88.5%;    Pred. No. 2.8e-265;
Matches 1255;  Conservative  0;  Mismatches 154;  Indels  9;  Gaps  3;
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Qy   137 GCTC---CATCAGCGGTTACTACTGGAGCTGGATCCGGCAGCCCCAGGGAGGGGAGGGAC  193
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Qy   314 CTGTGACCGACGCGGACACGGCGCCGTCTATTACTGTGGAGAGGCCCTCGCCCTGATTGCA  373
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Qy   554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCGGCTGTCCTACAGT  613
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Qy   914 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT  973
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Qy   974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1033
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Qy  1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1093
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Qy  1154 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG  1213
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Db  1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTC  1270

Qy  1274 CCGTGCTGGACTCCGACGCGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  1333
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Qy  1334 GGTGGCAGCAGGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1393
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Db  1331 GGTGGCAGCAGGGGAACGTGTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1390

Qy  1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
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Db  1391 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1428
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RESULT 13
US-08-770-057-17
; Sequence 17, Application US/08770057
; Patent No. 5998765
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Burns, Doane, Swecker & Mathis
;     STREET: P.O. Box 1404
;     CITY: Alexandria
;     STATE: Virginia
;     COUNTRY: United States
;     ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/7770,057
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
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Qy   974 ACAACAGCAGTACCGTGGTCAGCGTCCTGCTGACCAGGACTGCTGAATG 1033
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Qy  1034 GCAAGGAGTACAAGTGCAAGGTCTTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCA 1093
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Db  1031 GCAAGGAGTACAAGTGCAAGGTCTTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCA 1090

Qy  1094 TCTCCAAAGCCAAAGGGCCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1153
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Qy  1154 ATGAGCTGACCAAGAACCAGTCAGCCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1213
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Db  1151 ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1210

Qy  1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
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Db  1211 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTC 1270

Qy  1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1333
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Qy  1334 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393
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Db  1331 GGTGGCAGCAGGGGAACGTCTTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1390

Qy  1394 ACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db  1391 ACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428
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RESULT 12
US-08-635-878-17
; Sequence 17, Application US/08635878
; Patent No. 5955364
GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/635,878
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/488,376
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-150
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 836-6620

;   TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1428 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1428
US-08-635-878-17

Query Match   78.5%;   Score 1123.6; DB 2; Length 1428;
Best Local Similarity 88.5%;   Pred. No 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

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Qy   17 TCTTCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAGAGTGGGCTCCGAGGCTGCAGCAGT 76
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Db   17 TCTTGCTCTTCCTTGTCGCTGTGTCACGCGTGCCTGTCCCAGGTGACGTTGCAGGAGT 76

Qy   77 GGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGTCCCGGAGACCTGGGTTGTCTCTGGTG 136
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Qy  137 GCTC---CATCAGCGGTTACTACTACTGACCTGACCTGACCGCCAGACCCCAGGGAGGGGGAC 193
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Db  137 TCTCACTCAGCAACCCTAGAATGGGTGTGACCTGGATCCGTCAGCCCCCGGGAAGGGCCC 196

Qy  194 TGGAGTGGATTGGCCATATTATGTAATGGTGCGACCAACTACAATCCCTCCCTCA 253
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Db  197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAAGTC---CTTCAGTCCTTCTCTGA 253

Qy  254 AGAGTGCGAGTCACCATTCAAAAGACACAGTCAAGAACACCAGTTCTTCCTGAACTTGAATT 313
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Db  254 AGAGCAGACTCACCACCTCCAGGACACACTCCAGAAGCCAGGTGGTCCTAAGCTTGACCA 313

Qy  314 CTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGGAGAGAGCCCTCGCCCTGATTGCA 373
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Db  314 ACGTGGACCCTGTGGACACAGCCACATTATTACTGTGC---AGGGTAGGGACTGTATGCACA 370

Qy  374 CAACCATTGTTATGCGGCTGGGTCGATGTCTGGGGCCCGGGAGACCTGGTCACCGTCT 433
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Db  371 TCAATGCTTATTACCTATACTACCTGGATTATTGGGGCCAGGGAACCCTGGTCACCGTCT 430

Qy  434 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT 493
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Db  431 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT 490

Qy  494 CTGGGGCACAGCAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 553
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Db  491 CTGGGGCCACAGCAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG 550

Qy  554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 613
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Db  551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 610

Qy  614 CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 673
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Db  611 CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 670

Qy  674 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAACAAGGTGACAAGAAAGCAG 733
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Db  671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAACAAGGTGACAAGAAAGCAG 730

Qy  734 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCCTGG 793
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  731 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTCCTGG 790

Qy  794 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 853
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Db  791 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 850
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;       FEATURE:
;       NAME/KEY:    CDS
;       LOCATION:    1..1428
US-08-634-400-17

Query Match        78.5%;   Score 1123.6; DB 2; Length 1428;
Best Local Similarity 88.5%;   Pred. No. 2.8e-265;
Matches 1255;  Conservative   0;  Mismatches 154;  Indels   9;  Gaps   3;

Qy    17 TCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCCTGTCCCAGTGAAGCTGCAGCAGT 76
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Db    17 TCTTGCTCTTCCTTGTCGCGTGCTACGCGTGTCCTGTGCCCAGGTGCAGTTGCAGGAGT 76

Qy    77 GGGGCGGAGGACTTCGCAGCCTTCGGAGACCCTGTCCCGCACCTGACCTGGTCTCTGTG 136
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Db    77 CTGGTCCTGTGGTGTGAAACCCACAGAGACCCTCACGCTGACCTGCACCGTCTCTGGGT 136

Qy   137 GCTC---CATCAGCGGTTACTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAGGGGAC 193
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Db   137 TCTCACTCAGCAACCCTAGAATGGGTGTGACCTGGATCCGTCAGCCCCCAGGGAAGGGCC 196

Qy   194 TGGAGTGGATTGGCCATATTTATGGTAATGGTGACCACCAACTACAATCCCTCCCTCA 253
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Db   197 TAGAATGGCTTGGAAACATTTTTCGAGTGACGAGAGTC---CTTCAGTCCTTCTCTGA 253

Qy   254 AGAGTCGAGTCACACATTCAAAAGACACGTCAAGAACCAGTTCTTCCTGAACTTGAATT 313
         ||||  |||||||   || |||| |||| | |||| |||| ||  |  || ||| ||| |
Db   254 AGAGCAGACTCACCACCTCCAGACACACCCCAGAAGGCAGGTGGTGTCCTAAGCTGACCA 313

Qy   314 CTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGGCCCTCGCCCTGATTGCA 373
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Db   314 ACGTGGACCCGTGGACACAGCCACCATTACTGTGC---ACGGGTAGGACTGTATGACA 370

Qy   374 CAACCATTGTTATGGGGACGTGGGTCGATGTCTGGGGGCCCGGGAGACCTGGTCACCGTCT 433
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Db   371 TCAATGCTTATTACCTATACTACCTGGATTATTGGGGGCAGGGAACCCTGGTCACCGTCT 430

Qy   434 CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT 493
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Qy   554 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 613
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Db   551 TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT 610

Qy   614 CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 673
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Db   611 CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 670

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Db   671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG 730

Qy   734 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 793
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Db   731 AGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGG 790

Qy   794 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 853
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Db   791 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 850

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Db   851 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA 910

Qy   914 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 973
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Db   911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 970

Qy  1094 TCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGTGTACACCCTGCCCCATCCCGGG 1153
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Db  1091 TCTCCAAAGCCAAAGGGCAGCCCGAGAACCACAGTGTACACCCTGCCCCATCCCGGG 1150

Qy  1154 ATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1213
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Db  1151 ATGAGCTGACCAAGAACCAGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1210

Qy  1214 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
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Qy  1274 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1333
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Db  1271 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1330

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RESULT 11
US-08-634-400-17
; Sequence 17, Application US/08634400
; Patent No. 5939068
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/634,400
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/488,376
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-150
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 836-6620
;   TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1428 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)

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Qy    1214  ACATCGCGCTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC  1273
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Db    1211  ACATCGCGCTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTC  1270

Qy    1274  CCGTGCTGGACTCCGACGGCGCTCCTCCTTCTTTTTCTCTCTACAGCAAGCAAGCAGAGCA  1333
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Db    1271  CCGTGCTGGACTCCGACGGCGCTCCTCCTTCTTTTTCCTCTACAGCAAGCTCACCGGACAAGCA  1330

Qy    1334  GGTGGCAGCAGGGGAAGCGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT  1393
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Qy    1394  ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1431
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Db     137  TCTCACTCAGCAACCCTAGAATGGGTGTGATCCGTCCTGACCTGGATCCAGCCCCGGGAGGGCCC   196

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Db     254  AGAGCGATTCACCACCTCCAGGACACCTCCAGAAGCCAGGTGGTTCCTAAGCTTGACCA   313

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Db     371  TCAATGCTTATTACCTATACCTGGATTATTGGGGGCCAGGGAACCCTGGTCACCGTCT   430

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Db     431  CCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT   490

Qy     494  CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG   553
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Db     491  CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG   550

Qy     554  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT   613
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Db     551  TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGT   610

Qy     614  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC   673
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Db     611  CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC   670

Qy     674  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGAGCAG   733
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Db     671  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGAGCAG   730

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Db     731  AGCCCAAATCTTGTGACAAAACTCACACATGCCACCGTGCTGAGCGTGGACCACCGTGAACTCCTGG   790

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Db     791  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA   850

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Qy     974  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG  1033
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Qy    1034  GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  1093
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RESULT 10

US-08-634-224-17

; Sequence 17, Application US/08634224

; Patent No. 5866125

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward J.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Burns, Doane, Swecker & Mathis
  STREET: P.O. Box 1404
  CITY: Alexandria
  STATE: Virginia
  COUNTRY: United States
  ZIP: 22313-1404
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/634,224
  FILING DATE:
  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/488,376
  FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Teskin, Robin L.
  REGISTRATION NUMBER: 35,030
  REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (703) 836-6620
  TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 1428 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
FEATURE:
  NAME/KEY: CDS
  LOCATION: 1..1428

US-08-634-224-17

Query Match   78.5%; Score 1123.6; DB 2; Length 1428;
Best Local Similarity 88.5%; Pred. No. 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

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Db  1331 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1390

Qy  1394 ACACCGCAGAAGAGCTCTCCCTGTCTCCGGGTAAATGA 1431
         |||||||||||||||  |||||||||||||||||||||
Db  1391 ACACCGCAGAAGAGCCCTCCCTGTCTCCGGGTAAATGA 1428
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RESULT 9
US-08-634-223-17
; Sequence 17, Application US/08634223
; Patent No. 5840298
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/634,223
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/488,376
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-150
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 836-6620
;   TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1428 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1428
US-08-634-223-17

Query Match   78.5%; Score 1123.6; DB 2; Length 1428;
Best Local Similarity   88.5%; Pred. No. 2.8e-265;
Matches 1255; Conservative   0; Mismatches 154; Indels   9; Gaps   3;

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RESULT 8
US-08-488-376-17
; Sequence 17, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
;   APPLICANT: BRAMS, Peter
;   APPLICANT: CHAMAT, Soulaima Salim
;   APPLICANT: PAN, Li-Zhen
;   APPLICANT: WALSH, Edward E.
;   APPLICANT: HEARD, Cheryl Janne
;   APPLICANT: NEWMAN, Roland Anthony
;   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
;   TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burns, Doane, Swecker & Mathis
;   STREET: P.O. Box 1404
;   CITY: Alexandria
;   STATE: Virginia
;   COUNTRY: United States
;   ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/488,376
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Teskin, Robin L.
;   REGISTRATION NUMBER: 35,030
;   REFERENCE/DOCKET NUMBER: 012712-150
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 836-6620
;   TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1428 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1428
US-08-488-376-17

Query Match   78.5%; Score 1123.6; DB 1; Length 1428;
Best Local Similarity   88.5%; Pred. No. 2.8e-265;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

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GENERAL INFORMATION:
  APPLICANT: Hanna, Nabil
  APPLICANT: Newman, Roland A.
  APPLICANT: Reff, Mitchell E.
  TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
  TITLE OF INVENTION: Therapy
  NUMBER OF SEQUENCES: 59
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22314-3187
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/523,894
    FILING DATE: 06-SEP-1995
    CLASSIFICATION: 424
  ATTORNEY/AGENT INFORMATION:
    NAME: Teskin, Robin L.
    REGISTRATION NUMBER: 35,030
    REFERENCE/DOCKET NUMBER: 012712-165
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 703-836-6620
    TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1404 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  ORIGINAL SOURCE:
    ORGANISM: Homo sapiens
  POSITION IN GENOME:
    CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..1404
  FEATURE:
    NAME/KEY: mat_peptide
    LOCATION: 1..1404

US-08-523-894-9

Query Match   81.5%;   Score 1166.6;   DB 3;   Length 1404;
Best Local Similarity   89.8%;   Pred. No. 8.8e-276;
Matches 1285;   Conservative   0;   Mismatches   119;   Indels   27;   Gaps   2;

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Db     1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCAGGTAGTGCAGTGTCACCCTG    60

Qy    61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCCGCACC   120
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Qy   121 TGCGGTGTTCTCTGGTGGTCCATCAGCGGTTACTACTGGAGCTGGATCCGCCAGACC   180
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Db   121 TGCAGTGTCTCTGGTGGGTCTCCATCAGCGGTGACTATTGGTTCTGGATCCGCCAGTCC   180

Qy   181 CCAGGGAGGGGGACTGGAGTGGATTGGTCCCATATTTATGGTAATGGTGCGACCAACTAC   240
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Db   181 CCAGGGAAGGGGACTGGAGTGGATCGGCTACATCTATTCCAGTGGTAGCACACCCTACTAC   240

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Db   241 AATCCCCTCCCTCAACAATGCAGTCTCCATTTCAATAGACACGTCCAAGAACCAGTTCTCC   300
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           ------GTAATATATTGAAATATCTTCACTGGTTATTATACTGGGGCCCAGGGAGTC   402
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Qy   421 CTTGGTCACCGTCCTCCAGTCAGGACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC   480
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Db   643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG   702

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Db   754 CCTGAGTTCGAGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC   813

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Db   934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG   993

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Db   994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC   1053

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Db  1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT   1353

Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA   1431
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STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E
CHROMOSOME/SEGMENT: mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1404
US-08-523-894-11
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Query Match     81.6%;   Score 1168.2;   DB 3;   Length 1404;
Best Local Similarity  89.9%;
Matches 1286;   Conservative 0;   Mismatches 118;   Indels 27;   Gaps 2;
                                   Pred. No. 3.6e-276;
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Db 1354 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA  1404
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RESULT 7
US-08-523-894-9
; Sequence 9, Application US/08523894
; Patent No. 6136310
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;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/523,894
;       FILING DATE: 06-SEP-1995
;       CLASSIFICATION: 424
;  ATTORNEY/AGENT INFORMATION:
;       NAME: Teskin, Robin L.
;       REGISTRATION NUMBER: 35,030
;       REFERENCE/DOCKET NUMBER: 012712-165
;  TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 703-836-6620
;       TELEFAX: 703-836-2021
;  INFORMATION FOR SEQ ID NO: 7:
;  SEQUENCE CHARACTERISTICS:
;       LENGTH: 1404 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;  MOLECULE TYPE: DNA (genomic)
;  POSITION IN GENOME:
;       CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
;       CHROMOSOME/SEGMENT: 4
;  FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 1..1404
;  FEATURE:
;       NAME/KEY: mat_peptide
;       LOCATION: 1..1404
; US-08-523-894-7
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Query Match          81.9%;    Score 1171.4;    DB 3;    Length 1404;
Best Local Similarity 90.0%;   Pred. No. 5.9e-277;
Matches 1288;  Conservative   0;  Mismatches  116;  Indels  27;  Gaps  2;

Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGCTTCCAGATGGGTCCTGTCCCAG   60
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Db     1 ATGAAACACCTGTGGTTCTTCCTCCTGTGTGGCAGCCCCCAGATGGGTCTTGTCCCAG   60

Qy    61 GTGAAGCTGCGAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGAGACCCGTCCCGCACC  120
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Db    61 GTGCAGCTGCGAGGAGTGGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  120

Qy   121 TGCGTTGTCTCTGGTTGGCTCCATCAGCGGTTACTACTAGGCGGTTACTACTGGACCGGCAGAC  180
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Db   121 TGCAGTGTCTCTGGTGGCTCCATCAGCAGTGGTGACTATTATTGGTTCTGGATCCGCCAGTCC  180

Qy   181 CCAGGGAGGGACTGGAGTGATTGGCCATATTATTATGGTAATGGTGCGACCACCAACTAC  240
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Db   181 CCAGGGAAGGGACTGGAGTGGATCGGGTGGTTCTATTATTGGTTCTGGATCCGCCAGTCC  240

Qy   241 AATCCCCTCAAGAGTCCAGTGCAGCACCATTCAAAAGACACGTCCAAGAACCAGTTCTTC  300
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Db   241 AATCCCCTCCCCTCAACAATCGGATCTTCATTTCAATAGACACGTCCAAGAACCTCTTCTCC  300

Qy   301 CTGAACTTGAATTCTGTGACCGACGCGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT  360
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Db   301 CTGAAACTGAGTGTCTGACACGGCCGTGTACTATCGTGTTATTATACTGTGGGCCCAGGGAGTC  360

Qy   361 CGCCCTGATTGCACAACCATTTGTTATGGGGCGGCTGGGTCGATGTCTGGGGCCCGGAGAC  420
                 --------GTAATATATTGAAATATCTTCACTGTTTATTATACTGTGGGCCCAGGGAGTC  402

Qy   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC  480
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Db   403 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGC  462

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  540
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Db   463 TCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  522

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  600
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Db   523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG  582

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  660
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Db   583 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC  642

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG  720
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Db   643 AGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTG  702

Qy   721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA  780
         |||||||||||||||||| | ||| ||||||||||       |||||| |||||||||||||
Db   703 GACAAGAGAGTTGAGTCCAAATATG-------TCCCCATGCCCATCATGCCCAGCA  753

Qy   781 CCTGAACTCCTGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC  840
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Db   754 CCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTC  813

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT  900
         ||||| ||||||||||||||| |||||||||||||||||||||||||||||| ||||||
Db   814 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC  873

Qy   901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  960
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Db   874 GAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG  933

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
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Db   934 CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG  993

Qy  1021 GACTGGCTGAATGCCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
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Db   994 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCC 1053

Qy  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
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Qy  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
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Db  1114 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1173

Qy  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
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Db  1174 TTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1233

Qy  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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Db  1234 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCAACC 1293

Qy  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
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Db  1294 GTGGACAAGAGCAGGTGGCAGCAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCT 1353

Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA          1431
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Db  1354 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA          1404
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RESULT 6
US-08-523-894-11
; Sequence 11, Application US/08523894
; Patent No. 6136310
GENERAL INFORMATION:
     APPLICANT: Hanna, Nabil
     APPLICANT: Newman, Roland A.
     APPLICANT: Reff, Mitchell E.
     TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
     TITLE OF INVENTION: Therapy
     NUMBER OF SEQUENCES: 59
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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;     REGISTRATION NUMBER:  24,618
;     REFERENCE/DOCKET NUMBER:  660-118-0 PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-413-3000
;       TELEFAX:  703-413-2220
;     INFORMATION FOR SEQ ID NO:  7:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  1418 base pairs
;         TYPE:  nucleic acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1418
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  1..57
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  58..1418
;     OTHER INFORMATION:  /product= "IMMUNOGLOBIN, HEAVY
;     OTHER INFORMATION:  CHAIN"

US-08-793-450-7

Query Match        84.6%;   Score 1210.4;  DB 4;  Length 1418;
Best Local Similarity   92.4%;   Pred. No. 1.8e-286;
Matches 1310;   Conservative   0;   Mismatches   96;   Indels  12;   Gaps   3;
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Qy    13  TGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCGTGTCCCAGGTGAAGCTGCAG  72
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Db    13  TGTATCATCCTTCTTCTTGGTAGCAACAGCTACCAGGTGTCCACTCCCAGGTCCAACTGGAG  72

Qy    73  CAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGTCCCGCACCTGCGTTGTCTCT  132
              |||||||||||||||||||| ||||||||||||||||||||| || |
Db    73  CAGTGGGGCGAGGAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTGCACTGCTCTAT  132

Qy   133  GGTGGCTCCATCGGCGGTTACTACTGGAACTGGATCCGCCAGCCCCCAGGGCAGGGGA  192
              |||||||||||||| |||||||||||||| ||||| ||| |||||||||||||||
Db   133  GGTGGGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGG  189

Qy   193  CTGGAGTGGATTGGCCATATTTATGGTAATGTGCGACCACCAACTACAATCCCTCCCTC  252
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Db   190  CTGGAGTGGATTGGGAAATCAA---TCATAGTGGAAATACCAACTACAACCCGTCCCTC  246

Qy   253  AAGAGTCCAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTCCTGAACTTGAAT  312
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Db   247  AAGAGTCCAGTCAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTTCCTGAAACTGAAC  306

Qy   313  TCTGTGACCGACGGGGACACGGCCGTCTATTACTGTGCGAGAGGGGCCCCTGCCCTGATTGC  372
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Db   307  TCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGGG------CCCAGAGTAT  360

Qy   373  ACAACCATTGTTATGGCGGGCTGGGTCGATGTCTGGGGCCCCGGAGACCTGTCACCGTC  432
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Db   361  AAATGGAGAGTATCATGGGGACTGGTTCGACCCCTGGGGCCAAGGTACCACTGTCACCGTC  420

Qy   433  TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC  492
              ||||||||||| ||||||||||||||||||||||||||||||||
Db   421  TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACC  480

Qy   493  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG  552
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Db   481  TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACG  540

Qy   553  GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG  612
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Db   541  GTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAG  600

Qy   613  TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC  672
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC  660
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Qy   673  CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA  732
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Db   661  CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCA  720

Qy   733  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG  792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG  780

Qy   793  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG  852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG  840

Qy   853  ACCCCTGAGGTCACATGGTGTGGTGGTGGACGTGAGCCACGAGACCCTGAGGTCAAGTTC  912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  ACCCCTGAGGTCACATGGTGTGGTGGTGGACGTGAGCCACGAGACCCTGAGGTCAAGTTC  900

Qy   913  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG  972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG  960

Qy   973  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT  1032
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Db   961  TACAACAGCACTTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT  1020

Qy  1033  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC  1092
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATTGAGAAAACC  1080

Qy  1093  ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG  1140
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Db  1081  ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG  1140

Qy  1153  GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC  1212
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Db  1141  GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGTTTCTATCCTAGC  1200

Qy  1213  GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT  1272
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Db  1201  GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT  1260

Qy  1273  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC  1332
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Db  1261  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC  1320

Qy  1333  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC  1392
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Db  1321  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC  1380

Qy  1393  TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG  1430
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Db  1381  TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATG  1418
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INFORMATION FOR SEQ ID NO: 17:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 1567 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
   IMMEDIATE SOURCE:
      LIBRARY: PANCTUT01
      CLONE: 1513264
US-09-049-672A-17

Query Match      86.3%;  Score 1234.8;  DB 3;  Length 1567;
Best Local Similarity  92.9%;  Pred. No. 2e-292;
Matches 1332;  Conservative  0;  Mismatches  87;  Indels  15;  Gaps  3;

Qy     1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGTCCCAGATGGGTCGTCCTGTCCCAG   60
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Db    78 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGCAGTCCCAGATGGGTCCTGTCCTGTCCCAG  137

Qy    61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTGGACACCTGTCCCGCACC  120
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Db   138 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC  197

Qy   121 TGCGTTGTCTGTGGTGGCTCCATC--AGCGGTTACTACTGGAGCTGGATCCGCCAG  177
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Db   198 TGCGCTGTCTCTGGTGGCTCCATCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAG  257

Qy   178 ACCCCAGGGAAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCCACCAAC  237
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Db   258 CCCCCAGGGAAGGGGCTGGAGTGGATTGGGTACATCTA---TTACAGTGGGAGCACCCTC  314

Qy   238 TACAATCCTGCCCTCCCTCCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTC  297
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Db   315 TACAACCCGTCCCTCAAGAGTCGAGTCGTCGTGTGACACGCCAGAACCAGTTC  374

Qy   298 TTCCTGAACTTGAATTCTGTGACGACGGCGACACGGCCGTCTATTACTGTGCGAGAGGC  357
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Db   375 TCCCTGAAGCTGAGCTCTGTGACCGCTGCCGCAGACACGGCCGTGTATTACTGTGCGAGAG--  432

Qy   358 CCTGCGCCTGATTGCACAACCATTTGTTATGCGGCGTGGGTCGATGTCTGGGGCCCGGGA  417
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Db   433 ------ATGACGTAGTTTAAGGGGGGAACTACGGTACGTCTGGGGCCCAGGGA  485

Qy   418 GACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  477
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Db   486 ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC  545

Qy   478 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  537
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Db   546 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC  605

Qy   538 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  597
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Db   606 CCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTC  665

Qy   598 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  657
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Db   666 CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC  725

Qy   658 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  717
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Db   726 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAG  785

Qy   718 GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA  777
           |||||||||| || | ||||||||||||||||||||||||||||||||||||||||||||
Db   786 GTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA  845

Qy   778 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  837
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Db   846 GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC  905

Qy   838 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  897
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Db   906 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC  965

Qy   898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACACAAG  957
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Db   966 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG 1025

Qy   958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1017
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Db  1026 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC 1085

Qy  1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC 1077
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Db  1146 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC 1205

Qy  1138 CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1197
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Db  1206 CTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA 1265

Qy  1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1266 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1325

Qy  1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1326 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1385

Qy  1318 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG 1377
           |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1386 ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTTTTCTCATGCTCCGTGATGCATGAG 1445

Qy  1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db  1446 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGTAAATGA 1499
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;           LOCATION: 1..1431
US-08-487-550-11

Query Match      91.9%;  Score 1315.8;  DB 3;  Length 1431;
Best Local Similarity  95.0%;  Pred. No. 3.3e-312;
Matches 1359;  Conservative 0;  Mismatches 0;  Indels 72;  Gaps 0;

Qy     1 ATGAAACACCTGTGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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Db     1 ATGAAACACCTGTGTTCTTCCTCCTCCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60

Qy    61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTCGCAGCCTTCGGAGACCCTGTCCGCACC 120
           ||| |||||||| ||||  |||  ||||| |  |||||||||||||||||||||| ||||
Db    61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC 120

Qy   121 TGCGTGTCTCTGGTGGCTCCATCAGCGGTGGTTACTACTGGAGCTGGATCCGGCCAGCC 180
           |||||||||||||||||||||||||||||||| ||  | |||| | |||||||||||
Db   121 TGCGTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGTGGGAGCTGGATCCGGCCAGCCC 180

Qy   181 CCAGGAGGGGGACTGGAGTGGATTGGGAGTGGTTCTATATTATGGGAGTGCGACCACCAACTAC 240
           |||||||||||||||||||||||||||||||  | ||| | | ||  || | | ||||||||||
Db   181 CCAGGAAGGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240

Qy   241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAGACACGTCCAAGAACCAGTTCTTC 300
           |||||| ||||||||||||  |  |   ||||| |||||| | |||||||||||| |||
Db   241 AACCCCTCCCTCAAGAGTCGAGTCACCATTTCAACAGACAGTCCAAGAACCAGTTCTCC 300

Qy   301 CTGAACTTGAATTCTGTGACCGCCGACACGGCCGTCTATTACTGTGCGAGAGGGCCCT 360
           ||||||||||| | ||||  ||||| || ||||||||||||||||| ||| |||  |
Db   301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360

Qy   361 CGCCCTGATTGCACAACCATTTGTTATGGGCGGTCGATGTCTGGGGCCCGGGAGAC 420
           | ||| | ||   |  |  ||| ||| |  || |  |||||| | || | ||| |
Db   361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420

Qy   421 CTGGTCACGGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 480
           |||||||| ||| | |||||||| ||||||||||| |||||||||||||| ||| | |
Db   421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC 480

Qy   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540
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Db   481 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540

Qy   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600

Qy   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660
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Db   601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660

Qy   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720

Qy   721 GACAAGAAAGCAGAGAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GACAAGAAAGCAGAGAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA 780

Qy   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840

Qy   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 900

Qy   901 GAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAGGTGCATAAATGCCAAGACAAAGCCG 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAGGTGCATAAATGCCAAGACAAAGCCG 960

Qy   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020

Qy  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

Qy  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
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Db  1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140

Qy  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC 1200

Qy  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260

Qy  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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Db  1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320

Qy  1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
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Qy  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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Db  1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431


RESULT 3
US-09-049-672A-17
;  Sequence 17, Application US/09049672A
;  Patent No. 6135941
;  GENERAL INFORMATION:
;     APPLICANT: Hillman, Jennifer L.
;     APPLICANT: Lal, Preeti
;     APPLICANT: Tang, Y. Tom
;     APPLICANT: Yue, Henry
;     APPLICANT: Au-Young, Janice
;     APPLICANT: Corley, Neil C.
;     APPLICANT: Guegler, Karl J.
;     APPLICANT: Baughn, Mariah R.
;     TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;     NUMBER OF SEQUENCES: 28
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Incyte Pharmaceuticals, Inc.
;        STREET: 3174 Porter Drive
;        CITY: Palo Alto
;        STATE: CA
;        COUNTRY: USA
;        ZIP: 94304
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Diskette
;        COMPUTER: IBM Compatible
;        OPERATING SYSTEM: DOS
;        SOFTWARE: FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/09/049,672A
;        FILING DATE: HEREWITH
;        CLASSIFICATION: 536
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:
;        FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Cerrone, Michael C
;        REGISTRATION NUMBER: 39,132
;        REFERENCE/DOCKET NUMBER: PF-0497 US
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 650-855-0555
;        TELEFAX: 650-845-4166
;        TELEX:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG    60
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Db      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG    60

Qy     61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACAGTCGCGTCCGCACC   120
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Db     61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACAGTCGCGTCCGCACC   120

Qy    121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGTCCGATCGCCAGCCTCCAGACC   180
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Db    121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGTCCGATCGCCAGCCTCCAGACC   180

Qy    181 CCAGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC   240
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Db    181 CCAGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC   240

Qy    241 AATCCCTCCCTCAAGAGTCGAGTCACCGTCTCATTTCAAAGACACGTCCAAGAACCAGTTCTTC   300
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Qy    901 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG   960
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Db   1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC   1080

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Db   1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACCAGGTGTACACCCTG   1140

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Qy   1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTAC   1260
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RESULT 2
US-08-487-550-11
; Sequence 11, Application US/08487550
; Patent No. 6113898
GENERAL INFORMATION:
    APPLICANT: Anderson, Darrell R.
    TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
    TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
    TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
    TITLE OF INVENTION: IMMUNOSUPPRESANTS"
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
        STREET: 699 Prince Street
        CITY: Alexandria
        STATE: VA
        COUNTRY: USA
        ZIP: 22314
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/487,550
        FILING DATE: 07-JUN-1995
        CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
        NAME: Teskin, Robin L.
        REGISTRATION NUMBER: 35,030
        REFERENCE/DOCKET NUMBER: 012712-131
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 703-836-6620
        TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1431 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: not relevant
        TOPOLOGY: linear
    MOLECULE TYPE: peptide
    FEATURE:
        NAME/KEY: CDS
        LOCATION: 1..1431
    FEATURE:
        NAME/KEY: mat_peptide

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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April  5, 2003, 19:47:34 ; Search time 65.1566 Seconds
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Perfect score:  1431
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Scoring table:  IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched:   441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:   882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	1315.8	91.9	1431	3	US-08-487-550-11	Sequence 11, Appl
3	1234.8	86.3	1567	3	US-09-049-672A-17	Sequence 17, Appli
4	1210.4	84.6	1418	4	US-08-793-450-7	Sequence 7, Appli
5	1171.4	81.9	1404	3	US-08-523-894-7	Sequence 7, Appli
6	1168.2	81.6	1404	3	US-08-523-894-11	Sequence 11, Appl
7	1166.6	81.5	1404	3	US-08-523-894-9	Sequence 9, Appli
8	1123.6	78.5	1428	1	US-08-488-376-17	Sequence 17, Appl
9	1123.6	78.5	1428	2	US-08-634-223-17	Sequence 17, Appl
10	1123.6	78.5	1428	2	US-08-634-224-17	Sequence 17, Appl
11	1123.6	78.5	1428	2	US-08-634-400-17	Sequence 17, Appl
12	1123.6	78.5	1428	2	US-08-635-878-17	Sequence 17, Appli
13	1123.6	78.5	1428	4	US-08-770-057-17	Sequence 17, Appl
14	1123.6	78.5	1428	4	US-09-335-697B-17	Sequence 17, Appl
15	1123.6	78.5	1428	4	US-09-335-697B-17	Sequence 17, Appl
16	1117.2	78.1	1437	3	US-08-487-550-7	Sequence 7, Appli
17	1112.4	77.7	1428	1	US-08-488-376-19	Sequence 19, Appl
18	1112.4	77.7	1428	2	US-08-634-223-19	Sequence 19, Appl
19	1112.4	77.7	1428	2	US-08-634-224-19	Sequence 19, Appl
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21	1112.4	77.7	1428	2	US-08-635-878-19	Sequence 19, Appl
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23	1112.4	77.7	1428	4	US-09-335-697B-19	Sequence 19, Appl
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25	1111.6	77.7	19040	4	US-09-343-485A-3	Sequence 3, Appli
26	1103.6	77.1	1617	2	US-08-378-939-9	Sequence 9, Appli
27	1092.6	76.4	6557	1	US-08-286-740-3	Sequence 3, Appli
28	1092.6	76.4	6557	5	PCT-US95-09576-3	Sequence 3, Appli
29	1090.6	76.2	8120	3	US-09-027-449-68	Sequence 68, Appl
30	1090.6	76.2	8120	3	US-09-026-985-68	Sequence 68, Appl
31	1090.6	76.2	8120	4	US-09-121-952A-68	Sequence 68, Appl
32	1090.6	76.2	8120	4	US-09-234-340A-68	Sequence 68, Appl
33	1090.2	76.2	1576	1	US-08-157-101A-6	Sequence 6, Appli
34	1087	76.0	9209	1	US-08-149-099C-3	Sequence 3, Appli
35	1087	76.0	9209	2	US-08-476-275-2	Sequence 2, Appli
36	1087	76.0	9209	2	US-08-478-967A-3	Sequence 3, Appli
37	1087	76.0	9209	4	US-08-475-815B-3	Sequence 3, Appli
38	1087	76.0	18986	2	US-08-819-866-2	Sequence 2, Appli
39	1087	76.0	18986	2	US-09-023-715-2	Sequence 2, Appli
40	1087	76.0	18986	4	US-09-343-485A-2	Sequence 2, Appli
41	1080.2	75.5	1350	3	US-08-157-101A-9	Sequence 9, Appli
42	1049.8	73.4	1655	3	US-09-049-672A-21	Sequence 21, Appl
43	1044.6	73.0	1135	1	US-08-236-311-8	Sequence 8, Appli
44	1044.6	73.0	1135	3	US-08-457-918-8	Sequence 8, Appli
45	1040	72.7	6285	1	US-08-467-420A-49	Sequence 49, Appl

```
                              ALIGNMENTS

RESULT 1
US-08-487-550-3

;  Sequence 3, Application US/08487550
;  Patent No. 6113898
;  GENERAL INFORMATION:
;~   APPLICANT: Anderson, Darrell R.
;~   TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;~   TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;~   TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;~   TITLE OF INVENTION: IMMUNOSUPPRESANTS"
;~   NUMBER OF SEQUENCES: 12
;~   CORRESPONDENCE ADDRESS:
;~     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;~     STREET: 699 Prince Street
;~     CITY: Alexandria
;~     STATE: VA
;~     COUNTRY: USA
;~     ZIP: 22314
;~   COMPUTER READABLE FORM:
;~     MEDIUM TYPE: Floppy disk
;~     COMPUTER: IBM PC compatible
;~     OPERATING SYSTEM: PC-DOS/MS-DOS
;~     SOFTWARE: PatentIn Release #1.0, Version #1.30
;~   CURRENT APPLICATION DATA:
;~     APPLICATION NUMBER: US/08/487,550
;~     FILING DATE: 07-JUN-1995
;~     CLASSIFICATION: 435
;~   ATTORNEY/AGENT INFORMATION:
;~     NAME: Teskin, Robin L.
;~     REGISTRATION NUMBER: 35,030
;~     REFERENCE/DOCKET NUMBER: 012712-131
;~   TELECOMMUNICATION INFORMATION:
;~     TELEPHONE: 703-836-6620
;~     TELEFAX: 703-836-2021
;~   INFORMATION FOR SEQ ID NO: 3:
;~     SEQUENCE CHARACTERISTICS:
;~       LENGTH: 1431 base pairs
;~       TYPE: nucleic acid
;~       STRANDEDNESS: not relevant
;~       TOPOLOGY: linear
;~     MOLECULE TYPE: peptide
;~   FEATURE:
;~     NAME/KEY: CDS
;~     LOCATION: 1..1431
;~   FEATURE:
;~     NAME/KEY: mat_peptide
;~     LOCATION: 1..1431
US-08-487-550-3

Query Match             100.0%;  Score 1431;  DB 3;  Length 1431;
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Db   180 HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239
             |  |||||  ||||  ||||  ||||||:::||||||:||||||||  :|  ||||||
Qy   381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 440
             ||   :|::|||  :|||::||:|:||  ||||::| ||||:|||| ::|:|||||
Db   240 PPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLR 299
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SQ   SEQUENCE   399 AA;   44020 MW;   4C38138BFAED3FF0 CRC64;

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Query Match              43.3%;   Score 1117;  DB 1;  Length 399;
Best Local Similarity   63.4%;    Pred. No. 1.1e-71;
Matches 210;  Conservative  43;  Mismatches  74;  Indels   4;  Gaps   3;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
             |  :||||   :| :: ||||| |||||||  :|:|||||||||||| :||||||||||
Db     1 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD  60

Qy   207 GLYSLSSVVTVPSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 264
             :|||:  |||  :||  |||:|  |:||   ::||||||:||  |||||| |||||
Db    61 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118

Qy   265 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
             |||||||:|||||||||||  :::||:|||||||||||||||||||||||||:||| ::
Db   119 GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED 178

Qy   325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
             |||| |  :||||: |:|  ||||||||:||:|||||||:|||||  |  :|||||||||
Db   179 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE 238

Qy   385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
             :|  |||  :|||::||:|:||  ||||::|||||||:|||| ::|:|||||||
Db   239 EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 298

Qy   445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
             :| |  :||||:|||: ||||||:::||
Db   299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329
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Search completed: March 29, 2003, 09:11:13
Job time : 13.3492 secs

RESULT 15
GCAM_MOUSE

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ID   GCAM_MOUSE    STANDARD;    PRT;    399 AA.
AC   P01865;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2A chain C region, membrane-bound form.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC   -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC       SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC       GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC       BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC       IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC       SEGMENT OF MU CHAINS.
CC   -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC       IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC       THE A ALLELE.
```

```
DR   EMBL; J00471; AAB59661.1; ALT_INIT.
DR   PIR; A02154; G2MSAM.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
FT   DISULFID     15     15       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     82
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    110    110       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   TRANSMEM    346    363       POTENTIAL.
FT   DOMAIN      364    399       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
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Db   381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239
Qy   441 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db   300 VQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK 335
```

RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN   [4]
RP   MYELOMA PROTEIN MOPC 173.
RX   MEDLINE=74175517; PubMed=4831970;
RA   Bourgois A., Fougereau M., Rocca-Serra J.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT   for the evolution of immunoglobulin structure and function.";
RL   Eur. J. Biochem. 43:423-435(1974).
RN   [5]
RP   DISULFIDE BONDS.
RX   MEDLINE=7305687; PubMed=4565406;
RA   de Preval C., Fougereau M.;
RT   "Determination of the primary structure of a mouse gamma G2a
RT   immunoglobulin. Identification of the disulfide bridges.";
RL   Eur. J. Biochem. 30:452-462(1972).
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; V00798; CAA24178.1; -.
DR   PIR; A02152; G2MSA.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGC1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1   1
FT   DISULFID   15   15   INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID   27   82
FT   DISULFID   107   107   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   110   110   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   112   112   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   144   204
FT   DISULFID   250   308
FT   MOD_RES   330   330   REMOVED POST-TRANSLATIONALLY.
SQ   SEQUENCE   330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match   43.5%; Score 1122; DB 1; Length 330;
Best Local Similarity   63.6%; Pred. No. 4e-72;
Matches 211; Conservative 74; Mismatches 43; Indels   4; Gaps 3;

Qy 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
Db   1 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSD 60

Qy 207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 264
Db   61 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118

Qy 265 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
Db 119 GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED 178

Qy 325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
Db 179 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVVYLPPPE 238

Qy 385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
Db 239 EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 298

Qy 445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
Db 299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330

RESULT 14
GCAB_MOUSE
ID   GCAB_MOUSE   STANDARD;   PRT;   335 AA.
AC   P01864;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2A chain C region, B allele.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=82037861; PubMed=6170065;
RA   Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT   "Multiple differences between the nucleic acid sequences of the
RT   IgG2aa and IgG2ab alleles of the mouse.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN   [2]
RP   SEQUENCE.
RX   MEDLINE=82037777; PubMed=6794027;
RA   Dognin M.J., Lauwereys M., Strosberg A.D.;
RT   "Multiple amino acid substitutions between murine gamma 2a heavy
RT   chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC   -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC   FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR   PIR; A02153; G2MSAB.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGC1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1   1
SQ   SEQUENCE   335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match   43.4%; Score 1119.5; DB 1; Length 335;
Best Local Similarity   61.3%; Pred. No. 6.1e-72;
Matches 206; Conservative 52; Mismatches 71; Indels   7; Gaps 2;

Qy 147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
Db   1 AKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQ-S 59

Qy 207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK------SCDKTHTCPPCPA 260
Db   60 GLYTLSSSVTVTSNTWPSQTTCNVAHPASSTKVDKKIEPRVPITQNPCPPHQRVPPCAA 119

Qy 261 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 320
Db 120 PDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 179

Qy 321 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380

```
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    113       HINGE.
FT   DOMAIN      114    223       CH2.
FT   DOMAIN      224    327       CH3.
FT   TRANSMEM    346    362       POTENTIAL.
FT   DOMAIN      363    398       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT    333    333       E -> G (IN REF. 2).
FT   CONFLICT    342    342       E -> Q (IN REF. 2).
FT   CONFLICT    388    388       P -> F (IN REF. 2).
SQ   SEQUENCE    398 AA;  43929 MW;  CF7F264B50A41B95 CRC64;
```

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Query Match             43.7%;  Score 1126;  DB 1;  Length 398;
Best Local Similarity   63.8%;  Pred. No. 2.6e-72;
Matches  210;  Conservative  46;  Mismatches  69;  Indels  4;  Gaps  3;

Qy  148 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 207
            :|:||||| |||||||::|:|||||||| |||||||||:||| ||:||:.|.|||||: :||
Db    1 TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SG  59

Qy  208 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCP--PCPAPELLG 265
           |:|||| :|||||:   ||.||||| | :.|:|   :|::|:.   |||  .||| |:||
Db   60 FYSLSSLLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-IPKPSTPPGSSCPPGNILG 118

Qy  266 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 325
           ||||| ||||||| |||| ||:|||||||||:  |||  :|:||:||||:| ||||||:|
Db  119 GPSVFIFPPKPKDALMISLLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY 178

Qy  326 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 385
           ||||||| | | ||||:.||||:|||| |||||||||:|||| ||.|:|.|||:||| :|
Db  179 NSTFRVVSALPIQHQDMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPRE 238

Qy  386 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 445
              :.|||||||| :||| ||:||||| |||.| ||.|||:||||||:|||||||||| :.
Db  239 QMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDTDS 298

Qy  446 WQQGNVFSCSVMHEALHNHYTQKSLSLSP 474
           | ||::|:||| |||||||:|||.|| ||
Db  299 WLQGEIFTCSVVHEALHNHHTQKNLSRSP 327
```

```
RESULT 13
GCAA_MOUSE
ID   GCAA_MOUSE     STANDARD;      PRT;   330 AA.
AC   P01863;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ig gamma-2A chain C region, A allele.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81076554; PubMed=6777755;
RA   Sikorav J.-L., Auffray C., Rougeon F.;
RT   "Structure of the constant and 3' untranslated regions of the murine
RT   Balb/c gamma 2a heavy chain messenger RNA.";
RL   Nucleic Acids Res. 8:3143-3155(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81198976; PubMed=6262729;
RA   Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT   "The complete nucleotide sequence of mouse immunoglobin gamma 2a gene
RT   and evolution of heavy chain genes: further evidence for intervening
RT   sequence-mediated domain transfer.";
RL   Nucleic Acids Res. 9:1365-1381(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81223894; PubMed=6787604;
RA   Ollo R., Auffray C., Morchamps C., Rougeon F.;
RT   "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT   suggests that exons can be exchanged between genes in a multigenic
```

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Db    1 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD  60

Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 264
           .|:|||| :|||||:|   |:| |||| | :.:::   .|..|   |  .  .|| ||:
Db   61 -LYTLSSSVVTVPSSSPRPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 114

Qy  265 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
            .||||| ||||||| | | ||:||||||||:| |||| :|:||:||||:| |||||:||
Db  115 --SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPRREQ 172

Qy  325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
           :|||| |||: | ||||||||||:||.||:||  |||||||||| ||.|:|.|||:|||:
Db  173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 232

Qy  385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
           :|  .|.|||||| : ||| ||:||||: |||.:||.| ||::|:.|||:|:||||.|:|
Db  233 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS 292

Qy  445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
           .||:|| |:|||| ||||||||::||| ||||
Db  293 NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 323
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RESULT 12
GC3M_MOUSE
ID   GC3M_MOUSE     STANDARD;      PRT;   398 AA.
AC   P03987;
DT   23-OCT-1986 (Rel. 02, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-3 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
RN   [2]
RP   SEQUENCE OF 328-398 FROM N.A.
RX   MEDLINE=84041483; PubMed=6314258;
RA   Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA   Wall R.;
RT   "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT   segment.";
RL   Nucleic Acids Res. 11:6775-6785(1983).
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DR   EMBL; J00451; AAB59655.1; -; ALT_SEQ.
DR   EMBL; V01526; CAA24767.1; ALT_SEQ.
DR   PIR; A02155; G3MSM.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC_1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER       1      1
```

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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00451, -; NOT_ANNOTATED_CDS.
DR   PIR; B02156; G3MSC.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Transmembrane; Alternative splicing.
FT   NON_TER   1   1
FT   DOMAIN   1   97   CH1.
FT   DOMAIN   98   113   HINGE.
FT   DOMAIN   114   223   CH2.
FT   DOMAIN   224   327   CH3.
SQ   SEQUENCE   329 AA; 36228 MW; F458271741B2BAD6 CRC64;

Query Match   44.1%; Score 1137; DB 1; Length 329;
Best Local Similarity   64.0%; Pred. No. 3.5e-73;
Matches 212; Conservative 46; Mismatches 69; Indels   4; Gaps   3;

Qy   148 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 207
              ||:|||:| || ||:|||||||||||||||||||||||||||||| :|||||||
Db   1 TTTAPSVPVPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNVGALSSGVRTVSSVLQ-SG 59

Qy   208 LYSLSSVVTVPSSSLGTGTYICNVNHKPSNTKVDKKAEPKSCDKTHTCP--PCPAPELLG 265
              ||||||||| ||: |: || ||:|::|||| :: || :|
Db   60 FYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKIREPR-IPKPSTPPGSSCPPGNILG 118

Qy   266 GPSVFLFPPKPKDTLMISRTEPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 325
              ||||| || | | |: |: |||||:|||| ::|||| | : || ||| | |:||| |:
Db   119 GPSVFIFPPKPKDALMLSLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY 178

Qy   326 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 385
              ||| ||||| | :|||:|| ||||||:|||| ||||| | || || | ||| |||:||
Db   179 NSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPRE 238

Qy   386 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 445
              ::|||||||||| ||||| | |:||| ||:| |||||| |||||||| ||||||||||||
Db   239 QMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDTDS 298

Qy   446 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
              |::| |||||||||||||:|||||||||||
Db   299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329

RESULT 11
GC1M_MOUSE
ID   GC1M_MOUSE   STANDARD;   PRT;   393 AA.
AC   P01869;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ig gamma-1 chain C region, membrane-bound form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]

RP   SEQUENCE OF 323-393 FROM N.A.
RX   MEDLINE=82197626; PubMed=6804950;
RA   Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT   "mRNA for surface immunoglobulin gamma chains encodes a highly
RT   conserved transmembrane sequence and a 28-residue intracellular
RT   domain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN   [3]
RP   SEQUENCE OF 323-366 FROM N.A.
RX   MEDLINE=82115295; PubMed=6799207;
RA   Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA   Eisenberg D., Wall R.;
RT   "Gene segments encoding transmembrane carboxyl termini of
RT   immunoglobulin gamma chains.";
RL   Cell 26:19-27(1981).
RN   [4]
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE=82221190; PubMed=6283537;
RA   Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT   "Nucleotide sequences of gene segments encoding membrane domains of
RT   immunoglobulin gamma chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC   SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC   GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC   BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC   IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC   SEGMENT OF MU CHAINS.
CC   ---
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   PIR; B02159; G1MSM.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   Alternative splicing; Transmembrane.
FT   NON_TER   1   1
FT   DOMAIN   1   97   CH1.
FT   DOMAIN   98   110   HINGE.
FT   DOMAIN   111   217   CH2.
FT   DOMAIN   218   324   CH3.
FT   DISULFID   27   82   INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID   102   102   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   104   104   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   107   107   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   109   109   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   138   198
FT   CARBOHYD   174   174   N-LINKED (GLCNAC...).
FT   DISULFID   244   302
FT   TRANSMEM   340   357   POTENTIAL.
FT   DOMAIN   358   393   CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match   44.0%; Score 1133; DB 1; Length 393;
Best Local Similarity   61.9%; Pred. No. 8.3e-73;
Matches 205; Conservative 55; Mismatches 61; Indels 10; Gaps   4;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
              || |||||| ||||| ||:||||:|||||||||| :|||||||

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KW   Alternative splicing.
FT   NON_TER       1      1
FT   DOMAIN        1     97       CH1.
FT   DOMAIN       98    110       HINGE.
FT   DOMAIN      111    217       CH2.
FT   DOMAIN      218    324       CH3.
FT   DISULFID     27     82
FT   DISULFID    102    102       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID    104    104       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    107    107       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    138    198
FT   CARBOHYD    174    174       N-LINKED (GLCNAC...).
FT                               /FTId=CAR_000055.
FT   DISULFID    244    302
FT   MOD_RES     324    324       REMOVED POST-TRANSLATIONALLY.
FT   CONFLICT    276    276       N -> D (IN REF. 3).
FT   CONFLICT    278    278       N -> D (IN REF. 3).
SQ   SEQUENCE    324 AA;     35704 MW;   A338812F3D1F2C93 CRC64;

Query Match             44.2%;
Best Local Similarity   62.0%;   Pred. No. 2.9e-73;    Score 1138;  DB 1;   Length 324;
Matches  206;   Conservative  55;   Mismatches  61;   Indels  10;   Gaps  4;

Qy   147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  206
               |||:||::|||| : :     |||||:||||||||:||:|:||:|||||||
Db     1  AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD   60

Qy   207  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL  264
               : |||||:: |||||||||||||||:: |||||: |       :|||| |||:
Db    61  -LYTLSSSVTVPSSPRPSEVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV-  114

Qy   265  GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ  324
               |||||||||||||| :|| |||||||||| |:||||||| |||||||::| ||||
Db   115  --SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEHTAQTQPREEQ  172

Qy   325  YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR  384
               ::|||| ||||||||:||::||::|||||:|: |||||||||||:::
Db   173  FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVVTIPPPK  232

Qy   385  DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS  444
               ::|:|||||||||:||||:::|||::| :||||||||||:|||:||::::|||
Db   233  EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS  292

Qy   445  RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
               |:  ||||:|||:|||||:||||:|||| |||
Db   293  NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK  324


RESULT 10
GC3_MOUSE
ID   GC3_MOUSE     STANDARD;      PRT;     329 AA.
AC   P22436;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-3 chain C region, secreted form.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85027161; PubMed=6092053;
RA   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA   Tucker P.W., Blattner F.R.;
RT   "Structural analysis of the murine IgG3 constant region gene.";
RL   EMBO J. 3:2041-2046(1984).
```

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RESULT 9
GC1_MOUSE
ID   GC1_MOUSE     STANDARD;      PRT;     324 AA.
AC   P01868;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ig gamma-1 chain C region.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80045036; PubMed=115593;
RA   Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA   Takahashi N., Mano Y.;
RT   "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT   gamma 1 chain gene.";
RL   Cell 18:559-568(1979).
RN   [2]
RP   SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX   MEDLINE=80202559; PubMed=6769752;
RA   Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA   Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT   "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT   cloned in a bacterial plasmid.";
RL   Gene 9:87-97(1980).
RN   [3]
RP   SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=80012837; PubMed=113776;
RA   Rogers J., Clarke P., Salser W.;
RT   "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT   heavy chain.";
RL   Nucleic Acids Res. 6:3305-3321(1979).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX   MEDLINE=78242288; PubMed=98524;
RA   Adetugbo K.;
RT   "Evolution of immunoglobulin subclasses. Primary structure of a
RT   murine myeloma gamma1 chain.";
RL   J. Biol. Chem. 253:6068-6075(1978).
RN   [5]
RP   DISULFIDE BONDS (MOPC 21).
RX   MEDLINE=73008889; PubMed=5073237;
RA   Svasti J., Milstein C.;
RT   "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL   Biochem. J. 126:837-850(1972).
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DR   EMBL; V00793; CAA24172.1; -.
DR   EMBL; V00793; CAA24173.1; -.
DR   EMBL; V00793; CAA24174.1; -.
DR   EMBL; V00795; CAA24175.1; -.
DR   EMBL; V00795; CAA24176.1; -.
DR   PIR; A02159; G1MS.
DR   HSSP; P01842; 7FAB.
DR   GlycoSuiteDB; P01868; -.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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Qy   371 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 430
         ||||||||||||| :|||||||||||||||||||||||||||||||||| ||||||
Db   185 QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPMLDSD 244

Qy   431 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         |||||||||||||||||||| ||||||||||||||||:||||||||
Db   245 GSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 290

RESULT 7
GC1_RAT
ID   GC1_RAT   STANDARD;   PRT;   326 AA.
AC   P20759;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-1 chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89232738; PubMed=3149946;
RA   Brueggemann M.;
RT   "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL   Gene 74:473-482(1988).
DR   PIR; PS0017; PS0017.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT   NON_TER   1   1
FT   DOMAIN   1   97   CH1.
FT   DOMAIN   98   112   HINGE.
FT   DOMAIN   113   219   CH2.
FT   DOMAIN   220   326   CH3.
FT   DISULFID   27   82
FT   DISULFID   102   102   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   106   106   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   109   109   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   111   111   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   140   200
FT   DISULFID   246   304
FT   CARBOHYD   176   176   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   326 AA;   35946 MW; 013BAB45EF49B9DA CRC64;

Query Match   44.5%;
Best Local Similarity   63.1%;
Matches 210; Conservative 52; Mismatches 61; Indels 10; Gaps 4;

Score 1148; DB 1; Length 326;
Pred. No. 5.7e-74;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
         ||:||| :| ||:| ||||||||||||||:|||||||||||||||||||:||||||||:|
Db   1 AETTAPSVYPLAPGTALKSNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQ-S 59

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
         |||| ||| :|: | ||| ||||| ::|::||||||||| : |
Db   60 GLYTLTSSVT--SSTWPSQTVTCNVAHPASSTKVDKKIVPRNCG---GDCKPC----ICTG 113

Qy   267 ---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 323
         :::||:||||||||||: :||||||||||:|| : ::||:|:||||||||:| |:::
Db   114 SEVSSVVFIFPPKPKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEE 173

Qy   324 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 383
         ||||||||:|| ||||||||||:: ||:|: : |||:||||||: | |: | :|
Db   174 QFNSTFRSVSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMSPT 233

Qy   384 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 443
         ||:|||||||||||||||||||||||||| ||||||:|||||||||||||||||:|
Db   234 KEEMTQNEVSITCMVKGFYPPDIYEWQMNGQQPENYKNTPPTMDTDGSYFLYSKLNVKK 293

Qy   444 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         :||||| :|| ||||||||:|:|||||||||||
Db   294 EKWQQGNTFTCSVLHEGLHNHTEKSLSHSPGK 326

RESULT 8
GCB_RAT
ID   GCB_RAT   STANDARD;   PRT;   333 AA.
AC   P20761;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2B chain C region.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89232738; PubMed=3149946;
RA   Brueggemann M.;
RT   "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL   Gene 74:473-482(1988).
DR   PIR; PS0018; PS0018.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1   1
FT   DISULFID   15   15   INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID   27   80
FT   DISULFID   106   106   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   109   109   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   112   112   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   115   115   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   147   207
FT   DISULFID   253   311
SQ   SEQUENCE   333 AA;   36497 MW; 55F8B64D48D460A6 CRC64;

Query Match   44.3%;
Best Local Similarity   63.7%;
Matches 214; Conservative 44; Mismatches 69; Indels 9; Gaps 3;

Score 1142.5; DB 1; Length 333;
Pred. No. 1.4e-73;

Qy   147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
         |: :|||||| :| | :||||||||||||:||||||||||||||||||:||||||||:
Db   1 AQTTAPSVYPLAPGCGDTTSSTVLGCLVKGYFPEPVTVTWNSGALSSDVHTFPAVLQ-S 59

Qy   207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKS------CDKTHTCPPCPA 260
         |||| |||||: |:|: :|| ||||:|:|||||||| ::   ::
Db   60 GLYTLTSSVT--SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCPTCPTCHKCPV 117

Qy   261 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 320
         |||||||||||||||||||:| :|| |||||:||:::|:|||:|:||||||||:| ||
Db   118 PELLGGPSVFIFPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEVHTAQTQP 177

Qy   321 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380
         |||||||||:|| |||||||||||: : ||:|: :||||||||||||| | ||:
Db   178 REEQYNSTFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVRKPQVYVM 237

Qy   381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 440
         |||::|| ||||||||||||||||||||||||:|||||:||||||||:| ||||||||
Db   238 GPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLN 297

Qy   441 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         | :::||| ::|| ||||||||:|::|||||:|||
Db   298 VERSRWDSRAPFVCSVVHEGLHNHHVEKSISRPPGK 333

```
Db    176  QYNTTFRVESVLPIQHQDWLRGKEFKCKVNKALPAPIEKTISKTKGAPRMPDVVTLPPS 235
           ||||:||  ||: ||||||||||||||||||||||||||||| |||||
Qy    384  RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 441
           ||||:|| |:||:||  |:|:|| ||||  | ||  ||  :||||||  : |||||||||
Db    236  RDELSKSKVSVSTCLINFPPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLTV 295
```

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Qy    442  DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
           |||  || ||| ||||||||||| |||||| ||
Db    296  DKSAWDQGTVVTCSVMHEALHNHVTQKAISRSPG 329
```

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RESULT 6
GC3_HUMAN
ID    GC3_HUMAN     STANDARD;      PRT;     290 AA.
AC    P01860;
DT    21-JUL-1986 (Rel. 01, Created)
DT    21-JUL-1986 (Rel. 01, Last sequence update)
DT    15-JUN-2002 (Rel. 41, Last annotation update)
DE    Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN    IGHG3.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE (DISEASE PROTEIN WIS).
RX    MEDLINE=81021548; PubMed=6774747;
RA    Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT    "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT    gamma 3 heavy-chain disease protein Wis.";
RL    Biochemistry 19:4304-4308(1980).
RN    [2]
RP    REVISIONS TO 12-97 (PROTEIN WIS).
RX    MEDLINE=77118561; PubMed=402363;
RA    Michaelsen T.E., Frangione B., Franklin E.C.;
RT    "Primary structure of the 'hinge' region of human IgG3. Probable
RT    quadruplication of a 15-amino acid residue basic unit.";
RL    J. Biol. Chem. 252:883-889(1977).
RN    [3]
RP    REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX    MEDLINE=77021516; PubMed=823945;
RA    Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT    "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT    Structure of the Fc fragment of immunoglobulin G3.";
RL    Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN    [4]
RP    SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX    MEDLINE=82247835; PubMed=6808505;
RA    Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA    Franklin E.C., Hood L., Buxbaum J.N.;
RT    "Gamma heavy chain disease in man: cDNA sequence supports partial
RT    gene deletion model.";
RL    Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC    -!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC        INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC        NORMALLY PRESENT IN THE HINGE REGION.
CC    -!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC    -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC        REF.2.
CC    -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC        AND ALL OF THE CH1 REGION.
CC    -!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC        OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC        GAMMA-3 HEAVY CHAINS.
CC    -!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC        OR ANOTHER GAMMA CHAIN SUBCLASS.
CC    -!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC        TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC        IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC        SEGMENT (12-28).
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DR    EMBL; J00231; AAA52805.1; ALT_SEQ.
DR    PIR; A02149; G3HUWI.
DR    HSSP; P01857; 1FC1.
DR    Genew; HGNC:5527; IGHG3.
DR    MIM; 147120; -.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003597; Ig_C1.
DR    InterPro; IPR003600; Ig_like.
DR    Pfam; PF00047; ig; 2.
DR    SMART; SM00410; IG_like; 1.
DR    SMART; SM00407; IGc1; 1.
DR    PROSITE; PS00290; IG_MHC; 1.
KW    Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT    DOMAIN        12     73       HINGE.
FT    DOMAIN        74    183       CH2.
FT    DOMAIN       184    289       CH3.
FT    REPEAT        29     43
FT    REPEAT        44     58
FT    REPEAT        59     73
FT    MOD_RES        1      1       PYROLIDONE CARBOXYLIC ACID.
FT    CARBOHYD       6      6       N-LINKED (GLCNAC...).
FT    DISULFID       7      7       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      24     27       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      27     27       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      33     33       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      39     39       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      42     42       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      48     48       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      54     54       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      57     57       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      63     63       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      69     69       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    DISULFID      72     72       INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT    CARBOHYD     140    140       N-LINKED (GLCNAC...).
FT    MOD_RES      290    290       REMOVED POST-TRANSLATIONALLY.
FT    VARIANT      126    127       QV -> EB (IN ZUC).
FT                                  /FTId=VAR_003890.
FT    VARIANT      134    134       P -> L (IN OMM).
FT                                  /FTId=VAR_003891.
FT    VARIANT      139    139       F -> Y (IN OMM).
FT                                  /FTId=VAR_003892.
FT    VARIANT      182    182       T -> A (IN OMM).
FT                                  /FTId=VAR_003893.
FT    VARIANT      227    227       S -> N (IN OMM).
FT                                  /FTId=VAR_003894.
FT    VARIANT      227    227       MISSING (IN ZUC).
FT                                  /FTId=VAR_003895.
FT    VARIANT      279    279       F -> Y (IN OMM).
FT                                  /FTId=VAR_003896.
SQ    SEQUENCE   290 AA;  32331 MW;  E69CBC95705B2F46 CRC64;
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Query Match             44.9%;  Score 1157;  DB 1;  Length 290;
Best Local Similarity   76.2%;  Pred. No. 1.1e-74;
Matches  218;  Conservative   20;  Mismatches  26;  Indels  22;  Gaps  2;

Qy    210  SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV-----------DKKAEPKSCD 250
           |:||||||||||||||||||||||||||||||           ||||||||||
Db      8  TVSSELKTP---LGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCD 64

Qy    251  KTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 310
           |:||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db     65  TPPPCPRCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDG 124

Qy    311  VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 370
           |:|||||||||||:||||||||||||||||:||||||||||||||||||||||||||
Db    125  VQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTKG 184
```

DR   InterPro; IPR003597; Ig_cl.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER   1   1
FT   VARIANT   104   104   T -> M (IN D11 MARKER).
FT   VARIANT   185   185   T -> A (IN E15 MARKER).
FT   CONFLICT   48   48   N -> E (IN REF. 2).
FT   CONFLICT   71   71   V -> VPV (IN REF. 2).
FT   CONFLICT   144   144   E -> E (IN REF. 3 AND 4).
FT   CONFLICT   173   173   N -> D (IN REF. 5).
FT   CONFLICT   187   187   Q -> E (IN REF. 3 AND 5).
FT   CONFLICT   201   201   N -> D (IN REF. 5).
FT   CONFLICT   218   218   Q -> E (IN REF. 5).
FT   CONFLICT   233   233   E -> Q (IN REF. 5).
FT   CONFLICT   246   246   E -> D (IN REF. 5).
FT   CONFLICT   256   256   N -> G (IN REF. 5).
FT   CONFLICT   260   260   N -> D (IN REF. 5).
FT   CONFLICT   266   266   N -> D (IN REF. 5).
FT   CONFLICT   280   280   Y -> W (IN REF. 5).
FT   CONFLICT   284   284   N -> S (IN REF. 5).
SQ   SEQUENCE   323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match   47.6%; Score 1226.5; DB 1; Length 323;
Best Local Similarity   69.7%; Pred. No. 1.7e-79;
Matches 228; Conservative   34; Mismatches   58; Indels   7; Gaps   2;

Qy   150 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 209
                |||||||||||| ||||||| ||:|||||||||||||||||||||||||||:| ||||
Db   4 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLY 63

Qy   210 SLSSVVSVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSV 269
                ||||| || :|||||| : ||| | || | ::||:||||||||||
Db   64 SLSSVVSVTSSS---QPVTCNVAHPATNTKVDKTVAPSTCSK----PTCPPPELLGGPSV 116

Qy   270 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 329
                |||||||||||||||||||||||||||| : :|:| :| | | ||:::|::||
Db   117 FIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTI 176

Qy   330 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDELTK 389
                ||||| |||||||||||:: :|| ||||||||||||||||| || ::|| |: ||||
Db   177 RVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYIMGPPREELSS 236

Qy   390 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 449
                ||||||||:|||||||:::|| || |||| ||||||||||||| :||:|:|||:|||||
Db   237 RSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRG 296

Qy   450 NVFSCSVMHEALHNHYTQKSLSLSPGK 476
                 || ||||||||||||||||:| ||||
Db   297 DVFTCSVMHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO
ID   GC2_CAVPO   STANDARD;   PRT;   329 AA.
AC   P01862;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma-2 chain C region.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE OF 1-3.
RA   Trischmann T.M.;
RL   Submitted (APR-1975) to the PIR data bank.
RN   [2]
RP   SEQUENCE OF 4-68.
RX   MEDLINE=71058471; PubMed=5538606;
RA   Birshtein B.K., Hussain Q.Z., Cebra J.J.;

RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT   half-cystine joining heavy and light chains.";
RL   Biochemistry 10:18-25(1971).
RN   [3]
RP   SEQUENCE OF 69-133 AND 312-329.
RX   MEDLINE=71058486; PubMed=5538616;
RA   Turner K.J., Cebra J.J.;
RT   "Structure of heavy chain from strain 13 guinea pig
RT   immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT   and hinge region cyanogen bromide fragments.";
RL   Biochemistry 10:9-17(1971).
RN   [4]
RP   SEQUENCE OF 134-226.
RX   MEDLINE=75036072; PubMed=4429665;
RA   Tracey D.E., Cebra J.J.;
RT   "Primary structure of the CH2 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4796-4803(1974).
RN   [5]
RP   SEQUENCE OF 227-311.
RX   MEDLINE=75036073; PubMed=4609467;
RA   Trischmann T.M., Cebra J.J.;
RT   "Primary structure of the CH3 homology region from guinea pig IgG2
RT   antibodies.";
RL   Biochemistry 13:4804-4811(1974).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71058474; PubMed=4922544;
RA   Oliveira B., Lamm M.E.;
RT   "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL   Biochemistry 10:26-31(1971).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC   13 INBRED GUINEA PIGS.
DR   PIR; A02151; G2GP.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT   NON_TER   1   1
FT   DISULFID   16   16   INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID   28   79   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   105   105   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   107   107   INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID   110   110
FT   CARBOHYD   142   202   N-LINKED (GLCNAC...).
FT   DISULFID   178   178
FT   DISULFID   248   308
SQ   SEQUENCE   329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match   47.1%; Score 1212.5; DB 1; Length 329;
Best Local Similarity   70.1%; Pred. No. 1.6e-78;
Matches 234; Conservative   28; Mismatches   63; Indels   9; Gaps   4;

Qy   146 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 205
                | | |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1 SARTTAPSVFPLAASCVDTSGSMWTLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVLQ- 59

Qy   206 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTH--TCPPCPAPEL 263
                |||||||| ||||||||:||||| | :|: | ::||:||:||:|||:   : |:|:|:|
Db   60 SGLYSLSSVVTVPSSQKAT-----CNVAHPASSTKVDKTVEPIRTPZPBCTCPKCPPPEN 115

Qy   264 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 323
                |||||:|:||||||||||||||||||||||||| | :| | || ||:::|:::::
Db   116 LGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRVE 175

Qy   324 QYNSTYRVRVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 383
                ||:||::|::|::|:|||||||||||:| :|:|||||| ||||| || ||||:|| ||
Db   324 ...

```
Db  178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
            :|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy  447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
            |:||||||||||||||||||||||||| ||
Db  298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
```

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RESULT 4
GC_RABIT
ID   GC_RABIT               STANDARD;      PRT;    323 AA.
AC   P01870;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig gamma chain C region.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84030930; PubMed=6313520;
RA   Bernstein K.E., Alexander C.B., Mage R.G.;
RT   "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT   F-I haplotype.";
RL   Immunogenetics 18:387-397(1983).
RN   [2]
RP   SEQUENCE OF 1-128.
RX   MEDLINE=76135469; PubMed=1243651;
RA   Pratt D.M., Mole L.E.;
RT   "Sequence studies on the constant region of the Fd sections of rabbit
RT   immunoglobulin G of different allotype.";
RL   Biochem. J. 151:337-349(1975).
RN   [3]
RP   SEQUENCE OF 88-266 FROM N.A.
RX   MEDLINE=83299917; PubMed=6193512;
RA   Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT   "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT   heavy chain and identification of two genomic C gamma genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN   [4]
RP   SEQUENCE OF 132-161.
RX   MEDLINE=7011015; PubMed=5461106;
RA   Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT   "Sequence studies of the Fd section of the heavy chain of rabbit
RT   immunoglobulin G.";
RL   Biochem. J. 116:249-259(1970).
RN   [5]
RP   SEQUENCE OF 129-131 AND 155-322.
RA   Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL   (In) Killander J. (eds.);
RL   Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL   Stockholm (1967).
CC   -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC       104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC       MARKERS AND REF.5 THE E15 MARKER.
CC   --------------------------------------------------------------------------
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC       or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M16426; AAA31289.1; -.
DR   PIR; A02161; GHRB.
DR   HSSP; P01857; 1FC1.
DR   InterPro; IPR003006; Ig_MHC.
```

```
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-4 chain C region.
GN   IGHG4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81157104; PubMed=6299662;
RA   Ellison J.W., Buxbaum J.N., Hood L.E.;
RT   "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL   DNA 1:11-18(1981).
RN   [2]
RP   SEQUENCE OF 1-30 AND 81-326.
RX   MEDLINE=70207560; PubMed=4192699;
RA   Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT   "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT   constant region of a gamma 4 chain.";
RL   Biochem. J. 117:33-47(1970).
CC   --------------------------------------------------------------------------
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; K01316; AAB59394.1; ALT_INIT.
DR   PIR; A02150; G4HU.
DR   HSSP; P01842; 7FAB.
DR   Genew; HGNC:5528; IGHG4.
DR   MIM; 147130;
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region.
FT   NON_TER        1      1
FT   DOMAIN         1     98       CH1.
FT   DOMAIN        99    110       HINGE.
FT   DOMAIN       111    220       CH2.
FT   DOMAIN       221    327       CH3.
FT   DISULFID      14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID      27     83
FT   DISULFID     106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID     109    109       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID     141    201
FT   DISULFID     247    305
SQ   SEQUENCE   327 AA;  35940 MW;  3EDDB811EF208E7A CRC64;
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Query Match             61.6%;  Score 1586.5;  DB 1;  Length 327;
Best Local Similarity   90.6%;  Pred. No. 6.9e-105;
Matches  299;  Conservative  12;  Mismatches  16;  Indels  3;  Gaps  1;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
            ||||||||||||| ||| :|||:||||||||||||||||||||||||||||||||||||
Db    1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
            |||||||||||| |||| ||| ||||||| |||||||   ||  |  : |  |  |||
Db   61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117
Qy  267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
            ||||||||||||||||||||||||||||||||:|:||||| ||||| |||||||||:|
Db  118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQBDPEVQFNWYVDGVEVHNAKTKPREEQFN 177
Qy  327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
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OX   NCBf_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-326 FROM N.A.
RX   MEDLINE=82197521; PubMed=6804948;
RA   Ellison J.W., Hood L.E.;
RT   "Linkage and sequence homology of two human immunoglobulin gamma
RT   heavy chain constant region genes";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN   [2]
RP   SEQUENCE OF 88-115 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=83001943; PubMed=6811139;
RA   Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT   "Structure of human immunoglobulin gamma genes: implications for
RT   evolution of a gene family.";
RL   Cell 29:671-679(1982).
RN   [3]
RP   SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=84235992; PubMed=6329676;
RA   Krawinkel U., Rabbitts T.H.;
RT   "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT   genes.";
RL   EMBO J. 1:403-407(1982).
RN   [4]
RP   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX   MEDLINE=81007873; PubMed=6774012;
RA   Wang A.-C., Tung E., Fudenberg H.H.;
RT   "The primary structure of a human IgG2 heavy chain: genetic,
RT   evolutionary, and functional implications.";
RL   J. Immunol. 125:1048-1054(1980).
RN   [5]
RP   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX   MEDLINE=80001357; PubMed=113060;
RA   Connell G.E., Parr D.M., Hofmann T.;
RT   "The amino acid sequences of the three heavy chain constant region
RT   domains of a human IgG2 myeloma protein.";
RL   Can. J. Biochem. 57:758-767(1979).
RN   [6]
RP   SEQUENCE OF 238-275 (ZIE).
RX   MEDLINE=80114419; PubMed=118920;
RA   Hofmann T., Parr D.M.;
RT   "A note of the amino acid sequence of residues 381-391 of human
RT   immunoglobulin gamma chains.";
RL   Mol. Immunol. 16:923-925(1979).
RN   [7]
RP   REVISIONS TO 25, 59, 60 AND 264-268 (ZIE).
RA   Hofmann T., Parr D.M.;
RL   Submitted (MAR-1980) to the PIR data bank.
RN   [8]
RP   SEQUENCE OF 1-121 (DQT).
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=72035500; PubMed=4940472;
RA   Milstein C., Frangione B.;
RT   "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL   Biochem. J. 121:217-225(1971).
RN   [10]
RP   DISULFIDE BONDS.
RX   MEDLINE=69064124; PubMed=5782707;
RA   Frangione B., Milstein C., Pink J.R.L.;
RT   "Structural studies of immunoglobulin G.";
RL   Nature 221:145-148(1969).
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00230; AAB59393.1; -.
DR   PIR; A02148; G2HU.
DR   HSSP; P01857; 1FC1.
DR   Genew; HGNC:5526; IGHG2.
DR   MIM; 147110; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
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FT   DOMAIN       99    110       CH1.
FT   DOMAIN      111    219       HINGE.
FT   DOMAIN      220    326       CH2.
FT   DOMAIN                       CH3.
FT   DISULFID     14     14       INTERCHAIN (WITH A LIGHT CHAIN).
FT   DISULFID     27     83       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    102    102       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    103    103       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    106    106       INTERCHAIN (WITH A HEAVY CHAIN).
FT   DISULFID    109    109
FT   DISULFID    140    200
FT   DISULFID    246    304
FT   SITE        156    156       AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT   MOD_RES     326    326       REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT   VARIANT      60     60       S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT                                /FTId=VAR_003889.
FT   CONFLICT    109    109       C -> S (IN REF. 3).
SQ   SEQUENCE   326 AA;  35884 MW;  8310878C6878CF9C CRC64;

Query Match             62.1%;
Best Local Similarity   90.9%;
Pred. No. 7.7e-106;  DB 1;  Score 1600;  Length 326;
Matches  300;  Conservative   12;  Mismatches   14;  Indels    4;  Gaps     2;

Qy  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
            ||||||||||||| :|||  |||||||||||||||||||||||||||||||||||||||||
Db    1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
            ||||||||||||||  |||||  ||||||||||||| :| | | |        ||||||| :  |
Db   61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy  267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
            ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||:| 
Db  117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy  327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
            ||:||||||||:||||||||||||||||| ||||||||||| |||||||||||||||||:|
Db  177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy  387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446
            :||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db  237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy  447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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Db  297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326

RESULT 3
GC4_HUMAN
ID   GC4_HUMAN      STANDARD;      PRT;   327 AA.
AC   P01861;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
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RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC       G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC       MARKER & THE G1M (NON-1) MARKERS.
CC   -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC       35,116,198,269 & 272.
CC   -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC       155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC       268-272.
CC   -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC       RESIDUES 198,267&272.
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CC   --------------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A02146; GHHU.
DR   PDB; 1FC1; 15-JUL-92.
DR   PDB; 1FC2; 15-JUL-92.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00407; IGC1; 2.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW   3D-structure.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       HINGE.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    109
FT   DISULFID    109    109       INTERCHAIN (WITH LIGHT CHAIN).
FT   DISULFID    112    112       INTERCHAIN (WITH HEAVY CHAIN).
FT   DISULFID    144    204       INTERCHAIN (WITH HEAVY CHAIN).
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FT   VARIANT      97     97       K -> R (IN G1M(3) MARKER).
FT                                /FTId=VAR_003886.
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FT                                /FTId=VAR_003887.
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FT   STRAND      141    148
FT   STRAND      158    162
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FT   HELIX       193    197
FT   TURN        198    199
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FT   STRAND      227    227
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FT   STRAND      238    240
FT   HELIX       241    242
FT   TURN        245    256
FT   STRAND      260    266
FT   TURN        267    268
FT   STRAND      269    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      306    312
FT   TURN        313    314
FT   TURN        316    317
FT   STRAND      320    324
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Query Match             68.4%;  Score 1763;  DB 1;  Length 330;
Best Local Similarity   99.7%;  Pred. No. 2.5e-117;
Matches  329;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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Db     61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy    267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
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Qy    327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
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Qy    447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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RESULT 2
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ID   GC2_HUMAN     STANDARD;     PRT;    326 AA.
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DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-2 chain C region.
GN   IGHG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OM protein - protein search, using sw model

Run on:   March 29, 2003, 09:06:23 ; Search time 11.3492 Seconds
                               (without alignments)
                               1739.566 Million cell updates/sec

Title:     US-09-758-173-4
Perfect score: 2577
Sequence:  1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
          Gapop 10.0 , Gapext 0.5

Searched:  112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:  112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 45 summaries

Database :  SwissProt_40:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1763	68.4	330	1	GC1_HUMAN	P01857 homo sapien
2	1600	62.1	326	1	GC2_HUMAN	P01859 homo sapien
3	1586.5	61.6	327	1	GC4_HUMAN	P01861 homo sapien
4	1226.5	47.6	323	1	GC_RABIT	P01870 oryctolagus
5	1212.5	47.1	329	1	GC2_CAVPO	P01862 cavia porce
6	1157	44.9	290	1	GC3_HUMAN	P01860 homo sapien
7	1148	44.5	326	1	GC1_RAT	P20759 rattus norv
8	1142.5	44.3	333	1	GCB_RAT	P20761 rattus norv
9	1138	44.2	324	1	GC1_MOUSE	P01868 mus musculu
10	1137	44.1	329	1	GC3_MOUSE	P22436 mus musculu
11	1133	44.0	393	1	GC1M_MOUSE	P01869 mus musculu
12	1126	43.7	398	1	GC3M_MOUSE	P03987 mus musculu
13	1122	43.5	330	1	GCAA_MOUSE	P01863 mus musculu
14	1119.5	43.4	335	1	GCAB_MOUSE	P01864 mus musculu
15	1117	43.3	399	1	GCAM_MOUSE	P01865 mus musculu
16	1114.5	43.2	329	1	GCC_RAT	P20762 rattus norv
17	1108	43.0	322	1	GCA_RAT	P20760 rattus norv
18	1085	42.1	336	1	GCB_MOUSE	P01866 mus musculu
19	1080	41.9	405	1	GCBM_MOUSE	P01867 mus musculu
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21	483.5	18.8	429	1	EPC_RAT	P01855 rattus norv
22	468	18.2	146	1	HV2I_HUMAN	P06331 homo sapien
23	465	18.0	421	1	EPC_MOUSE	P06336 mus musculu
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26	437	17.0	458	1	MUC_RABIT	P03988 oryctolagus
27	431.5	16.7	476	1	MUCM_MOUSE	P01873 mus musculu
28	427	16.6	479	1	MUCM_RABIT	P04221 oryctolagus
29	425	16.5	457	1	MUC_SUNMU	P20768 suncus muri
30	420	16.3	450	1	MUC_CANFA	P01874 canis famil
31	415.5	16.1	454	1	MUC_MESAU	P06337 mesocricetu
32	403	15.6	391	1	MUCB_HUMAN	P04220 homo sapien
33	394	15.3	438	1	HVCS_HETFR	P23087 heterodontu
34	390.5	15.2	370	1	HVC1_HETFR	P23084 heterodontu
35	386.5	15.0	438	1	HVC2_HETFR	P23085 heterodontu
36	385	14.9	461	1	HVCM_HETFR	P23088 heterodontu
37	383.5	14.9	353	1	ALC1_HUMAN	P01876 homo sapien
38	380.5	14.8	353	1	ALC1_GORGO	P20758 gorilla gor
39	379	14.7	340	1	ALC2_HUMAN	P01877 homo sapien
40	371	14.4	129	1	HV2F_HUMAN	P01824 homo sapien
41	362.5	14.1	393	1	HV3C_HETFR	P23086 heterodontu
42	361	14.0	117	1	HV2G_HUMAN	P01825 homo sapien
43	356.5	13.8	137	1	HV46_MOUSE	P01822 homo sapien
44	355	13.8	116	1	HV60_MOUSE	P18531 mus musculu
45	344	13.3	344	1	ALC_MOUSE	P01878 mus musculu

ALIGNMENTS

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RESULT 1
GC1_HUMAN
ID   GC1_HUMAN     STANDARD;      PRT;    330 AA.
AC   P01857;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig gamma-1 chain C region.
GN   IGHG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82274238; PubMed=6287432;
RA   Ellison J.W., Berson B.J., Hood L.E.;
RT   "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL   Nucleic Acids Res. 10:4071-4079(1982).
RN   [2]
RP   SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX   MEDLINE=71064024; PubMed=5489771;
RA   Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA   Waxdal M.J., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL   Biochemistry 9:3161-3170(1970).
RN   [3]
RP   SEQUENCE OF 136-329 (EU).
RX   MEDLINE=71064025; PubMed=5530842;
RA   Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA   Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT   acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL   Biochemistry 9:3171-3181(1970).
RN   [4]
RP   SEQUENCE (MYELOMA PROTEIN NIE).
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [5]
RP   SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
```

Left column

```
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   597 AA;  65300 MW;  2DAFAD50A63175851 CRC64;

Query Match
Best Local Similarity   37.7%;   Pred. No. 5.1e-70;
Matches  222;   Conservative   75;   Mismatches  169;   Indels  123;   Gaps  20;

Qy    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT  60
Db    1 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFSG-YYWSWIRQP  59

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR--  118
Db   60 PGKGLEWIGEINHSG-ITNYNPSLKSRVTISVDTSKKQLSLKLLSSVNAADTAVYYCARVI  118

Qy  119 --GPRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCL  174
Db  119 TRASPGTDGR---YG--MDVWGQGTTVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCL  173

Qy  175 VKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-IC  229
Db  174 AQDFLPDSITFSWKYKNNSDISSTRGFPSVLR--GGKYAATSQVLLPSKDVMQGTDEHVVC  232

Qy  230 NVNHKPSN----------------------TKVDKKAEPKS----------CDKTHTCP------  256
Db  233 KVQHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSW  292

Qy  257 ------------------PCPAPELLGGPS------------------------  268
Db  293 LREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQ  352

Qy  269 ----------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV  313
Db  353 NASSMCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEA  410

Qy  314 HNAKTKPREQYNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-  372
Db  411 VKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVAL  470

Qy  373 REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD-  428
Db  471 HRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEP  530

Qy  429 -SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
Db  531 QAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK  579
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RESULT 15
Q8WUX4
ID   Q8WUX4      PRELIMINARY;       PRT;    588 AA.
AC   Q8WUX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 64.4 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019235; AAH19235.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
```

Right column

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DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   588 AA;  64438 MW;  FC60DBAD82B39FD7 CRC64;

Query Match
Best Local Similarity   36.5%;   Pred. No. 2.3e-69;
Matches  220;   Conservative   76;   Mismatches  167;   Indels  123;   Gaps  20;

Qy    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT  60
Db    1 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFSG-YYWSWIRQP  59

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR--  118
Db   60 PGKGLEWIGEINHSG-STNYNPSLKSRVTISVDTSKKQLSLKLLSSVNAADTAVYYCARVI  118

Qy  119 --GPRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCL  174
Db  119 TRASPGTDGR---YG--MDVWGQGTTVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCL  173

Qy  175 VKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-IC  229
Db  174 AQDFLPDSITFSWKYKNNSDISSTRGFPSVLR--GGKYAATSQVLLPSKDVMQGTDEHVVC  232

Qy  230 NVNHKPSN----------------------TKVDKKAEPKS----------CDKTHTCP------  256
Db  233 KVQHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSW  292

Qy  257 ------------------PCPAPELLGGPS------------------------  268
Db  293 LREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQ  352

Qy  269 ----------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV  313
Db  353 NASSMCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEA  410

Qy  314 HNAKTKPREQYNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-  372
Db  411 VKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVAL  470

Qy  373 REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD-  428
Db  471 HRPDVYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEP  530

Qy  429 -SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS  473
Db  531 QAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS  576
```

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Search completed: March 29, 2003, 09:14:37
Job time : 46.1716 secs
```

```
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT   NON_TER        1      1
SQ   SEQUENCE   337 AA;  37438 MW;  A60BF2B01DEFD1F6 CRC64;

Query Match             49.0%;  Score 1262.5;  DB 6;  Length 337;
Best Local Similarity   69.2%;  Pred. No. 2.3e-96;
Matches   234;  Conservative   42;  Mismatches   53;  Indels    9;  Gaps    3;

Qy  147  ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  206
              ||||||||:||||||||:|:||||:||||||||||||||||||:||||||||
Db    1  ASTTAPKVFALAPGCGTTSDSTVALGCLVSGYFPEPVKVSWNSGSLTSGVHTFPSVLQSS   60

Qy  207  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP------KSCDKTHTCPPCPA  260
              |||||||:::||||||| :||||:||:||||:||||||      | ||::|| |||
Db   61  GFYSLSSMVTVPASTWTSETYICNVVHAASNFKVDKKRIEPIPDNHQKVCDMS-KCPKCPA  119

Qy  261  PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP  320
              ||||||||||:|||:|||||||:||||||||||||||:|||:|::||||||||| ||:
Db  120  PELLGGPSVFIFPPNPKDTLMIRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTRP  179

Qy  321  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPQVYTL  380
              :|||:|||||||:||| ::||||:||||:|||||| ||| ||:||| ||:|||||||:|
Db  180  KEEQFNSTYRVVSVLRIQHQDWLSGKEFKCKVNNQALPQPIERTITKTKGRSQEPQVYVL  239

Qy  381  PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK  438
              .|:|||:|:|||:||||||:|||| |||||||||  ||||||| |||||||||||:|||
Db  240  APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYISTTQAQQDSDGSYFLYSK  299

Qy  439  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
              |:||| :||||| ||| ||||||||||||:|| |||
Db  300  LSVDRNRRWQQGTFTCGVMHEALHNHYQKNVSKNPGK  337

RESULT 13
Q9BU10
ID   Q9BU10         PRELIMINARY;       PRT;   597 AA.
AC   Q9BU10;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 65.3 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002963; AAH02963.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   597 AA;  65274 MW;  2DAFA8FB7E055851 CRC64;

Query Match             36.9%;  Score 950.5;  DB 4;  Length 597;
Best Local Similarity   37.7%;  Pred. No. 3.5e-70;
Matches   222;  Conservative   76;  Mismatches  168;  Indels  168;  Gaps   20;

Qy    1  MKHLWFFLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWIWIRQT   60
```

```
Db    1  MCHLWFFLLVAAPRWVLSQVLQQWGAGLLKPSETLSLTCGVYGGSFSG-YYWSWIRQP   59
              |||||||||||||||||||:|||| ||| |||||| ||.| ||| ||| ||||||
Qy   61  PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR--  118
              .| |||||| |:.:| .:|||||||||||| |||| ||: | .||.||||||||||
Db   60  PGKGLEWIGEINHSG-STNYNPSLKSRVTISVDTSKKQLSKLSSVNAADTAVYYCARVI  118

Qy  119  ---GPRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCL  174
              .| ||| :| :: || |||||||||||| |||||||||| :|::||||| ||||||
Db  119  TRASPGTDGR---YG--MDVWGQGTTVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCL  173

Qy  175  VKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL-GTQTY-IC  229
              ||:| | .: .|  |:| | .| :..|| || . |.| .: :: ||| |  |.: |
Db  174  AQDFLPDSIIFSWKYKNSDISSTRGFPSVLR-GGKYAATSQVLLPSKDVWQGTDEHVVC  232

Qy  230  NVNHKPSN----------TKVDKKAEPKS-------CDKTHTCP------  256
              .: |:|.|          |:| ||| |         ||| |||
Db  233  KVQHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFGNPRKSKLICQATGSPRQIQVSW  292

Qy  257  ----------PCPAPELLGGPS-----------------------  268
              .||||||||| .|
Db  293  LREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQ  352

Qy  269  ------------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV  313
              .:| ||||| | ||.||||||| . | : ::
Db  353  NASSMCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEA  410

Qy  314  HNAKTKPREEQYNSTYRVRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQP-  372
              .: : || :|.: .: |:. :. ..:| |: | |: |. : | :: :| :
Db  411  VKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVAL  470

Qy  373  REPQVVTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD-  428
              :|||:||||| .:| ||||||||||||||||| ||||||||  |:|||| |||
Db  471  HRPDVVLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEP  530

Qy  429  -SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
              .| || . |:|||.:  : | ||.||||||||| .| ||:||| ||
Db  531  QAPGRYFAHSILTVSEEWNTGEYTCVVAHEALPNRVTERTVDKSTGK  579

RESULT 14
Q9BQB8
ID   Q9BQB8         PRELIMINARY;       PRT;   597 AA.
AC   Q9BQB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Unknown (protein for MGC:1905) (protein for MGC:1228).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MUSCLE;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006180; AAH06180.1; -.
DR   EMBL; BC001872; AAH01872.1; -.
DR   HSSP; P01825; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 5.
DR   SMART; SM00407; IGc1; 4.
```

```
DE   Hypothetical 51.7 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025447; AAH25447.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA;  51748 MW;  8608B57C6CD2874A CRC64;

Query Match             51.4%;  Score 1325;  DB 11;  Length 474;
Best Local Similarity   54.0%;  Pred. No. 2.5e-101;
Matches  257;  Conservative  73;  Mismatches  130;  Indels  16;  Gaps  5;

Qy    8  LLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEW   67
         |  :|  ||   |||:||  :  : .:||:| |::|:|  ||||:|||  :||:||||||||
Db    8  LFLLSVTEGVHSQVQLLQSGPELVKPGASVKISCRASGYAFS-KSWMNWVKRRPGKGLEW   66

Qy   68  IGHIYGNGATTNVNPSLKSRVTISKDTSKNQFLNLNSVTDADTAVYYCARGPRPDCTTI   127
         ||  : :| .: .:    : |:|  :| |::: : |:  ::|  ||:| |
Db   67  IGRIFPGDGDTHYSGKFQGKAKLTADKSSVTAFLQLTSLTSEDSAVYFCARDSD------   120

Qy  128  CYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW   187
         |    || |  : ||::||     || |||||     |||||  :|| ||||| |||:|||
Db  121  -YGDYFDDWGQGATVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTW   179

Qy  188  NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK   247
         |||| |||||||||| ||||:|||||||||||  |  ||| | |||:|||  : |||| ||
Db  180  NSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS   238

Qy  248  SCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP   300
         |||:| |:||||      |||  ||| |||| |   :|::: |  || ||||||:|:::|
Db  239  GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDP   298

Qy  301  EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP   360
         :||||| ||||| || ||::|: |::||:|::|| :|: : |:  :|| |||| :|||
Db  299  DVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSP   358

Qy  361  IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY   420
         |:||||| ||  |  ||| |||::|::: |||| :|  |:|||| ||| || |  : :||
Db  359  IERTISKIKGLVRAPQVVILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENY   418

Qy  421  KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   476
         | |  |||||||||||||:|::| ::|:  |||:| |||||:::|||| | : |||
Db  419  KDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK   474

RESULT 11
Q96PQ8
ID   Q96PQ8
AC   Q96PQ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Factor VII active site mutant immunoconjugate.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21477448; PubMed=11593034;
RA   Hu Z., Garen A.;
RT   "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT   cells for immunotherapy in mouse models of prostatic cancer.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR   EMBL; AF272274; AAK58686.1; -.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   InterPro; IPR000294; VitK_dep_GLA.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00594; gla; 1.
DR   Pfam; PF00047; ig; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   SMART; SM00181; EGF; 2.
DR   PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS01187; EGF_CA; UNKNOWN_1.
DR   PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW   Hydrolase; Serine protease.
SQ   SEQUENCE   701 AA;  77826 MW;  94AC6CEB42CC992F CRC64;

Query Match             49.2%;  Score 1268;  DB 4;  Length 701;
Best Local Similarity   82.7%;  Pred. No. 2.2e-96;
Matches  244;  Conservative  4;  Mismatches  29;  Indels  18;  Gaps  3;

Qy  185  VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS---NTKVD   241
         |||  |  :|                             :|:
Db  422  VSWGQGATVG---------------HFGVY-----TRVSYIEWLQKLMRSEPRPGVLLRAPFP   466

Qy  242  KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE   301
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  467  GSAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE   526

Qy  302  VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI   361
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  527  VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI   586

Qy  362  EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK   421
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  587  EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK   646

Qy  422  TTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   476
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  647  TTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK   701

RESULT 12
Q95M34
ID   Q95M34                     PRELIMINARY;       PRT;   337 AA.
AC   Q95M34;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Immunogobulin gamma 1 heavy chain constant region
DE   (Fragment).
GN   IGHC1.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagner B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9383416; PubMed=9717671;
RA   Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA   Leibold W., Radbruch A.;
RT   "Organization of the equine immunoglobulin heavy chain constant region
RT   genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL   Immunobiology 199:105-119(1998).
DR   EMBL; AJ300675; CAC44624.1; -.
```

Db   400 LNVQKSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK 437

RESULT 8
Q99L25
ID   Q99L25   PRELIMINARY;   PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH03888.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM0409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;   52449 MW; BE9889B7986DA155 CRC64;

Query Match   53.7%; Score 1383.5; DB 11; Length 473;
Best Local Similarity   55.3%; Pred. No. 3.5e-106;
Matches 269; Conservative   71; Mismatches 123; Indels 23; Gaps

Qy   1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWT------ 55
           :::| || |||||||||||:: ||:| |||| :   :| ||::| |||
Db   1 MEWSWVFLFFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSG-----YTFTDHTIH 54

Qy   56 WIRQTPGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYY 115
           ||||| | |||||| | || : : | : ||||||||| ||||||||||||||||||
Db   55 WVKQRPEQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCF 114

Qy   116 CARGPRPDCTTICYG----GWDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG 172
           | |:: |:|||||||||||||||||||||||||||||||||||||||
Db   115 CSRG------GSIYYGYGLYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLG 169

Qy   173 CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN 232
           ||||||||||||| ||||||| ||||||||||| |||||||||||||| : |||||||||
Db   170 CLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVA 228

Qy   233 HKPSNTKVDKKAEPKSCDKTHTCPP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC 290
           ||||||||| | ||| : : | ||||||||||||||||||||||||||||||||
Db   229 HPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTC 287

Qy   291 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC 350
           ||||| |||||||||:|||||||||||||||||||||||| |||||||||||||||||||
Db   288 VVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKC 347

Qy   351 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 410
           ||:||||||||||||| | || ||||| : :: || ||||||||||||||:| |||
Db   348 KVNNKALPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLICMVTDFMPEDIYVEW 407

Qy   411 ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 470
           : ||| ||| ||||||||||||:| |: :::| |::|::|:| |||:|| ||||||:|:
Db   408 TNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTKSF 467

Qy   471 SLSPGK 476
           ||||||
Db   468 SRTPGK 473

RESULT 9
Q91Z05
ID   Q91Z05   PRELIMINARY;   PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.9 kDa protein.
GN   AU044919.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
DR   MGD; MGI:2144967; AU044919.
DR   InterPro; IPR000345; CytC heme_bind.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;   51946 MW; CF625F008932AF12 CRC64;

Query Match   51.7%; Score 1333.5; DB 11; Length 473;
Best Local Similarity   54.0%; Pred. No. 4.9e-102;
Matches 259; Conservative   72; Mismatches 124; Indels 25; Gaps

Qy   7 FLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLE 66
           |||:|::|::|: ||:|||||:::||: || ||:| : ::|:|::||||:||:||:
Db   9 FLVLIL--KGVQCEVQLVESGGGLVKPGGSRKLSCAASGFTFSD-YGMHVRQAPEKGLE 65

Qy   67 WIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDCTT 126
           ||| |||||::: : ||: |||:||: : | |::|: || : | |:|:||:|||:|:
Db   66 WVAYINSGSTIYYADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCAREL------- 119

Qy   127 ICYGGW---VDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 183
           :| | :: :|::|||||:|:|::||||||||||::::|:|:||:|||||||||||:
Db   120 ----WLRRIDYWGQGTTITVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESV 174

Qy   184 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK 243
           |::||||: ||||||||||| | :|||:|||||| ::| |:|| |||:| ||| |||||
Db   175 TVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVSSTWPSQTVTCSVAHPASSTTVDKK 233

Qy   244 AEPKSCDKT-HTCPP------CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 296
           | | | : ::| | ||||:||||||||:||||:||:||||:: |:||||||||
Db   234 LEPSGPISTNPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVS 293

Qy   297 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 356
           :|||:||:|::|||:|||||::| ::|||||| ||||:| |:::|| :|||:||||:|
Db   294 EDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKD 353

Qy   357 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 416
           ||||||:||| | || ||| | | :: || ||||||||:||||::|:|||| |:|
Db   354 LPSPIERTISKIGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHT 413

Qy   417 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
           |||:| |||||||||||:| || :::| |::|::| | |||:||:|||:|:|:|:|||||
Db   414 EENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYLKKTISRSPGK 473

RESULT 10
Q8R3H6
ID   Q8R3H6   PRELIMINARY;   PRT;   474 AA.
AC   Q8R3H6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez J., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match   54.5%; Score 1403.5; DB 11; Length 473;
Best Local Similarity   54.9%; Pred. No. 7.7e-108;
Matches 265; Conservative   79; Mismatches 122; Indels   17; Gaps   5;

Qy   1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT 60
          ||| : || : || | : |: |||::|| : ||| :: : || ||| ||||||
Db   1 MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFTDYYI-NWVKQR 59

Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCAR-G 119
          ||:|||||||||||| ::: || |||||||||||||::|| : :::::|||||:||||:|
Db   60 PGQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVFCARSG 119

Qy   120 PRPDCTTICYGGWVDWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
          | : | : ||:|||||||||||||::::||||||| | || ||||: |||| ||
Db   120 YDYD-------WFAYWGQGTLVTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYF 171

Qy   180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
          |||||||||||| :|||||| || |||| ||||||| :| : ||| |:||||||| : |
Db   172 PEPVLTWNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTK 230

Qy   240 VDKKAEPK------SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 293
          ||||: | : | | ||| | |::||||||| |||| | : :|| |||:|||||
Db   231 VDKKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVV 290

Qy   294 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 353
          ||| :|||| | : :: |:: :|| ||::|||||| :| ||| || ||:|||| |||
Db   291 DVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVN 350

Qy   354 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 413
          |||| |||||||||:|| | | | ||||| :: |||:||| ||:| ::|||||||| |
Db   351 NRALPSPIEKTISKPRGPVRAPQVVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSN 410

Qy   414 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
          | ||||||||||||||||| | |||| |||| |: ||||||||||||||||||||:| :
Db   411 GRTEQNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLFACSVVHEGLHNHLTTKIISRS 470

Qy   474 PGK 476
          |||
Db   471 LGK 473

RESULT 7
Q9R1A4
ID   Q9R1A4   PRELIMINARY;   PRT;   437 AA.
AC   Q9R1A4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Gammal heavy chain of Mab7 (Fragment).
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152372; AAD40243.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER   1   1
FT   NON_TER   437   437
SQ   SEQUENCE   437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match   53.9%; Score 1389.5; DB 11; Length 437;
Best Local Similarity   56.6%; Pred. No. 1e-106;
Matches 259; Conservative   76; Mismatches 100; Indels   23; Gaps   8;

Qy   21 VKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPGRGLEWIGHIYGNGATTNY 80
          :||:|| || :||::|||| ||| :||||||| ||:||||:|||||||||||| |:::
Db   1 VQLQESGGGLVKPGGSLKLSCAASGFTFSS-YAMSWVRQTPEKRLEWVAS-FSSGGIIYY 58

Qy   81 NPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDCTTICYGGWVDWGPGD 140
          : ::||||||||||::| : ::: | |:|| :||||| :: ||: |||
Db   59 TDSVKGRFTIYKDRNILSLQMSSLRSEDTAMYYCARGD--------YSAY--WGPGT 107

Qy   141 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 200
          |||||:::| |||||||| || :| ||||:|||||||||| ||:||||| ||||| |
Db   108 LVTVSAAKTTPFSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFP 167

Qy   201 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--C 258
          | || ||| ||| ||| ||: : || :||| ||| :: | : | | || : :
Db   168 AVLQSD-LYTLSSSVTVPSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCIC 222

Qy   259 PAPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
          ||| :||||||| |||| : :|| |||:|||||||| :||||| | : :: |:: :
Db   223 TVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQT 279

Qy   319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
          : |:||||||| :| ||| || ||:||||| |||||| |||||||||:|| | | | |
Db   280 QPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTGRPKAPQVY 339

Qy   379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
          ||||| :: ||||:||| ||:| ::|||||||| || |||||||||||||||| | |||
Db   340 TIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQNGQPAENVKNTQPIMDTDGSYFVYSK 399

Qy   439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSLSPGK 476
          | |||| |: ||||||||:||:|||| ||||:| : ||||

```
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96446; Igh-4.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM004409; IG; 2.
DR   SMART; SM004407; IGc1; 2.
DR   SMART; SM004406; IGv; 1.
DR   SMART; SM004410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

Query Match             55.2%;  Score 1423.5;  DB 11;  Length 463;
Best Local Similarity   54.8%;  Pred. No. 1.7e-109;
Matches  262;  Conservative  84;  Mismatches 115;  Indels  17;  Gaps  6;

Qy         1  MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT  60
              ||||||| || |||||| |  | | ||  : :||:|  || |:||| |||: ||:||||||
Db         1  MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFTGYV-SWVKQR  59

Qy        61  PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP  120
              |||||||||| ||||  ||:| ||:||||||:||::| ||||:|||:  :||||||||
Db        60  TGGGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMLSSLTSEDSAVYFCARSS  119

Qy       121  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
              ||:||| | |  | |||||:|||||||||||||||||| | :  || |:||||||||||
Db       120  YYSYDLFAY------WGGGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP  173

Qy       181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
              ||||| |||| |:|||||||||||| || ||||:| |||| || |||||||||:|||:||
Db       174  EPVTVTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSETVTCNVAHPASSTKV  232

Qy       241  DKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  298
              ||| |   |  | |     |    : |  :|:  |||||||:||:|||:||||||||:|
Db       233  DKKIVPRDCG----CKPCICTVPEV--SSVFIFPPKPKDVLTITLTPKVTCVVVDISKD  285

Qy       299  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  358
              |||::|  |||||||||| || |||:|||||:||:|  : |||||||||||||||||||
Db       286  DPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFP  345

Qy       359  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  418
              |||||||||  | ||  || |:|| | |::|||||||||||| ||: ||||||||||| :
Db       346  APIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAE  405

Qy       419  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
              ||| |||||||||||| ||||   || |  |:: :|  ||| |||||||::|| |||
Db       406  NYKNTQPIMDTDGSYFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK  463
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RESULT 5
Q99L31
ID   Q99L31             PRELIMINARY;       PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM004409; IG; 2.
DR   SMART; SM004407; IGc1; 3.
DR   SMART; SM004406; IGv; 1.
DR   SMART; SM004410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE   468 AA;  51661 MW;  96352328B3332ADB CRC64;

Query Match             54.5%;  Score 1405;  DB 11;  Length 468;
Best Local Similarity   56.7%;  Pred. No. 5.7e-108;
Matches  271;  Conservative  65;  Mismatches 130;  Indels  12;  Gaps  5;

Qy         1  MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT  60
              ||||| || |:||||  | | | ||  :  :::  |  ||:|||| |||:||||||||
Db         1  MKCCSWIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKD-SLMHWVKQR  59

Qy        61  PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP  120
              :|:||||||:||| |  |:| ||:|| |||||:|: :| | |||:  :||||||||||--
Db        60  PEQGLEWIGWIDPEDGETKYAPKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCAR--  117

Qy       121  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP  180
              :    |  | |  | |||| ||||||  |||||||||||   :   ||:|||||||||||
Db       118  ------NLLYGGYYDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFP  172

Qy       181  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV  240
              ||||| |||| |:|||||||||||| || ||||:| |||: || |||||||: :| |:||
Db       173  EPVTLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSVTWPSQSITCNVAHPASSTKV  231

Qy       241  DKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE  298
              |||  |   |  | |     || |: |  :|::|||||||:::|:: :|:|||||||:||
Db       232  DKKIEPRG-PTIKPCPPCKPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSED  290

Qy       299  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  358
              ||||:|||||||||:||| |: |||:|||| |:|||   || | : |||:|| |::| ||
Db       291  DPDVQISWFVNNVEVLTAQTQTHREDYNSTLRVSALPIQHQDWMSGKEFKCKVNNKALP  350

Qy       359  APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  418
              |||||||||||| ||  || |:|| |  |::| |||||||| | ||: |:||:||||| |
Db       351  APIERTISKPKGSVRAPQVYLPPPEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTEL  410

Qy       419  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  476
              ||| ||||||||||||:|||  :||:|:|:|::|||||:||| |||| :::||| |||
Db       411  NYKNTEPVLDSDGSYFMYSKLRVEKQNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK  468
```

```
RESULT 6
Q9D8L4
ID   Q9D8L4             PRELIMINARY;       PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   1810060009Rik protein.
GN   IGH-1 OR 1810060009RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
```

```
Db  180 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV 239

Qy  245 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTEPTCVVVDVSHEDPEVKF 304
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  240 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTEPTCVVVDVSHEDPEVKF 299

Qy  305 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 364
        ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 359

Qy  365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 424
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  360 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 419

Qy  425 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  420 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471


RESULT 2
Q8TC63
ID   Q8TC63      PRELIMINARY;      PRT;   473 AA.
AC   Q8TC63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025985; AAH25985.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  51986 MW;  E29920B09BA369F5 CRC64;

Query Match             78.3%;  Score 2017;  DB 4;  Length 473;
Best Local Similarity   81.3%;  Pred. No. 1.2e-158;
Matches  388;  Conservative  29;  Mismatches  48;  Indels  12;  Gaps  4;

Qy    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSI-SGYYYWTWIRQ 59
        ||||||  |||||||||||||  ||||:|:||:||  :|:|::||.:|:  .|||.||||:|
Db    8 MKHLWFLLLLVAAPRWVLSRLQLQESGGGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQ 67

Qy   60 TPGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVVYCARG 119
         ||.||||||: . |.:  |||  :.|::|: :|:::| ::      ||:|:|: ||||.|
Db   68 PPGKGLEWIGTINFSG-NMYYSPSLRSRVTMSADMSENSFYLKLDSVTAADTAVYYCAAG 126

Qy  120 PRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
         |||   |  |.:|  |  ||||||||||||||||||||||||||||||||||||||||||
Db  127 H------LVMGFGAHWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF 179

Qy  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239

Qy  240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTEPTCVVVDVSHED 299
        |||| :: ||:||| |...||||| ||||:||.|||||||||||||||||||||||||||
Db  240 VDKRVESK--YGPCPSCCPAPEFLGGPSVFLFPPKPKDTLMISRTEPTCVVVDVSQED 296

Qy  300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
        |||:||||||||||||||||||||||:|||||||||||||||||||||||||||||||:
Db  297 PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS 356

Qy  360 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
         |||||||||||||||||||||||:|:|:|||||||||||||||||||||||||||||||
Db  357 SIEKTISKAKGQPRREPQVTLPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 416

Qy  420 YKTTPPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  417 YKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 473


RESULT 3
Q8R3V9
ID   Q8R3V9      PRELIMINARY;      PRT;   469 AA.
AC   Q8R3V9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 52.0 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024405; AAH24405.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   469 AA;  51976 MW;  534793F155D05457 CRC64;

Query Match             55.5%;  Score 1429;  DB 11;  Length 469;
Best Local Similarity   56.0%;  Pred. No. 5.9e-110;
Matches  270;  Conservative  78;  Mismatches 110;  Indels 24;  Gaps  9;

Qy    4 LWF-FLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPG 62
        ||   |  | | |  :| : |  |: :    |::  ::   :  ||.:|:|  ||  |
Db    3 LWLNWIFLVTLLNGIQCEVNLVESGGGLVQPGGSLRLSCAASGFTFTD-YYMSWVRQPPG 61

Qy   63 RGLEWIGHI--YGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVVYCARGP 120
        : :|||| |   ||.|:|.|| :.: :.  ::::: ::      :  | .:|: ||||:|
Db   62 KALEWLGFIRNKANGYTTEYSASVKGRFTISRDNSQSILYLQMNALRAEDSATYYCARDR 121

Qy  121 RPDC----TTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK 176
        |:| |    ::  |.:||      ||:|||:|
Db  122 RSSYYYSGTSFAY------WGQGTLVTVSAAKTPPSVYPLAPGSAAQTNSMVTLGCLVK 175

Qy  177 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS 236
        ||||||| ||||||| :|:|:| ||:|::: | :|:::| .  .|    | .|.|.|.|
Db  176 GYFPEPVTWTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTWPSQTVTCNVAHPAS 234

Qy  237 NTKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTEPTCVVVD 294
        .|||||| :||: |  | ||    |    ::     || | | |  |:   :: |.|: :
Db  235 STKVDKKIVPRDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTITLTPKTCVVVD 287

Qy  295 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 354
        .|.:||||:|.||:|||||::|:.|||||||||||||:||||||.|||||||: .|||:|
Db  288 ISKDDPEVQFSWFVDDVEVHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS 347

Qy  355 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 414
        ||  |||:||||| .|:| |||| | |||::|| |:|:||||| .|:|  ||:|:|||.|
Db  348 AAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNG 407

Qy  415 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 474
        |||||||||||||||||||||||:||||||||||||||||||||||||||||:|||||:|
Db  408 QPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP 467

Qy  475 GK 476
        ||
Db  468 GK 469


RESULT 4
Q99LC4
ID   Q99LC4      PRELIMINARY;      PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
```

```
                 GenCore version 5.1.4 p5.4578
       Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:       March 29, 2003, 09:06:23 ; Search time 43.1716 Seconds
                              (without alignments)
                              2271.829 Million cell updates/sec

Title:        US-09-758-173-4
Perfect score: 2577
Sequence:     1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:     671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:      671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    SPTREMBL 21:*
              1: sp_archea:*
              2: sp_bacteria:*
              3: sp_fungi:*
              4: sp_human:*
              5: sp_invertebrate:*
              6: sp_mammal:*
              7: sp_mhc:*
              8: sp_organelle:*
              9: sp_phage:*
             10: sp_plant:*
             11: sp_rodent:*
             12: sp_virus:*
             13: sp_vertebrate:*
             14: sp_unclassified:*
             15: sp_rvirus:*
             16: sp_bacteriap:*
             17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result         Query                                   %
No.    Score   Match Length DB   ID       Description
-----  ------  ----- ------ --  ------     -----------
  1    2041.5  79.2   471   4   Q8TC77     Q8tc77 homo sapien
  2    2017    78.3   473   4   Q8TC63     Q8tc63 homo sapien
  3    1429    55.5   469  11   Q8R3V9     Q8r3v9 mus musculu
  4    1423.5  55.2   463  11   Q99LC4     Q99lc4 mus musculu
  5    1405    54.5   468  11   Q99L31     Q99l31 mus musculu
  6    1403.5  54.5   473  11   Q9D8L4     Q9d8l4 mus musculu
  7    1389.5  53.9   437  11   Q9R1A4     Q9r1a4 mus musculu
  8    1383.5  53.7   473  11   Q99L25     Q99l25 mus musculu
  9    1333.5  51.7   473  11   Q91Z05     Q91z05 mus musculu
 10    1325    51.4   474  11   Q8R3H6     Q8r3h6 mus musculu
 11    1268    49.2   701   6   Q96PQ8     Q96pq8 homo sapien
 12    1262.5  49.0   337   6   Q95M34     Q95m34 equus cabal
 13    950.5   36.9   597   4   Q9BU10     Q9bu10 homo sapien
 14    948.5   36.8   597   4   Q9BQB8     Q9bqb8 homo sapien
 15    940.5   36.5   588   4   Q8WUX4     Q8wux4 homo sapien
 16    940.5   36.5   618   4   Q96AA6     Q96aa6 homo sapien
 17    931     36.1   613   4   Q96EY0     Q96ey0 homo sapien
 18    856     33.2   496   4   Q96KX8     Q96kx8 homo sapien
 19    745.5   28.9   597   4   Q96BB9     Q96bb9 homo sapien
 20    727.5   28.2   479  11   Q99M22     Q99m22 mus musculu
 21    719     27.9   613  11   Q8VCX7     Q8vcx7 mus musculu
 22    718     27.9   613   4   Q8WUK1     Q8wuk1 homo sapien
 23    712     27.6   278  11   Q921K1     Q921k1 mus musculu
 24    691.5   26.8   614   4   Q96GA6     Q96ga6 homo sapien
 25    688     26.7   482  11   Q91X92     Q91x92 mus musculu
 26    665     25.8   494   4   Q96K68     Q96k68 homo sapien
 27    651     25.3   496   4   Q96DK0     Q96dk0 homo sapien
 28    640     24.8   500   4   Q9BRV0     Q9brv0 homo sapien
 29    632     24.5   488  11   Q91WR1     Q91wr1 mus musculu
 30    631.5   24.5   487  11   Q99KA4     Q99ka4 mus musculu
 31    630.5   24.5   497   4   Q8WY24     Q8wy24 homo sapien
 32    629.5   24.4   481  11   Q91WT1     Q91wt1 mus musculu
 33    625     24.3   486  11   Q91Z07     Q91z07 mus musculu
 34    621.5   24.1   481  11   Q8VCV5     Q8vcv5 mus musculu
 35    620.5   24.1   479  11   Q91WP5     Q91wp5 mus musculu
 36    618.5   24.0   484  11   Q8VEA0     Q8vea0 mus musculu
 37    617.5   24.0   480  11   Q91XE1     Q91xe1 mus musculu
 38    607.5   23.6   481  11   Q91WT3     Q91wt3 mus musculu
 39    600.5   23.3   489  11   Q8VCX4     Q8vcx4 mus musculu
 40    584     22.7   416   4   Q9NPP6     Q9npp6 homo sapien
 41    578     22.4   484  11   Q99LA6     Q99la6 mus musculu
 42    509     19.8   573   4   Q8WU38     Q8wu38 homo sapien
 43    506.5   19.7   150   4   O95973     O95973 homo sapien
 44    504.5   19.6   426  11   Q9DCD9     Q9dcd9 mus musculu
 45    457     17.7   384   4   Q9UP60     Q9up60 homo sapien
```

ALIGNMENTS

```
RESULT 1
Q8TC77
ID   Q8TC77       PRELIMINARY;     PRT;     471 AA.
AC   Q8TC77;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 51.8 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC024289; AAH24289.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE  471 AA;  51791 MW;  388F74CF58B660E CRC64;

Query Match             79.2%;  Score 2041.5; DB 4; Length 471;
Best Local Similarity   82.8%;  Pred. No. 1.1e-160;
Matches  391; Conservative  22; Mismatches  52; Indels  7; Gaps  4;

Qy     5 WFPLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPGRG 64
           |||  ||| |||||||| :  ||  : | :|:|    :| ||||||| ||| ||  |||
Db     7 WVF--LVAILEGVQCEVQLVESGGGLVKPGGSLRLSCAASGFTFSS-YSMNWVRQAPGKG 63

Qy    65 LEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDC 124
           || :| |||| :||:| | ::|::|| |:|:| | :||   :::: |||||  |    |
Db    64 LEWVSSMSSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLR-QL 122

Qy   125 TTICYGGWDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 184
          : |  |  |    | : | :||:||||||||||||||||||||||||||||||||||||
Db   123 TSTWY---FDLWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 179

Qy   185 VSWNSGALTSGVHTFPAVLQSGSGLYSLSSVVTVPSSSLGTQYICNVNHKPSNTKVDKKA 244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  235 DKRVESK--YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDP 291

Qy  301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db  292 EVQPNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS 351

Qy  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  352 IEKTISKAKGQPREPQVYTLPPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411

Qy  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db  412 KTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 467
```

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RESULT 15
AAG63640
ID   AAG63640 standard; Protein; 475 AA.
XX
AC   AAG63640;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Amino acid sequence of a single chain antibody.
XX
KW   Complementarity determining region; CDR; single chain antibody; ScFv;
KW   hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW   envelope glycoprotein.
XX
OS   Homo sapiens.
XX
PN   WO20015849-A1.
XX
PD   16-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-JP00967.
XX
PR   14-FEB-2000; 2000JP-0034906.
XX
PA   (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI   Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
XX
DR   WPI; 2001-496986/54.
DR   N-PSDB; AAH74680.
XX
PT   Remedies for hepatitis C containing substances with antiviral effects
PT   e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT   compounds, by inhibiting binding of hepatitis C virus envelope
PT   glycoprotein or CD81 -
XX
PS   Disclosure; Page 105-108; 138pp; Japanese.
XX
CC   The present sequence represents a single chain antibody of the invention.
CC   The specification describes a substance can inhibit the binding between
CC   hepatitis C virus (HCV) and cells with potential HCV infection, cells
CC   with expression of CD81, or CD81. This substance is especially an
CC   antibody with affinity towards HCV E2/NS1 protein, containing amino
CC   acid sequences based on the complementarity determining region (CDR) 1,
CC   CDR2 and CDR3 of the H and L chain variable regions. The antibody
CC   inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor.
CC   The antibodies and drugs are used for treatment and/or prevention of
CC   hepatitis C, or for diagnosis of hepatitis C.
XX
SQ   Sequence  475 AA;
```

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Qy   61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
         |:||:|||||| : :     |||  .: :.: :    || |.|||| :||:||||||
Db   60 PGQGLEWMGGIIPLSGPPHYAQKFQGKVSITADESTSTAYLELTSLTSEDTAVYYCARVL 119

Qy  121 RPDCTT-ICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
         : |:: : |:: :.:     ||||||||||||||||||||||||||||||||||||||
Db  120 RGYCRRGSCY-DWLDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 178

Qy  180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  179 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 238

Qy  240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239 VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 298

Qy  300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 358

Qy  360 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  359 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 418

Qy  420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  419 YKTTPPVLDSDGSFFLYSRLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
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Search completed: March 29, 2003, 09:10:16
Job time : 50.9575 secs
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Query Match       81.8%;   Score 2107.5;   DB 22;   Length 475;
Best Local Similarity 84.3%;   Pred. No. 1.6e-118;
Matches 402;   Conservative 19;   Mismatches 53;   Indels 3;   Gaps 3;

Qy    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQT 60
         ||||||||||||||||||||||||||||||||  |.:: .|. .:|:|||| ||:|||
Db    1 MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGSSVKVSCKASGGTYIDQPI-GWVRQA 59
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